```
1 import pandas as pd
2 import numpy as np
3 import matplotlib.pyplot as plt
4 import seaborn as sn
5 %matplotlib inline
6 import scipy.stats as stats
```

```
1 data = pd.read_csv('/content/sample_data/DataClustering.csv')
```

```
1 data.head()
```

	x1	x2	x3	x4
0	0.832354	1.389428	0.962226	0.993671
1	1.256087	1.500487	0.904118	0.738035
2	0.976953	1.058524	1.217530	1.357238
3	1.014365	1.122684	1.195847	0.984144
4	1.041386	1.219014	0.864819	1.720825

```
1 data.shape
```

```
(351, 4)
```

```
1 data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 351 entries, 0 to 350
Data columns (total 4 columns):
 #   Column  Non-Null Count  Dtype  
---  ------  --------------  -----  
 0   x1      351 non-null    float64
 1   x2      351 non-null    float64
 2   x3      351 non-null    float64
 3   x4      351 non-null    float64
dtypes: float64(4)
memory usage: 11.1 KB
```

```
1 data.columns
```

```
Index(['x1', 'x2', 'x3', 'x4'], dtype='object')
```

```
1 columns = ['x1', 'x2', 'x3', 'x4']
2 print(columns)
```

```
['x1', 'x2', 'x3', 'x4']
```

```
1 #unique and null values
2 for col in data.columns.values:
```

```
for col in data.columns.values:
  list_vals = pd.unique(data[col]) #list of unique values
  print('\033[1m' + col + '\033[0m' + ' has ' + str(len(list_vals))  +' unique
  if len(list_vals) < 10:
    list_str = ''
    for n in range(0, len(list_vals)):
      list_str = list_str + str(list_vals[n]) + ', '
    print('\033[1m' + '    ##### These are: '+ '\033[0m' +list_str[0:len(list_s
```

x1 has 351 unique values, **0** null entries and datatype **float64**
x2 has 351 unique values, **0** null entries and datatype **float64**
x3 has 351 unique values, **0** null entries and datatype **float64**
x4 has 351 unique values, **0** null entries and datatype **float64**

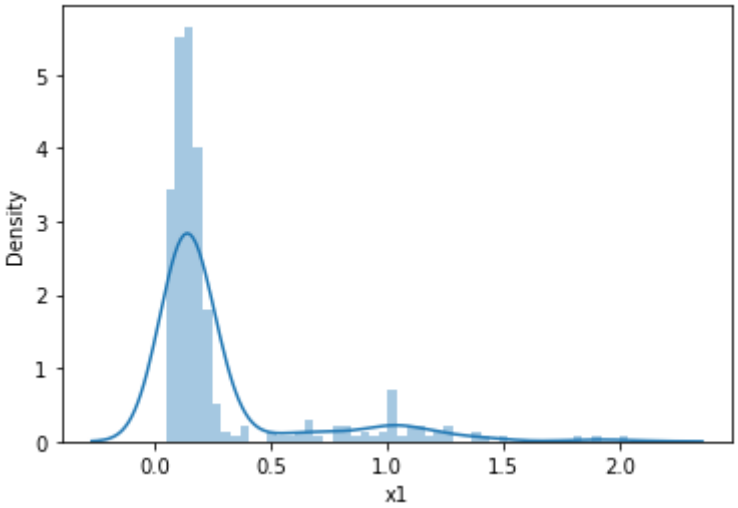
```
data.describe()
```

	x1	x2	x3	x4
count	351.000000	351.000000	351.000000	351.000000
mean	0.278820	0.472738	1.643857	1.482918
std	0.341446	0.511023	1.668052	0.964016
min	0.048604	0.047022	0.367717	0.232562
25%	0.111341	0.115257	0.815180	0.857948
50%	0.153383	0.165684	1.083528	1.190996
75%	0.212564	0.854725	1.557597	1.724461
max	2.037125	2.476118	12.635585	7.726843

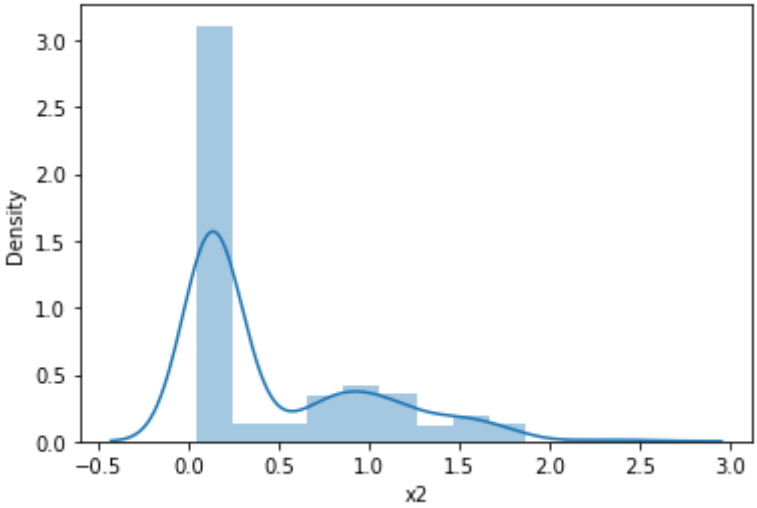
Data Visualization

```
from matplotlib import pyplot as plt
for col in data.columns.values:
  sn.distplot(data[col])
  plt.show()
```

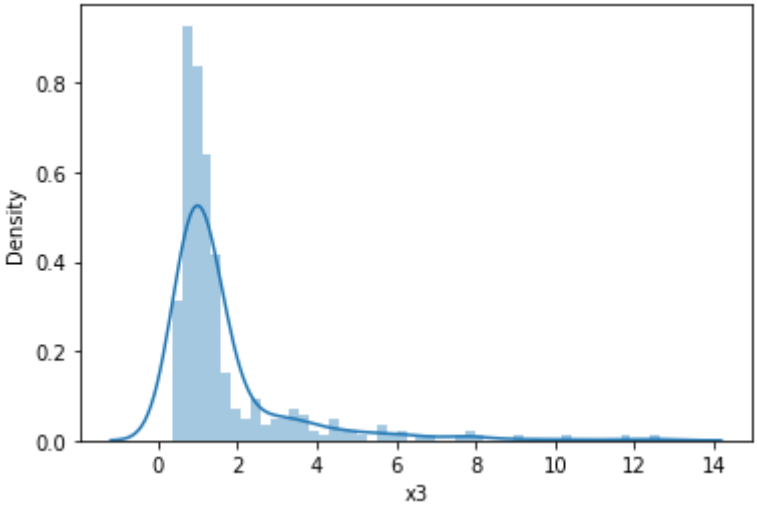
```
/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureW
  warnings.warn(msg, FutureWarning)
```




```
/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureW
  warnings.warn(msg, FutureWarning)
```



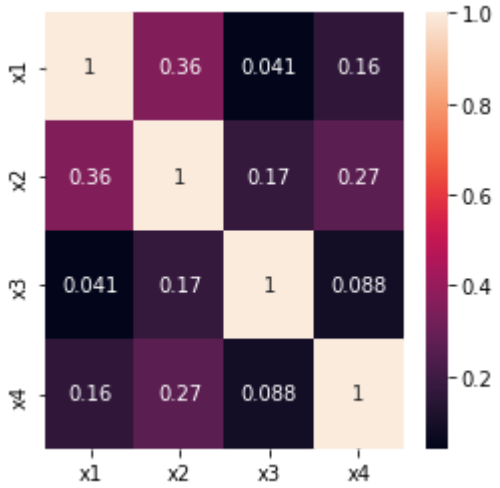

```
/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureW
  warnings.warn(msg, FutureWarning)
```




```
/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureW
  warnings.warn(msg, FutureWarning)
```

```
1 # visualization of correlation
2 corr = data.corr(method = 'spearman')
3 fig, ax = plt.subplots(figsize = (4,4))
```

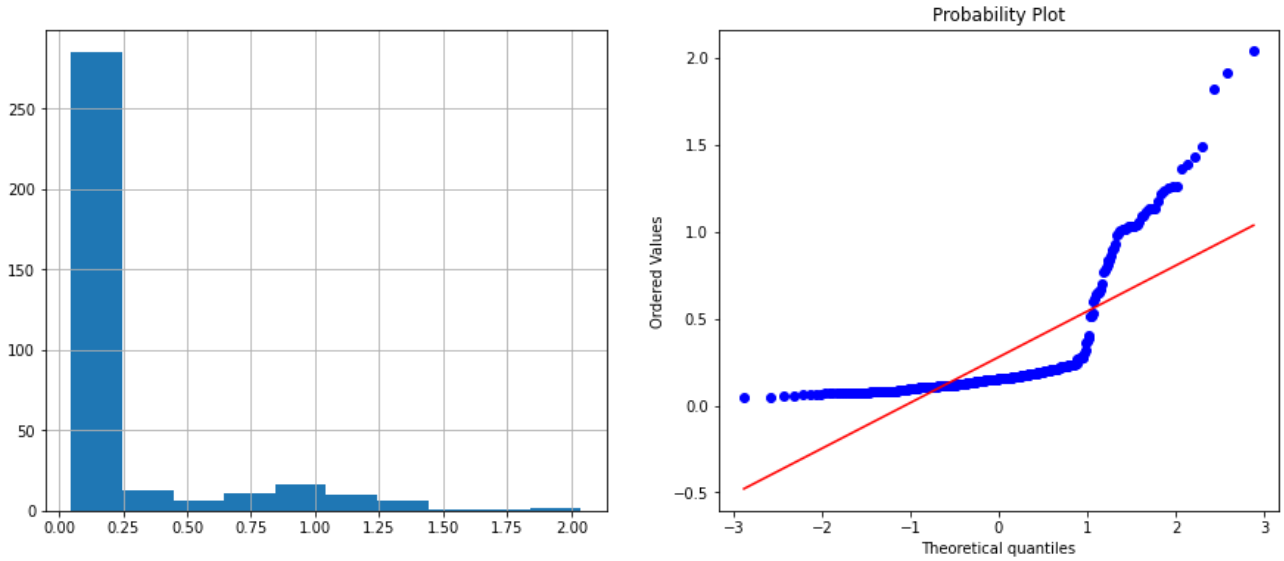
```
4 sn.heatmap(abs(corr), annot = True)
5 plt.show()
```



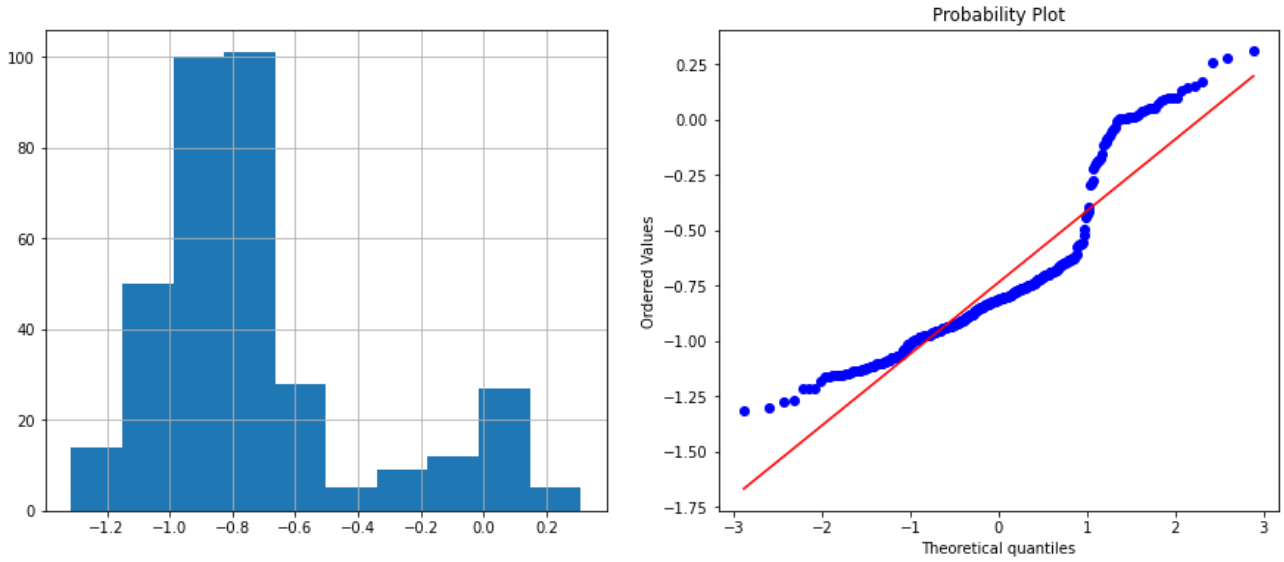
Data Pre-Processing

```
1 def diagnostic_plots(data,x):
2   plt.figure(figsize = (15,6))
3   plt.subplot(1,2,1)
4   data[x].hist()
5   plt.subplot(1,2,2)
6   stats.probplot(data[x], dist = "norm" , plot = plt)
7   plt.show()
```

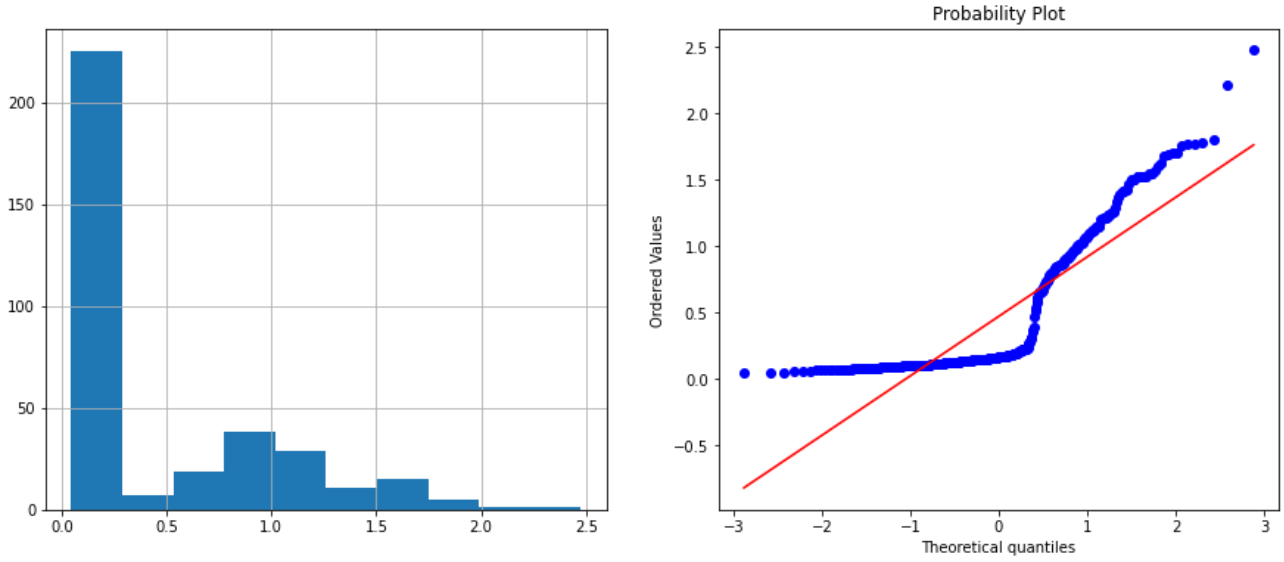
```
1 diagnostic_plots(data,'x1')
```



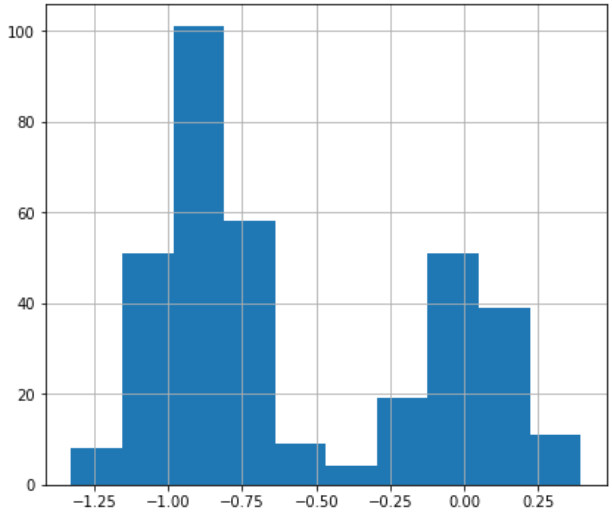
```
1 data['e_x1'] = np.log10(data['x1'])
2 diagnostic_plots(data,'e_x1')
```

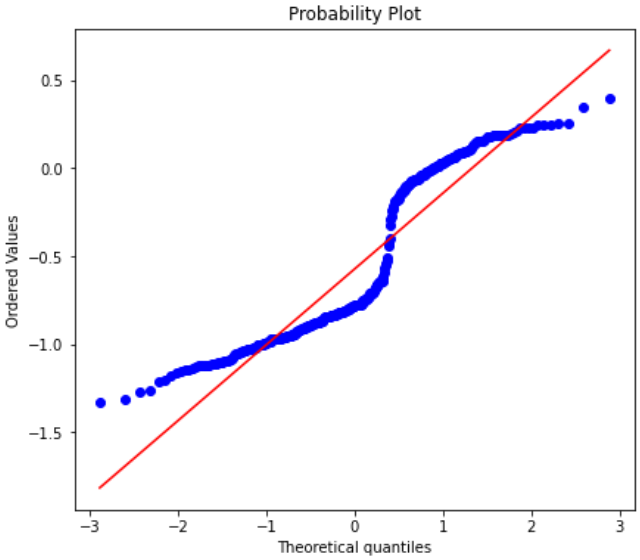



```
1 diagnostic_plots(data,'x2')
```

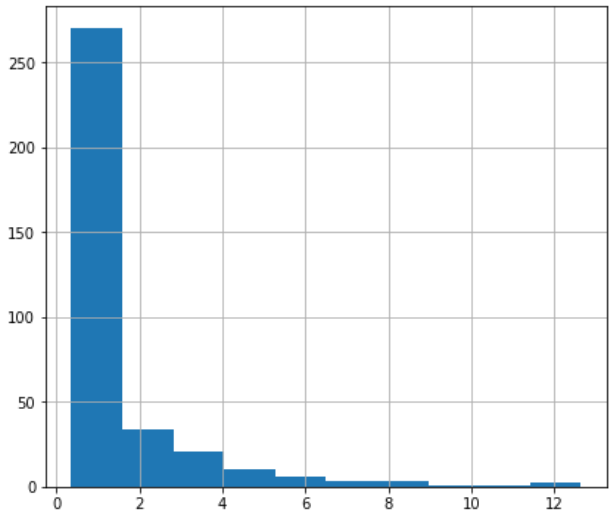


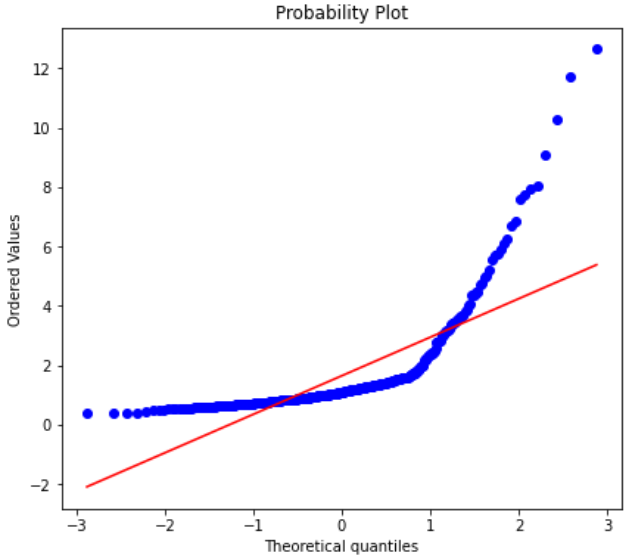

```
1 data['e_x2'] = np.log10(data['x2'])
2 diagnostic_plots(data,'e_x2')
```



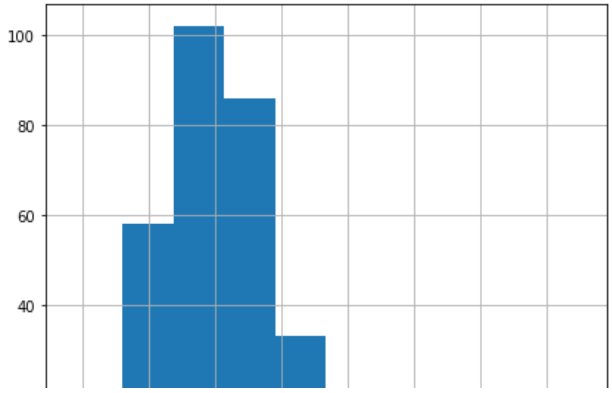


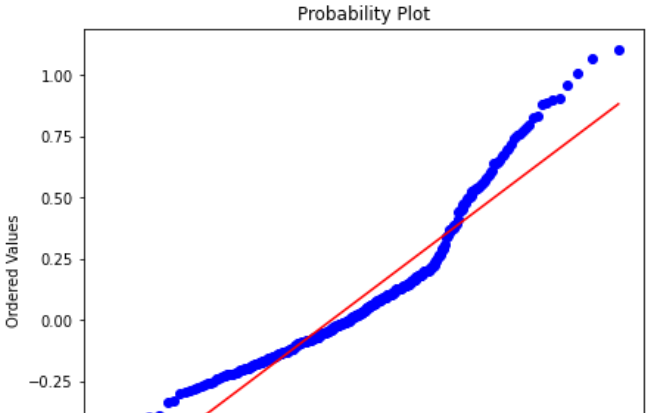

```
1 diagnostic_plots(data,'x3')
```



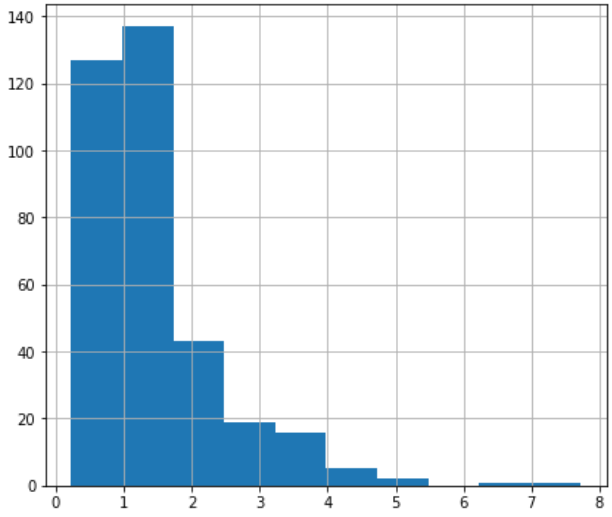


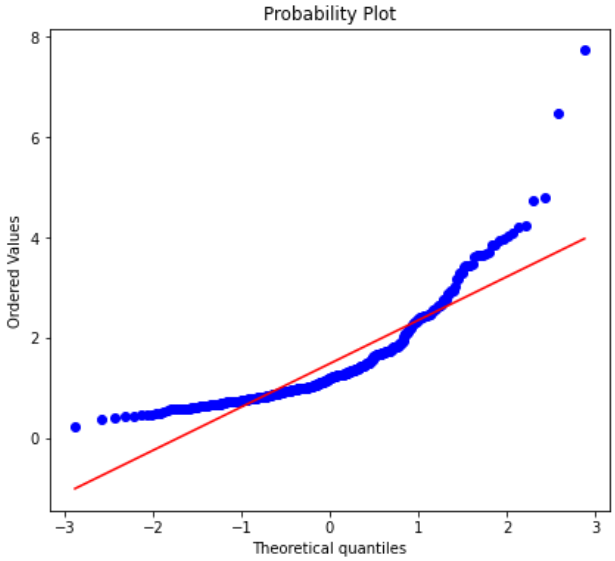

```
1 data['e_x3'] = np.log10(data['x3'])
2 diagnostic_plots(data,'e_x3')
```



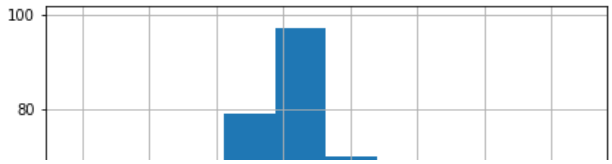


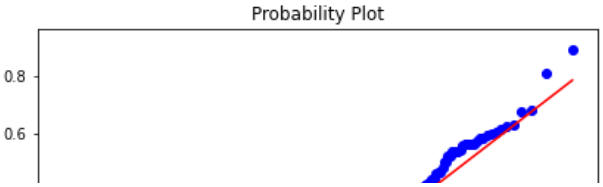

```
1 diagnostic_plots(data,'x4')
```



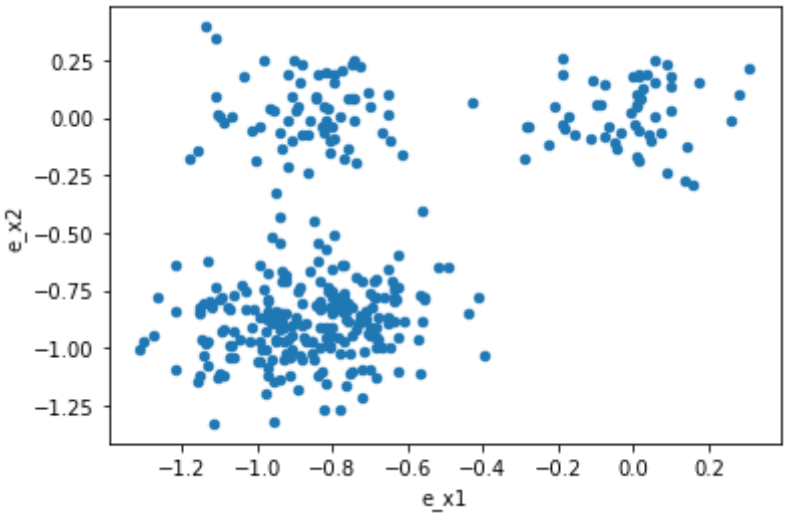



```
1 data['e_x4'] = np.log10(data['x4'])
2 diagnostic_plots(data,'e_x4')
```

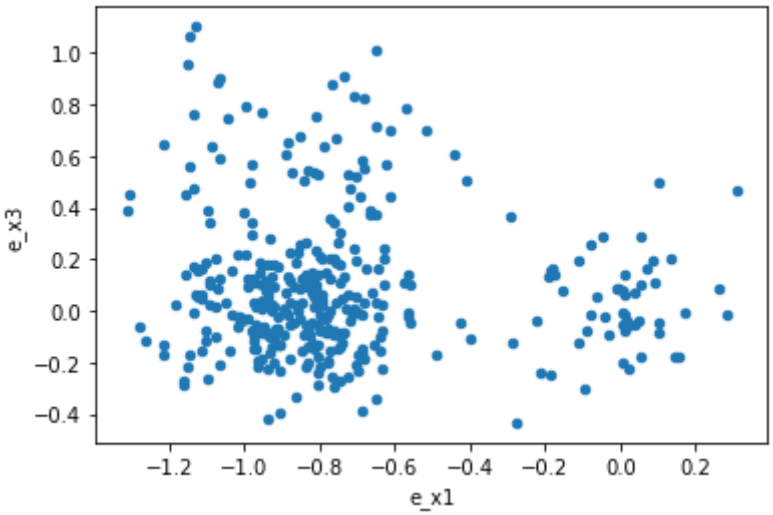




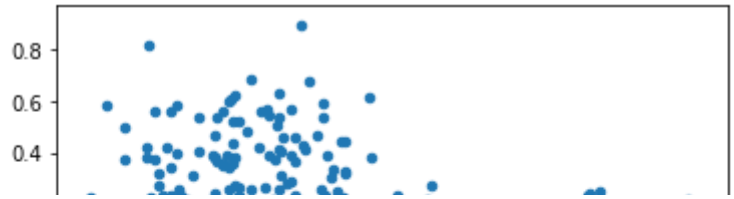

```
1 data.plot(kind = 'scatter', x = 'e_x1',y = 'e_x2');
2 plt.show()
```



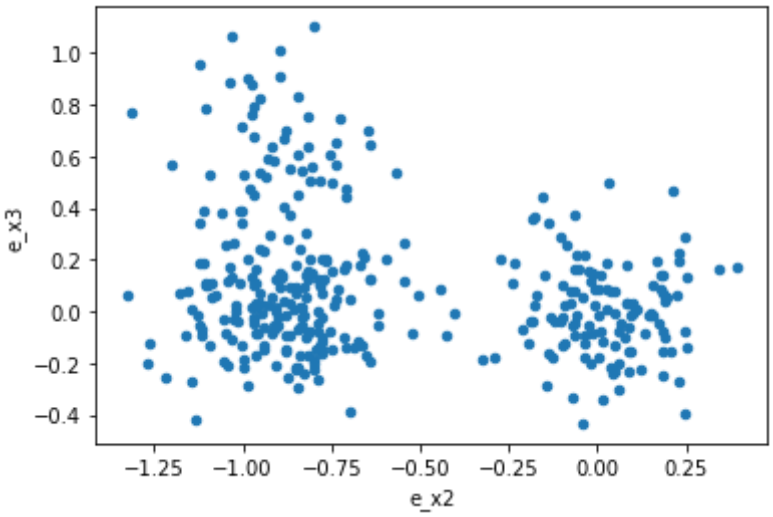

```
1 data.plot(kind = 'scatter', x = 'e_x1',y = 'e_x3');
2 plt.show()
```



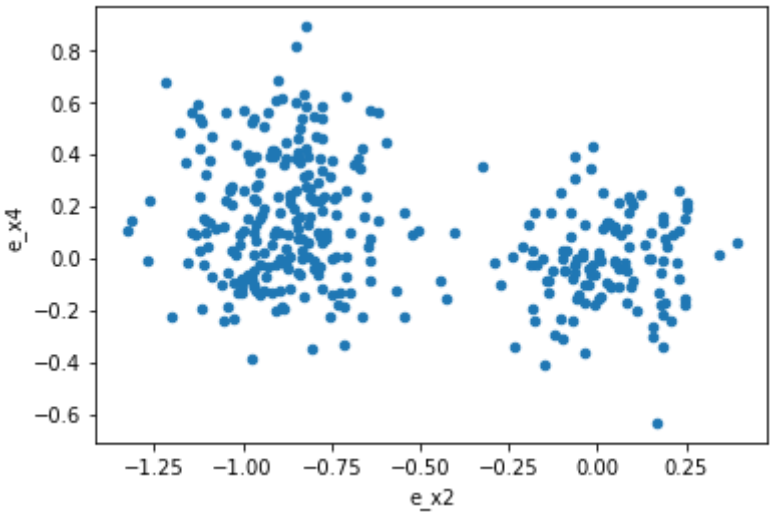

```
1 data.plot(kind = 'scatter', x = 'e_x1',y = 'e_x4');
2 plt.show()
```



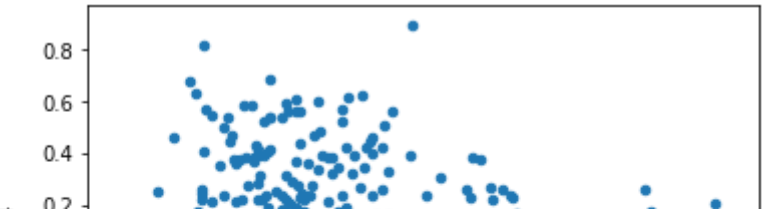

```
1 data.plot(kind = 'scatter', x = 'e_x2',y = 'e_x3');
2 plt.show()
```




```
1 data.plot(kind = 'scatter', x = 'e_x2',y = 'e_x4');
2 plt.show()
```




```
1 data.plot(kind = 'scatter', x = 'e_x3',y = 'e_x4');
2 plt.show()
```




```
1 data.head()
```

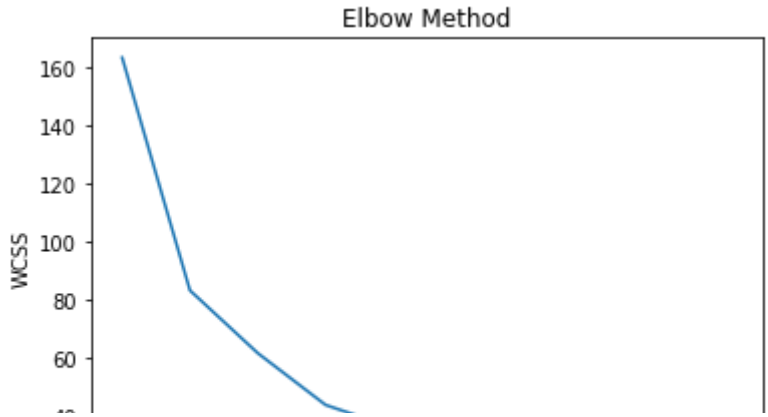
	x1	x2	x3	x4	e_x1	e_x2	e_x3	e_x4
0	0.832354	1.389428	0.962226	0.993671	-0.079692	0.142836	-0.016723	-0.002757
1	1.256087	1.500487	0.904118	0.738035	0.099020	0.176232	-0.043775	-0.131923
2	0.976953	1.058524	1.217530	1.357238	-0.010126	0.024701	0.085480	0.132656
3	1.014365	1.122684	1.195847	0.984144	0.006194	0.050257	0.077675	-0.006941
4	1.041386	1.219014	0.864819	1.720825	0.017612	0.086009	-0.063075	0.235737

```
1 data1 = data.drop(['x1','x2','x3','x4'],axis=1)
2 data1.head()
```

	e_x1	e_x2	e_x3	e_x4
0	-0.079692	0.142836	-0.016723	-0.002757
1	0.099020	0.176232	-0.043775	-0.131923
2	-0.010126	0.024701	0.085480	0.132656
3	0.006194	0.050257	0.077675	-0.006941
4	0.017612	0.086009	-0.063075	0.235737

k means clustering

```
 1 from sklearn.cluster import KMeans
 2 wcss = []
 3 for i in range(1, 11):
 4     kmeans = KMeans(n_clusters=i, init='k-means++', max_iter=300, n_init=10, ra
 5     kmeans.fit(data1)
 6     wcss.append(kmeans.inertia_)
 7 plt.plot(range(1, 11), wcss)
 8 plt.title('Elbow Method')
 9 plt.xlabel('Number of clusters')
10 plt.ylabel('WCSS')
11 plt.show()
```



so we are getting sharp elbow at k=2, k=4 and k=5, so it creates a confusion regarding taking proper value of k

```
# # define and map colors
# colors = ['#DF2020', '#81DF20', '#2095DF']
# data1['c'] = df.cluster.map({0:colors[0], 1:colors[1], 2:colors[2]})
# plt.scatter(data1, c=df.c, alpha = 0.6, s=10)
```

```
# Silhoute's Method
```

```
from sklearn.metrics import silhouette_samples, silhouette_score
silhouette_score(data, kmeans.labels_)
```

```
0.09684349876691904
```

```
kmeans_per_k = [KMeans(n_clusters=k, random_state=42).fit(data) for k in range(
silhouette_scores  = [silhouette_score(data, model.labels_) for model in kmeans
```

```
print(silhouette_scores)
```

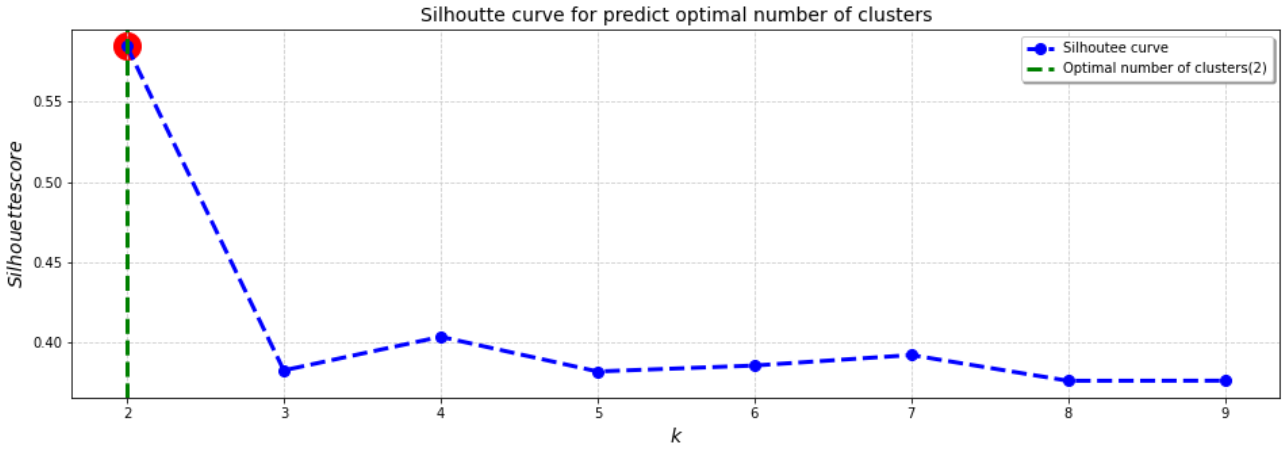
```
[0.5845000763505325, 0.38250695193757606, 0.40344396087241646, 0.381813824664
```

```
#Plotting the silhoutee score graph
from pylab import rcParams
rcParams['figure.figsize'] = 16, 5
plt.plot(range(2,10), silhouette_scores, "bo--", color = 'blue', linewidth=3, m
plt.xlabel("$k$", fontsize = 14, family = 'Arial')
plt.ylabel("$Silhouette score$", fontsize = 14, family = 'Arial')
plt.grid(which='major', color='#cccccc', linestyle='--')
plt.title('Silhoutte curve for predict optimal number of clusters', family='Ari

#Calculate number of Clusters
k = np.argmax(silhouette_scores)+2

#Draw a vertical line to mark optimal number of clusters
plt.axvline(x=k, linestyle='--', c='green', linewidth=3, label='Optimal number
plt.scatter(k, silhouette_scores[k-2], c='red', s=400)
```

```
16 plt.legend(shadow=True)
17 plt.show()
```




```
1 #predict the labels of clusters.
2 km=KMeans(n_clusters=2,init='k-means++',random_state=0)
3 label = km.fit_predict(data1)
4 y=label
```

```
1 y1=data1[label==0];y2=data1[label==1]
```

```
1 # plt.scatter(data1[0],data1[1])
```

DBSCAN

```
1 from sklearn.preprocessing import StandardScaler
```

```
1 data1 = StandardScaler().fit_transform(data1)
```

```
1 print(data1)
```

```
[[ 1.89424203  1.56511437 -0.40751579 -0.43845215]
 [ 2.41013978  1.6380821  -0.50317506 -0.9824951 ]
 [ 2.09506138  1.30699788 -0.04611686  0.13190639]
 ...
 [-0.81524501 -0.863918   -0.4323532   1.83027114]
 [-0.62386411 -0.67588521 -0.20351956  1.09332909]
 [-0.5985845   0.05797759  0.07595381  0.30786994]]
```

```
1 from sklearn.cluster import DBSCAN
2 dbscan = DBSCAN(eps = 0.8, min_samples = 4)
```

```
model = dbscan.fit(data1)
```

```
labels = model.labels_
```

```
from sklearn import metrics
```

```
sample_cores = np.zeros_like(labels,dtype = bool)
```

```
sample_cores[dbscan.core_sample_indices_]=True
```

```
n_clusters = len(set(labels))
```

```
print(n_clusters)
```

```
3
```

```
#Step 1. epsilon hyperparameter tuning
#Using the elbow point i.e. the point of the maximum curvature
from sklearn.cluster import DBSCAN
from sklearn import metrics
from sklearn.neighbors import NearestNeighbors

neigh = NearestNeighbors(n_neighbors=2)
nbrs = neigh.fit(data1)
distances, indices = nbrs.kneighbors(data1)
distances = np.sort(distances, axis=0)
distances = distances[:,1]
#plt.plot(distances)
indices[:,1].shape
plt.plot(indices[:,0], distances)
plt.grid()
```

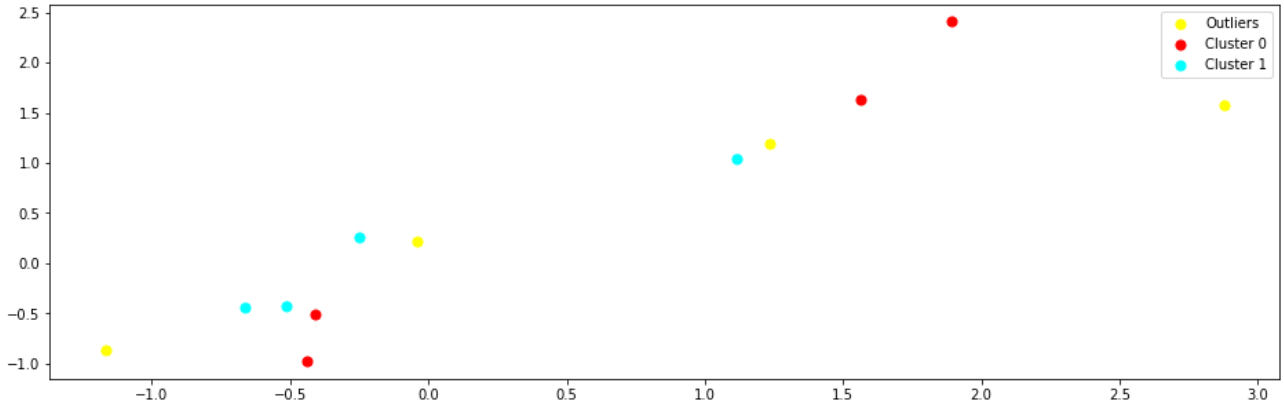
```
##interpretation of the epsilon
!pip install kneed
from kneed import KneeLocator
kn = KneeLocator(indices[:,0], distances, curve='convex', direction='increasing
#import scipy.interpolate as interp
#np.interp(kn.knee,indices[:,0], distances) #this gives the corrosponding $\eps
```

```
Looking in indexes: https://pypi.org/simple, https://us-python.pkg.dev/colab-
Requirement already satisfied: kneed in /usr/local/lib/python3.7/dist-package
Requirement already satisfied: scipy>=1.0.0 in /usr/local/lib/python3.7/dist-
Requirement already satisfied: numpy>=1.14.2 in /usr/local/lib/python3.7/dist
```

```
##Clustering using the DBSCAN
m = DBSCAN(eps=0.6, min_samples=4)
label_db = m.fit_predict(data1)
np.unique(label_db) # checking the no
```

```
array([-1,  0,  1,  2,  3,  4])
```

```
y1=data1[label_db==-1];y2=data1[label_db==0];y3=data1[label_db==1];
# y4=data1[label_db==2];y5=data1[label_db==3];y6=data1[label_db==4]
plt.scatter(y1[0],y1[1], s=50, c='yellow', label ='Outliers')
plt.scatter(y2[0],y2[1], s=50, c='red', label ='Cluster 0')
plt.scatter(y3[0],y3[1], s=50, c='cyan', label ='Cluster 1')
# plt.scatter(y4[0],y4[1], s=50, c='magenta', label ='Cluster 2')
# plt.scatter(y5[0],y5[1], s=50, c='pink', label ='Cluster 3')
# plt.scatter(y6[0],y6[1], s=50, c='blue', label ='Cluster 4')
plt.legend()
plt.show()
```




```
#Visualisation of the data using tsne
from sklearn.manifold import TSNE

```

```
tsne = TSNE(n_components=2, verbose=1, perplexity=30, n_iter=300, random_state=
tsne_results = tsne.fit_transform(data1)

x = tsne_results[:,0]
y = tsne_results[:,1]
target=label_db

plt.figure(1)
plt.title('Clustering Using KMeans')
sn.scatterplot( x, y, hue= label, palette=sn.color_palette("hls",2 ), data=data
print('No in legends corrosponds to the cluster nos.')
plt.figure(2)
plt.title('Clustering Using DBSCAN')
sn.scatterplot( x, y, hue= label_db, palette=sn.color_palette("hls",4 ), data=d
print('-1 corrosponds to the outliers and rest are clusters')
```

```
/usr/local/lib/python3.7/dist-packages/sklearn/manifold/_t_sne.py:783: Future
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/manifold/_t_sne.py:793: Future
  FutureWarning,
[t-SNE] Computing 91 nearest neighbors...
[t-SNE] Indexed 351 samples in 0.001s...
[t-SNE] Computed neighbors for 351 samples in 0.009s...
[t-SNE] Computed conditional probabilities for sample 351 / 351
[t-SNE] Mean sigma: 0.628714
[t-SNE] KL divergence after 250 iterations with early exaggeration: 57.370380
[t-SNE] KL divergence after 300 iterations: 0.471396
No in legends corrosponds to the cluster nos.
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarni
  FutureWarning
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarni
  FutureWarning
---------------------------------------------------------------------------
ValueError                                Traceback (most recent call last)
<ipython-input-260-fe21387cd2cf> in <module>
     15 plt.figure(2)
     16 plt.title('Clustering Using DBSCAN')
---> 17 sn.scatterplot( x, y, hue= label_db,
palette=sn.color_palette("hls",4 ), data=data1)
     18 print('-1 corrosponds to the outliers and rest are clusters')

                                 4 frames
/usr/local/lib/python3.7/dist-packages/seaborn/_core.py in
categorical_mapping(self, data, palette, order)
    202                 if len(palette) != n_colors:
    203                     err = "The palette list has the wrong number of
colors."
--> 204                     raise ValueError(err)
```

PCA

```
ValueError: The palette list has the wrong number of colors
```

```
1 from sklearn.decomposition import PCA
2 from sklearn.preprocessing import StandardScaler
```

Clustering Using KMeans

```
1 df_pca =  pd.read_csv('/content/sample_data/DataPCA.csv')
2 df_pca.head()
```

	x1	x2	x3	x4	x5	x6	x7
0	0.840261	-1.088160	4.861744	4.273055	4.312457	-0.137834	0.076453
1	1.320591	-1.174113	5.247360	3.295027	4.283410	-0.363759	-0.170605
2	1.537909	-1.175882	5.556251	3.394183	3.971574	-0.888398	0.080617
3	0.363552	-1.130608	4.329890	5.547488	4.539732	0.342330	0.251953
4	1.567938	-1.114719	5.542104	2.493071	4.156157	-0.609694	-0.291367

```
1 #unique and null values
2 for col in df_pca.columns.values:
3   list_vals = pd.unique(df_pca[col]) #list of unique values
```

```
4   print('\033[1m' + col + '\033[0m' + ' has ' + str(len(list_vals))  +' unique
5   if len(list_vals) < 10:
6     list_str = ''
7     for n in range(0, len(list_vals)):
8       list_str = list_str + str(list_vals[n]) + ', '
9     print('\033[1m' + '    ##### These are: '+ '\033[0m' +list_str[0:len(list_s
```

x1 has 190 unique values, **0** null entries and datatype **float64**
x2 has 190 unique values, **0** null entries and datatype **float64**
x3 has 190 unique values, **0** null entries and datatype **float64**
x4 has 190 unique values, **0** null entries and datatype **float64**
x5 has 190 unique values, **0** null entries and datatype **float64**
x6 has 190 unique values, **0** null entries and datatype **float64**
x7 has 190 unique values, **0** null entries and datatype **float64**

```
1 df_pca.describe()
```

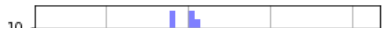
	x1	x2	x3	x4	x5	x6	
count	190.000000	190.000000	190.000000	190.000000	190.000000	190.000000	190.0000
mean	1.286644	-1.135656	5.254907	3.342504	4.233765	-0.412937	-0.1190
std	0.508765	0.233921	0.549171	0.995603	0.328327	0.482069	0.2396
min	-0.074116	-1.734167	3.967657	0.649854	3.306106	-1.936695	-0.7865
25%	0.928244	-1.298233	4.883782	2.645102	4.020569	-0.741547	-0.2781
50%	1.271034	-1.145689	5.249568	3.400840	4.242064	-0.377963	-0.1228
75%	1.637682	-0.997318	5.625487	3.996560	4.463035	-0.096413	0.0369
max	2.504835	-0.440730	6.857529	5.817673	5.056247	0.823165	0.5268

```
1 #Checking the data distribution of the variables
2 plt.figure()
3 df_pca.diff().hist(color="b", alpha=0.5, bins=50)
```

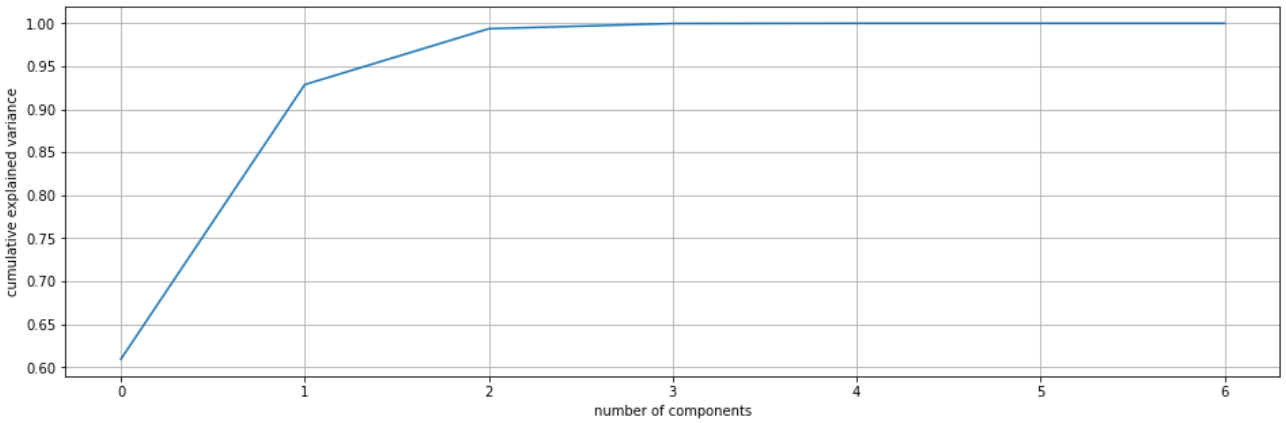
```
array([[<matplotlib.axes._subplots.AxesSubplot object at 0x7f50b87e3c10>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b87e39d0>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b83ea610>],
       [<matplotlib.axes._subplots.AxesSubplot object at 0x7f50b85cb790>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b88aac50>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b83d4050>],
       [<matplotlib.axes._subplots.AxesSubplot object at 0x7f50b88d3990>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b837b490>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b837bbd0>]],
      dtype=object)
<Figure size 1152x360 with 0 Axes>
```

```
#Apply Standard Scaling
col=df_pca.columns
feature=col.tolist()

sc=StandardScaler()  #as the PCA requirement making the mean as the origin i.e
X=sc.fit_transform(df_pca)
X=pd.DataFrame(X,columns=feature) #retaining the column names
```



```
#Plotting of the cumulative variance vs the no. of components
pca=PCA().fit(X)
plt.plot(np.cumsum(pca.explained_variance_ratio_)) #cumulative sum of the varia
plt.xlabel('number of components')
plt.ylabel('cumulative explained variance')
plt.grid()
#np.cumsum(PCA().fit(X).explained_variance_ratio_).dtype
```

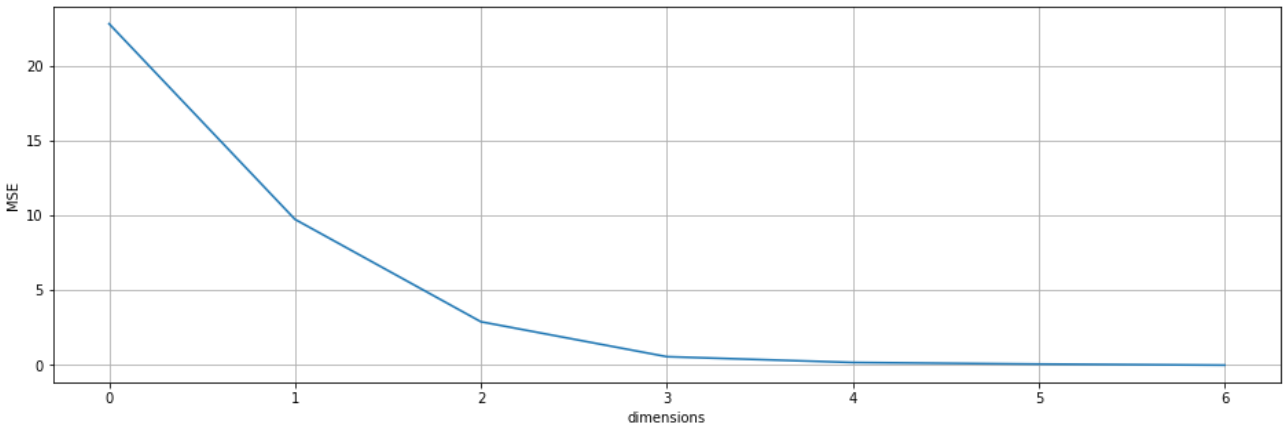



```
#taking the no of components as 4 as observed from above that the maximum varia
from numpy import linalg as LA
pca = PCA(n_components=4)
Xd = pca.fit_transform(X)
Xd_reconstructed=pca.inverse_transform(Xd)
MSE_for_reduction_upto4_components=LA.norm((X-Xd_reconstructed),None)
MSE_for_reduction_upto4_components
```

```
0.5648350714629252
```

```
#MSError visualisation for the various no of dimensions for PCA
from numpy import linalg as LA
loss=[]
for i in range(1,8):
    pca = PCA(n_components=i)
    Xd = pca.fit_transform(X)
    Xd_reconstructed=pca.inverse_transform(Xd)
    total_loss=LA.norm((X-Xd_reconstructed),None)
    loss.append(total_loss)

# Plottting
plt.ylabel('MSE')
plt.xlabel('dimensions')
plt.plot(loss)
plt.grid()
```



Part 3 Non-Linear Dimension Reduction

```
from sklearn.decomposition import KernelPCA
#from sklearn.model_selection import GridSearchCV
#from sklearn.pipeline import Pipeline
```

```
df_kpca = pd.read_csv('/content/sample_data/DataKPCA.csv')
```

```
#Visualisation of the data
# Check for unique and null values
Xk=df_kpca #data copied in Xk
for col in Xk.columns.values:
  list_vals = pd.unique(Xk[col]) #list of unique values
  print('\033[1m' + col + '\033[0m' + ' has ' + str(len(list_vals))  +' unique
  if len(list_vals) < 10:
    list_str = ''
    for n in range(0, len(list_vals)):
```

```
    list_str = list_str + str(list_vals[n]) + ', '
print('\033[1m' + '    ##### These are: '+ '\033[0m' +list_str[0:len(list_s
```

x1 has 190 unique values, **0** null entries and datatype **float64**
x2 has 190 unique values, **0** null entries and datatype **float64**
x3 has 190 unique values, **0** null entries and datatype **float64**
x4 has 190 unique values, **0** null entries and datatype **float64**
x5 has 190 unique values, **0** null entries and datatype **float64**
x6 has 190 unique values, **0** null entries and datatype **float64**
x7 has 190 unique values, **0** null entries and datatype **float64**

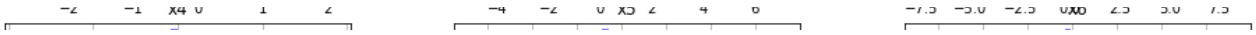
```
Xk.describe()
```

	x1	x2	x3	x4	x5	x6	
count	190.000000	190.000000	190.000000	190.000000	190.000000	190.000000	190.0000
mean	3.121555	14.985682	-47.909555	-8.811677	-2.175834	1.893953	1.9583
std	0.589013	1.298751	2.459375	2.337179	0.505819	0.159647	0.1087
min	1.964315	11.577329	-52.837231	-14.068488	-3.613443	1.750006	1.7613
25%	2.679532	14.087484	-49.736194	-10.392405	-2.512570	1.773690	1.8802
50%	3.039420	14.943396	-48.185549	-9.045948	-2.156469	1.852369	1.9423
75%	3.489341	15.764749	-46.405402	-7.235609	-1.828925	1.954614	2.0188
max	4.820967	18.747792	-40.772554	-1.907331	-0.972995	2.580983	2.3328

```
#Checking the data distribution of the variables
plt.figure()
Xk.diff().hist(color="b", alpha=0.5, bins=50)
```

```
array([[<matplotlib.axes._subplots.AxesSubplot object at 0x7f50b818c890>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b81a1f50>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b8103e90>],
       [<matplotlib.axes._subplots.AxesSubplot object at 0x7f50b80c53d0>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b8081910>,
        <matplotlib.axes._subplots.AxesSubplot object at 0x7f50b8037e10>],
       [<matplotlib.axes._subplots.AxesSubplot object at 0x7f50b7ffa3d0>,
```

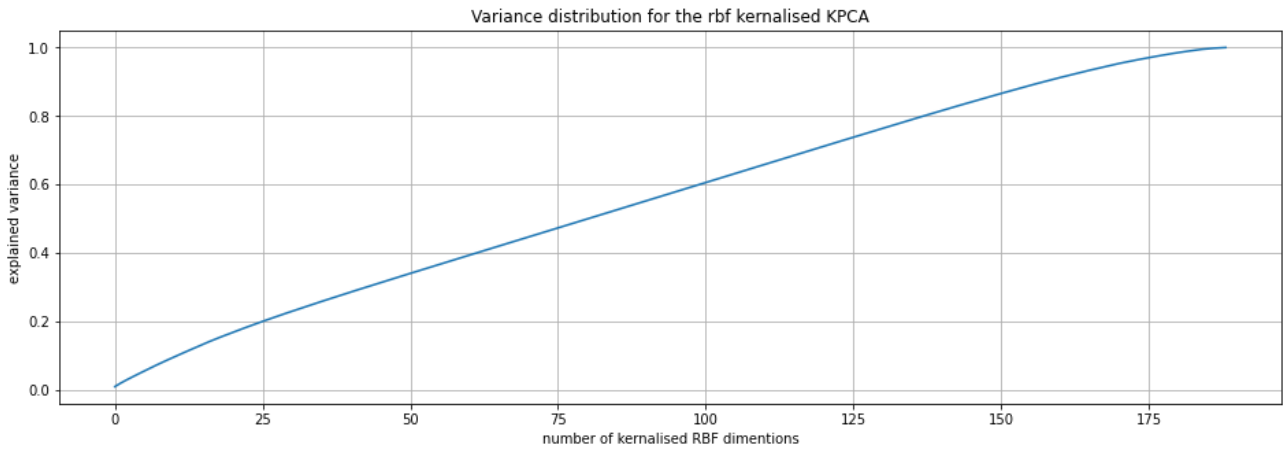
```
#standardisation of the data using the standard scaler
#Apply Standard Scaling
col=df_kpca.columns
feature=col.tolist()
sc=StandardScaler()  #as the PCA requirement making the mean as the origin i.e
Xk=sc.fit_transform(Xk)
Xk=pd.DataFrame(Xk,columns=feature)
```



Explained variance plotting in kpca

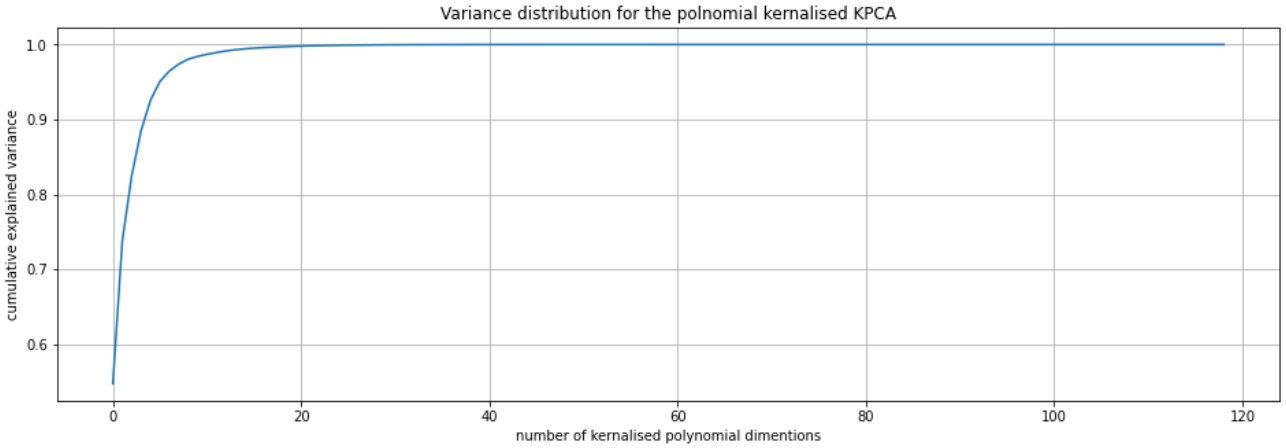
since we dont have any modeule as explained_variance ratio in sklearn.decomposition.KernelPCA so we will first transform using the kernel using the default n_components value as none, then we will apply the PCA to the kernelised input data.

```
kpca = KernelPCA(kernel="rbf", fit_inverse_transform=True, gamma=10)
Xkpca_rbf = kpca.fit_transform(Xk)
pca=PCA().fit(Xkpca_rbf)
plt.plot(np.cumsum(pca.explained_variance_ratio_)) #cumulative sum of the varia
plt.title('Variance distribution for the rbf kernalised KPCA')
plt.xlabel('number of kernalised RBF dimentions')
plt.ylabel('explained variance')
plt.grid()
```




```
kpca = KernelPCA(kernel="poly", fit_inverse_transform=True, gamma=10)
Xkpca_poly = kpca.fit_transform(Xk)
pca=PCA().fit(Xkpca_poly)
```

```
pca=PCA().fit(Xkpca_poly)
plt.plot(np.cumsum(pca.explained_variance_ratio_)) #cumulative sum of the varia
plt.title('Variance distribution for the polnomial kernalised KPCA')
plt.xlabel('number of kernalised polynomial dimentions')
plt.ylabel('cumulative explained variance')
plt.grid()
```

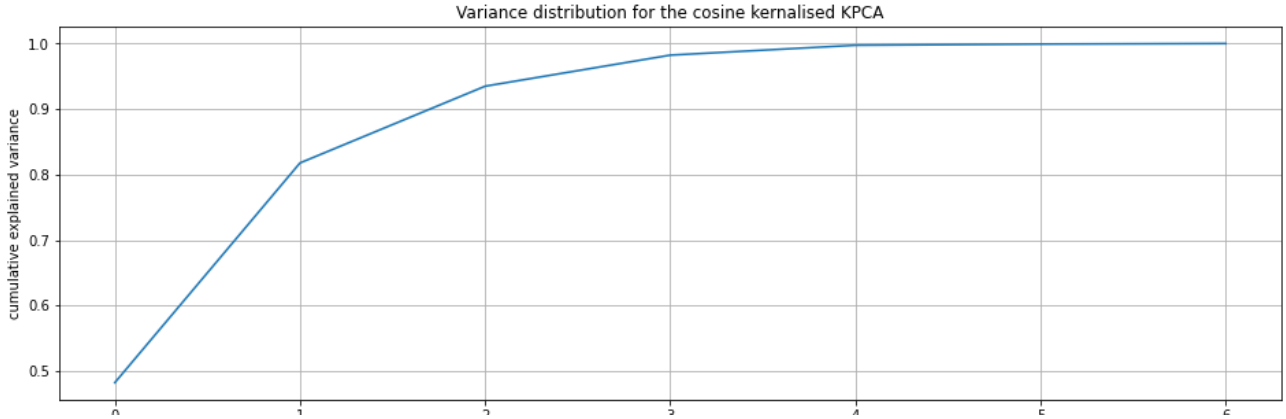



```
#fitting the KPCA dim reduction with optimal dimentions in the data
kpca = KernelPCA(kernel="poly", fit_inverse_transform=True, gamma=10)
Xkpca_poly = kpca.fit_transform(Xk)
pca=PCA(n_components=40).fit(Xkpca_poly)
Xkpca_trans=pca.fit_transform(Xkpca_poly)
Xkpca_trans.shape
#X2=pca.inverse_transform(Xkpca_trans)
```

```
(190, 40)
```

```
#KPCA with cosine kernel
kpca = KernelPCA(kernel="cosine", fit_inverse_transform=True, gamma=10)
Xkpca_cos = kpca.fit_transform(Xk)
pca=PCA().fit(Xkpca_cos)
plt.plot(np.cumsum(pca.explained_variance_ratio_)) #cumulative sum of the varia
plt.title('Variance distribution for the cosine kernalised KPCA')
plt.xlabel('number of kernalised cosine dimentions')
plt.ylabel('cumulative explained variance')
plt.grid()

```




```
Observations reg the applied Kernel

As we have applied the rbf cosine polynor
which the better results were given by th
kernel \ because as observed from the va
of rbf there was no significant lower dir
available which were covering the higher
```

Observations reg the applied Kernel

As we have applied the rbf cosine polynomial kernels out of which the better results were given by the polynomial kernel \ because as observed from the varince dist diagram of rbf there was no significant lower dimentions were available which were covering the higher variance ratio.

✓ 0s completed at 18:08