This is data analysis and model fit for human activity. Data is collected using smartphone sensors.

Data analysis

In [1]:
```
import numpy as np
import pandas as pd
import math
import matplotlib.pyplot as plt
import seaborn as sns
import psutil
import time

from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import normalize
from sklearn.cluster import DBSCAN
from sklearn import metrics
from sklearn.metrics import silhouette_score
from itertools import product
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis as LDA
from sklearn.neighbors import NearestNeighbors

#Setting the plot parameters for standardized graphs.
plt.rcParams["figure.figsize"] = (15, 7)
plt.style.use("ggplot")
```

In [2]:
```
#Read the data. 'train_data includes features and label.'
train_data = pd.read_csv("Dataset.csv") #Feature+labels.
X = np.array(pd.read_csv("X_train.csv", header=None)) #Only features.
label = pd.read_csv("y_train.csv", header=None)
```

In [ ]:
```
#Scatter plot of two features to see how data is spread. Data looks very dense and overlappin
sns.scatterplot(X[:,2], X[:,3], hue=train_data['Activity'], palette='bright')
```

In [ ]:
```
label.shape
```

In [ ]:
```
#Reference key for labels.
KeyRef = {1:"WALKING", 2:"WALKING_UPSTAIRS",3:"WALKING_DOWNSTAIRS",4:"SITTING",5:"STANDING",6
```

In [ ]:
```
#Check activity sample distribution.
train_data[('Activity')].groupby(train_data['Activity']).count()
```

In [ ]:
```
#Have a look on data details/feature.
train_data.describe()
```

In [6]:
```
#Check null values
train_data.isnull().groupby(train_data['Activity']).sum()
```

Out[6]:

Activity	1 tBodyAcc-mean()-X	2 tBodyAcc-mean()-Y	3 tBodyAcc-mean()-Z	4 tBodyAcc-std()-X	5 tBodyAcc-std()-Y	6 tBodyAcc-std()-Z	7 tBodyAcc-mad()-X	8 tBodyAcc-mad()-Y	9 tBodyAcc-mad()-Z	10 tBody max(
1	False	False	False	False	False	False	False	False	False	
2	False	False	False	False	False	False	False	False	False	
3	False	False	False	False	False	False	False	False	False	
4	False	False	False	False	False	False	False	False	False	
5	False	False	False	False	False	False	False	False	False	
6	False	False	False	False	False	False	False	False	False	

6 rows × 562 columns

In [4]:
```
#Check if data has any null values.
train_data.isnull().sum().sum()
```

Out[4]: 0

In [ ]:
```
#Print any features with null values. Not used now. Same as above.
nulls = train_data.isnull().sum().to_frame()
for index, row in nulls.iterrows():
    if row[0]>0:print(index, row[0])
```

In [5]:
```
#Study different acitivity sample data differences. MEan and variance selected.
train_data.groupby('Activity').agg(['mean','var'])
```

Out[5]:

	1 tBodyAcc-mean()-X		2 tBodyAcc-mean()-Y		3 tBodyAcc-mean()-Z		4 tBodyAcc-std()-X		5 tBodyAcc-std()-Y		...	557 ang
	mean	var	mean	var	mean	var	mean	var	mean	var	...	me
Activity												
1	0.276259	0.002536	-0.017767	0.000436	-0.108892	0.001052	-0.312640	0.020869	-0.020279	0.031568	...	
2	0.261925	0.006090	-0.026648	0.001372	-0.120423	0.003625	-0.221069	0.023843	-0.000344	0.040554	...	
3	0.288170	0.009044	-0.016368	0.000732	-0.105860	0.002566	0.139856	0.049337	0.079190	0.059430	...	
4	0.273450	0.001764	-0.012142	0.001050	-0.106576	0.002054	-0.983440	0.001042	-0.936213	0.016919	...	
5	0.279298	0.000404	-0.016124	0.000319	-0.107327	0.001273	-0.985346	0.000523	-0.936012	0.006714	...	
6	0.269187	0.010310	-0.018345	0.005405	-0.107178	0.008057	-0.959476	0.006196	-0.937598	0.021585	...	

6 rows × 1122 columns

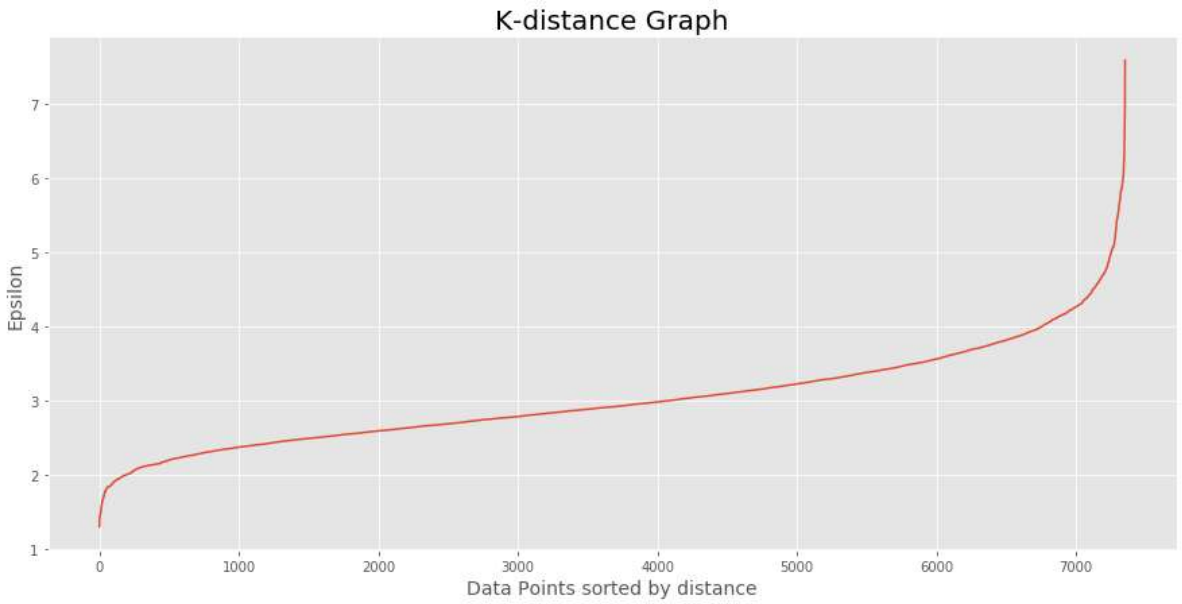
In [7]:
```
train_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 7352 entries, 0 to 7351
Columns: 562 entries, 1 tBodyAcc-mean()-X to Activity
dtypes: float64(561), int64(1)
memory usage: 31.5 MB
```

Use the input data without dimensionality reduction.

In [8]:

```
#Plot nearest neighbor grap for distance parameter setting.
neigh = NearestNeighbors(n_neighbors=10)
nbrs = neigh.fit(X)
distances, indices = nbrs.kneighbors(X)
# Plotting K-distance Graph
distances = np.sort(distances, axis=0)
distances = distances[:,1]
plt.plot(distances)
plt.title('K-distance Graph',fontsize=20)
plt.xlabel('Data Points sorted by distance',fontsize=14)
plt.ylabel('Epsilon',fontsize=14)
plt.show()
```



In [10]:

```
#Set range of values using above graph. This to fond optimal DBSCAN parameters
eps_values = np.arange(3.6,6,0.5) # with normalization and PCA
min_samples = np.arange(4,16,2) # with normalization and PCA 20,40,2
DBSCAN_params = list(product(eps_values, min_samples))
train_data.drop(columns=['Activity'])
```

Out[10]:

	1 tBodyAcc-mean()-X	2 tBodyAcc-mean()-Y	3 tBodyAcc-mean()-Z	4 tBodyAcc-std()-X	5 tBodyAcc-std()-Y	6 tBodyAcc-std()-Z	7 tBodyAcc-mad()-X	8 tBodyAcc-mad()-Y	9 tBodyAcc-mad()-Z	tBodyA max(
0	0.289	-0.02030	-0.133	-0.995	-0.98300	-0.9140	-0.995	-0.9830	-0.9240	-0.9
1	0.278	-0.01640	-0.124	-0.998	-0.97500	-0.9600	-0.999	-0.9750	-0.9580	-0.9
2	0.280	-0.01950	-0.113	-0.995	-0.96700	-0.9790	-0.997	-0.9640	-0.9770	-0.9
3	0.279	-0.02620	-0.123	-0.996	-0.98300	-0.9910	-0.997	-0.9830	-0.9890	-0.9
4	0.277	-0.01660	-0.115	-0.998	-0.98100	-0.9900	-0.998	-0.9800	-0.9900	-0.9
...	...	...	...	...	...	...	...	...	...	
7347	0.300	-0.05720	-0.181	-0.195	0.03990	0.0771	-0.282	0.0436	0.0604	0.2
7348	0.274	-0.00775	-0.147	-0.235	0.00482	0.0593	-0.323	-0.0295	0.0806	0.1
7349	0.273	-0.01700	-0.045	-0.218	-0.10400	0.2750	-0.305	-0.0989	0.3330	0.0
7350	0.290	-0.01880	-0.158	-0.219	-0.11100	0.2690	-0.310	-0.0682	0.3190	0.1
7351	0.352	-0.01240	-0.204	-0.269	-0.08720	0.1770	-0.377	-0.0387	0.2290	0.2

7352 rows × 561 columns

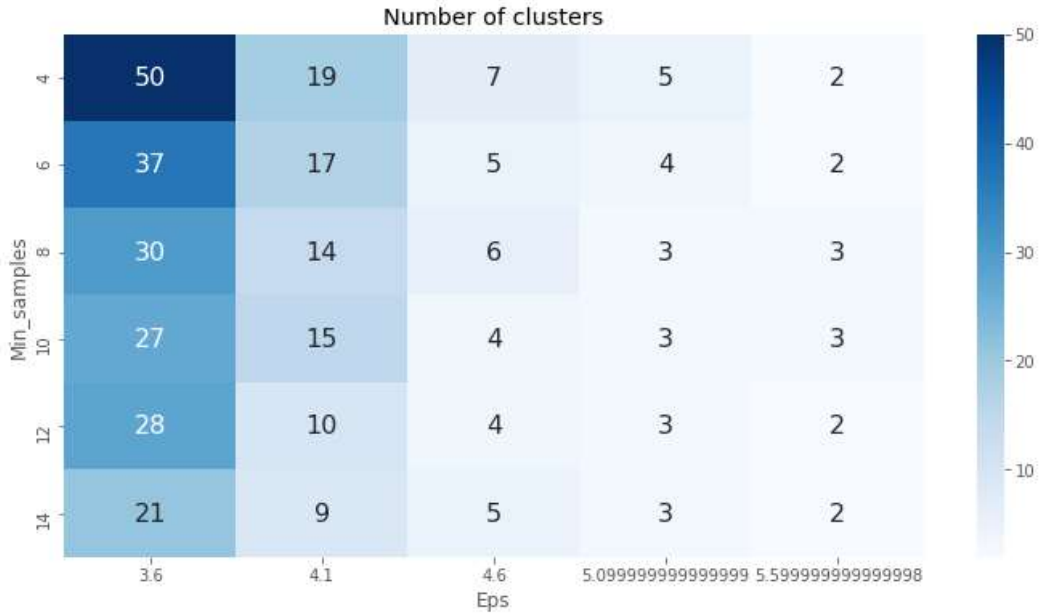
In [11]:

```
#THIS CAN TAKE ANYTHING FROM 30 MINUTES TO OVER ONE HOUR TO RUN!!! NOT NEEDED AS OPTIMAL PARA
#Run DBSCAN fit with multiple parameter sets to find optimal parameters for best most accurat
#Run timer to check computation time.
no_of_clusters = []
sil_score = []
print('PCU utilization:', psutil.cpu_percent(),'%')
print('Clusters created at each round. Looking for 6 with high silhouette score. Will take ab
start = time.time()

for p in DBSCAN_params:
    DBS_clustering = DBSCAN(eps=p[0], min_samples=p[1]).fit(train_data)
    no_of_clusters.append(len(np.unique(DBS_clustering.labels_)))
    #print(DBS_clustering.labels_)
    #print(no_of_clusters)
    #print(p[0],p[1])
    #print('PCU utilization%:', psutil.cpu_percent())
    if len(np.unique(DBS_clustering.labels_)) > 1:
        sil_score.append(silhouette_score(train_data, DBS_clustering.labels_))
        good_label = DBS_clustering.labels_
    else:
        sil_score.append(silhouette_score(train_data, good_label))

end = time.time()
print('PCU utilization:', psutil.cpu_percent(),'%')
print('Total time: %0.2f'%(end-start),'s')
```

```
PCU utilization: 23.3 %
Clusters created at each round. Looking for 6 with high silhouette score. Will take about 1800 t
o 3600s to run.
PCU utilization: 56.3 %
Total time: 2970.56 s
```

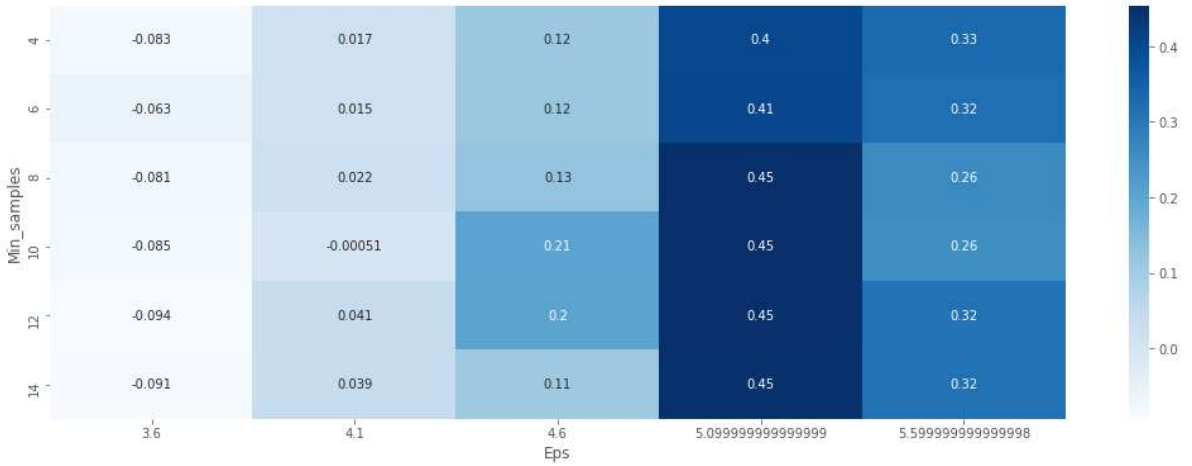
In [12]:

```
#Show clustering matrix with number of clusters, eps and min_samples (x,y).
tmp = pd.DataFrame.from_records(DBSCAN_params, columns =['Eps', 'Min_samples'])
tmp['No_of_clusters'] = no_of_clusters
pivot_1 = pd.pivot_table(tmp, values='No_of_clusters', index='Min_samples', columns='Eps')
fig, ax = plt.subplots(figsize=(12,6))
sns.heatmap(pivot_1, annot=True,annot_kws={"size": 16}, cmap="Blues", ax=ax)
ax.set_title('Number of clusters')
plt.show()
```



In [13]:

```
#Show clustering matrix with silhoutte score, eps and min_samples (x,y).
#Silhouette score indicates how well clusters are separates. Range is -1..1. 1 is the best sc
tmp = pd.DataFrame.from_records(DBSCAN_params, columns =['Eps', 'Min_samples'])
tmp['Sil_score'] = sil_score
pivot_1 = pd.pivot_table(tmp, values='Sil_score', index='Min_samples', columns='Eps')
fig, ax = plt.subplots(figsize=(18,6))
sns.heatmap(pivot_1, annot=True, annot_kws={"size": 10}, cmap="Blues", ax=ax)
plt.show()
```



In [14]:

```
#Final clustering with most optimal eps and min_samples parameters.
print('PCU utilization:', psutil.cpu_percent(),'%')
start = time.time()

DBS_clustering = DBSCAN(eps=4.5, min_samples=10).fit(X)
core_samples_mask = np.zeros_like(DBS_clustering.labels_, dtype=bool)
core_samples_mask[DBS_clustering.core_sample_indices_] = True
labels = DBS_clustering.labels_
n_clusters_ = len(set(labels)) - (1 if -1 in labels else 0)
n_noise_ = list(labels).count(-1)
DBSCAN_clustered = pd.DataFrame(X.copy())
DBSCAN_clustered.loc[:,'Cluster'] = DBS_clustering.labels_ # append labels to points

end = time.time()
print('PCU utilization:', psutil.cpu_percent(),'%')
print('Total time: %0.2f'%(end-start),'s')
```

```
PCU utilization: 34.9 %
PCU utilization: 74.1 %
Total time: 160.94 s
```

In [15]:

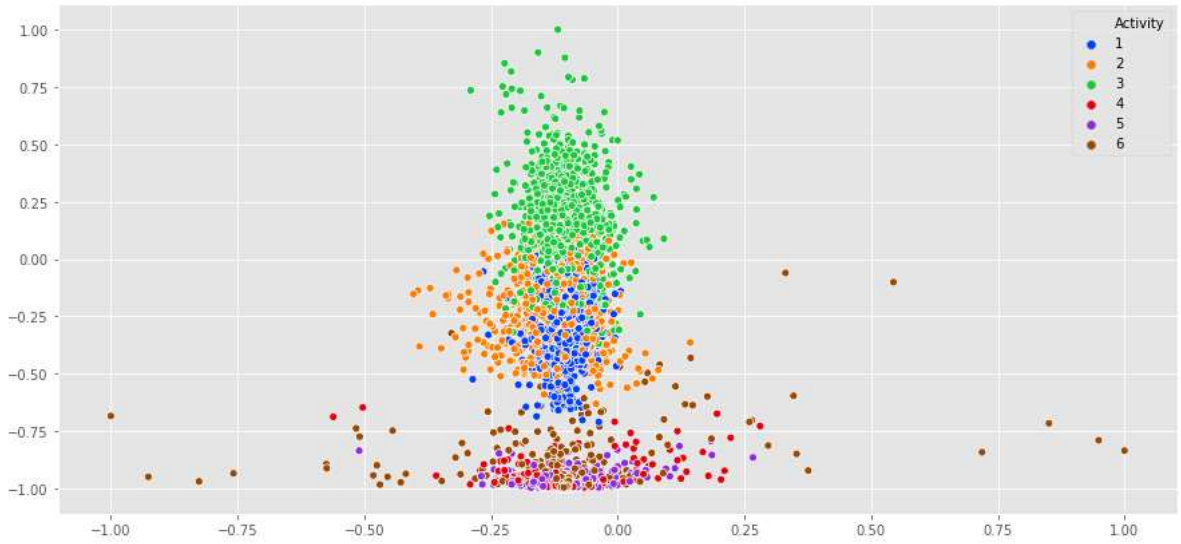
```
#Check number of clusters and amount of samples in each. DBSCAN only able to create two clust
DBSCAN_clust_sizes = DBSCAN_clustered.groupby('Cluster').size().to_frame()
DBSCAN_clust_sizes.columns = ["DBSCAN_size"]
DBSCAN_clust_sizes
```

Out[15]:

Cluster	DBSCAN_size
-1	499
0	3850
1	2970
2	33

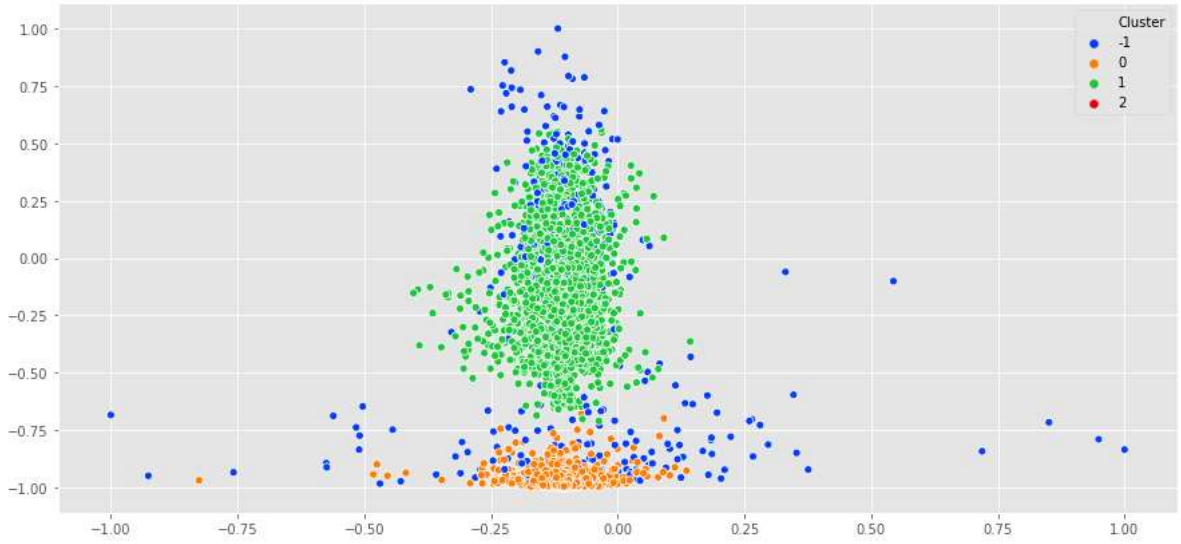
In [16]:
```
#Plot the original cluster assignments using given cluster assignments.
sns.scatterplot(X[:,2], X[:,3], hue=train_data["Activity"], palette="bright")
```

Out[16]: <matplotlib.axes._subplots.AxesSubplot at 0x231a40281c8>



In [17]:
```
#Plot DBSCAN predicted clusters. Label '-1' is outliers. Only two clusters identified.
sns.scatterplot(X[:,2], X[:,3], DBSCAN_clustered['Cluster'], palette="bright")
```

Out[17]: <matplotlib.axes._subplots.AxesSubplot at 0x231ab6578c8>



In [18]:
```
#Print the DBSCAN KPIs.
label_opt = np.array(np.reshape(label,-1))
label_opt = np.array(np.reshape(label_opt,-1))
label_opt
print('Estimated number of clusters: %d' % n_clusters_)
print('Estimated number of noise points: %d' % n_noise_)
print("Homogeneity: %0.3f" % metrics.homogeneity_score(label_opt, labels))
print("Completeness: %0.3f" % metrics.completeness_score(label_opt, labels))
print("V-measure: %0.3f" % metrics.v_measure_score(label_opt, labels))
print("Adjusted Rand Index: %0.3f" % metrics.adjusted_rand_score(label_opt, labels))
print("Adjusted Mutual Information: %0.3f" % metrics.adjusted_mutual_info_score(label_opt, la
print("Silhouette Coefficient: %0.3f" % metrics.silhouette_score(X, labels))
```

```
Estimated number of clusters: 3
Estimated number of noise points: 499
Homogeneity: 0.383
Completeness: 0.749
V-measure: 0.507
Adjusted Rand Index: 0.325
Adjusted Mutual Information: 0.507
Silhouette Coefficient: 0.197
```

Dimensionality reduction with LDA.

In [19]:
```
#Dimensionality reduction. Also called data extraction.
#Transform data to four components. This covers 99% of the variance. See variance ratio below
lda = LDA(n_components=4)
X_train = lda.fit_transform(X, label)
#X_train = lda.fit(X, label).transform(X)
```

```
C:\Users\marpulli\Anaconda3\lib\site-packages\sklearn\utils\validation.py:760: DataConversionWar
ning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to
(n_samples, ), for example using ravel().
  y = column_or_1d(y, warn=True)
```

In [20]:
```
pd.DataFrame(X_train).describe()
```

Out[20]:

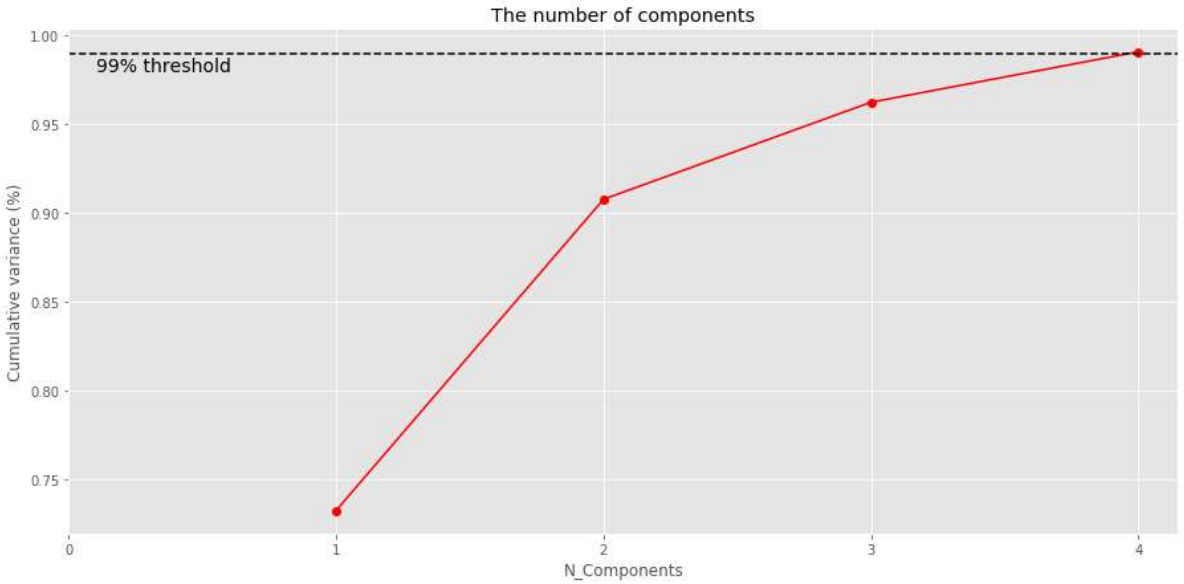
	0	1	2	3
count	7.352000e+03	7.352000e+03	7.352000e+03	7.352000e+03
mean	4.546048e-13	-7.486382e-14	1.874711e-13	-8.228927e-14
std	1.333182e+01	6.575960e+00	3.764320e+00	2.802709e+00
min	-1.924833e+01	-9.313733e+00	-1.110858e+01	-9.866220e+00
25%	-1.436734e+01	-7.036100e+00	-6.568213e-01	-5.025589e-01
50%	9.050437e+00	7.284046e-01	1.048651e-01	2.285788e-01
75%	1.027552e+01	2.084636e+00	7.346217e-01	1.607426e+00
max	2.125605e+01	1.452409e+01	1.123737e+01	7.138333e+00

In [21]:
```
#Check how much variance is covered with each component. With four componenets 99%.
lda.explained_variance_ratio_
```

Out[21]:
```
array([0.73276802, 0.17514607, 0.05460691, 0.02842483])
```

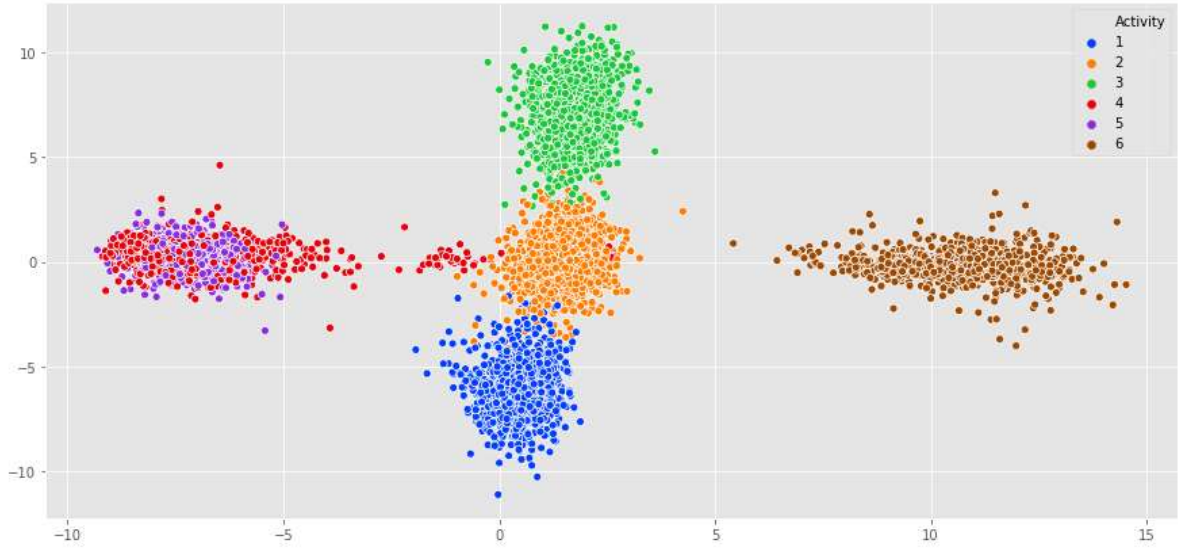
In [22]:
```
#Cumulative variance graph
y = np.cumsum(lda.explained_variance_ratio_)
xn = np.arange(1, 5, step=1)
plt.plot(xn, y, marker='o', color='r')
plt.axhline(y=0.99, color='black',linestyle='--')
plt.xticks(np.arange(0, 5, step=1))
plt.xlabel('N_Components')
plt.ylabel('Cumulative variance (%)')
plt.title('The number of components')
plt.text(0.1, 0.98, '99% threshold', color = 'black', fontsize=14)
```

Out[22]:
```
Text(0.1, 0.98, '99% threshold')
```



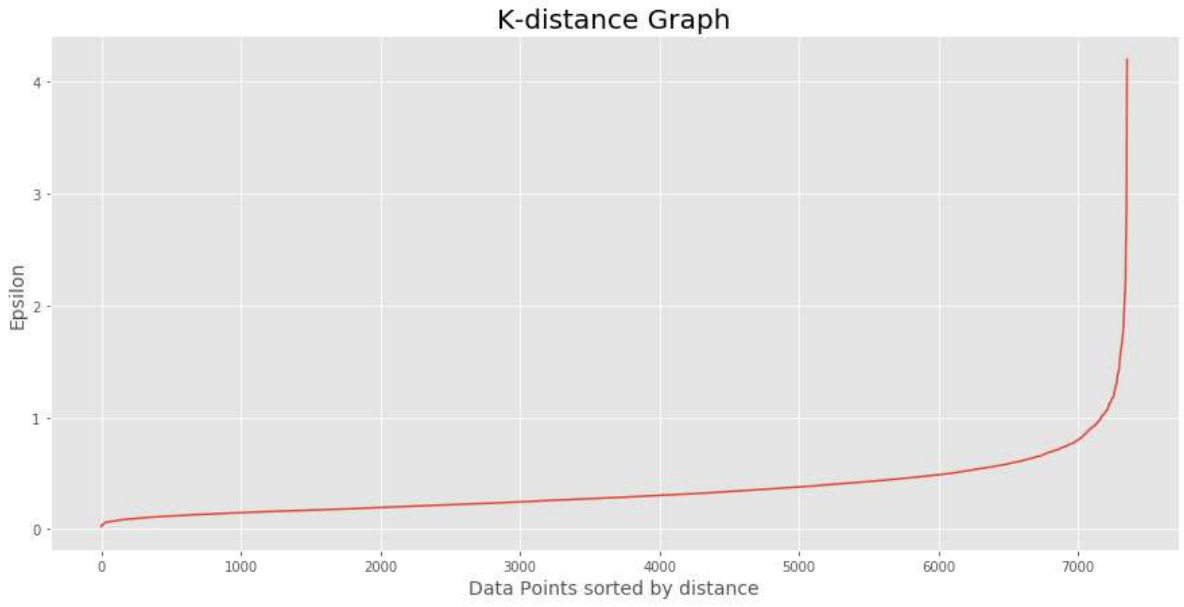
In [23]:
```
#Plot the data after dimensionality reduction with LDA data extraction.
sns.scatterplot(X_train[:,1], X_train[:,2], hue=train_data['Activity'], palette='bright')
```

Out[23]: <matplotlib.axes._subplots.AxesSubplot at 0x231b718fe48>



In [24]:
```
#Create nearest neighbor distances.
#X_data = StandardScaler().fit_transform(X_train)
X_data = X_train #No scaling after LDA.
neigh = NearestNeighbors(n_neighbors=4)
nbrs = neigh.fit(X_data)
distances, indices = nbrs.kneighbors(X_data)
```

In [25]:
```
# Plotting K-distance graph to find best DBSCAN eps value.
distances = np.sort(distances, axis=0)
distances = distances[:,1]
plt.plot(distances)
plt.title('K-distance Graph',fontsize=20)
plt.xlabel('Data Points sorted by distance',fontsize=14)
plt.ylabel('Epsilon',fontsize=14)
plt.show()
```



In [26]:
```
#Set range of values using above graph. This to fond optimal DBSCAN parameters
eps_values = np.arange(0.9,1.9,0.1) # no scaling + LDA these are good
min_samples = np.arange(4,18,2) # no scaling +LDA 4...18 these are good
DBSCAN_params = list(product(eps_values, min_samples))
```

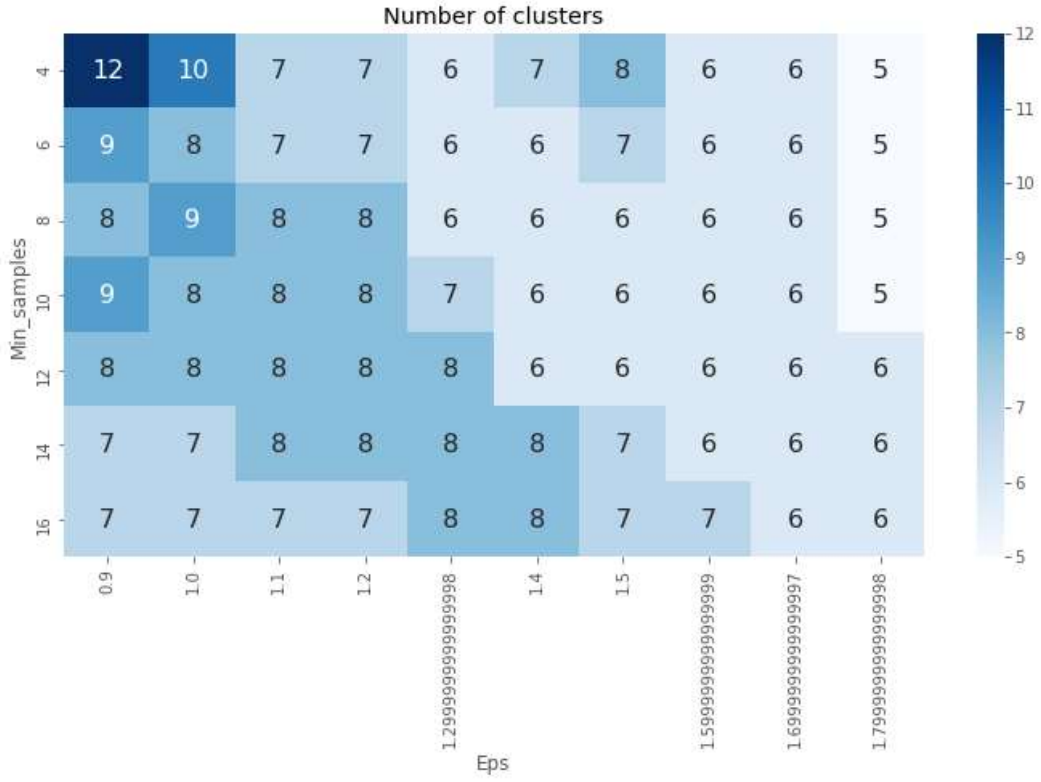
In [27]:

```
#Run DBSCAN fit with multiple parameter sets to find optimal parameters for best most accurat
#Run timer to check computation time.
no_of_clusters = []
sil_score = []
print('PCU utilization:', psutil.cpu_percent(),'%')
print('Clusters created at each round. Looking for 6 with high silhouette score. This will ta
start = time.time()

for p in DBSCAN_params:
    DBS_clustering = DBSCAN(eps=p[0], min_samples=p[1]).fit(X_data)
    no_of_clusters.append(len(np.unique(DBS_clustering.labels_)))
    #print(DBS_clustering.labels_)
    #print(no_of_clusters[-1])
    #print(p[0],p[1])
    #print('PCU utilization%:', psutil.cpu_percent())
    if len(np.unique(DBS_clustering.labels_)) > 1:
        sil_score.append(silhouette_score(X_data, DBS_clustering.labels_))
        good_label = DBS_clustering.labels_
    else:
        sil_score.append(silhouette_score(X_data, good_label))

end = time.time()
print('PCU utilization:', psutil.cpu_percent(),'%')
print('Total time: %0.2f'%(end-start),'s')
```

```
PCU utilization: 27.5 %
Clusters created at each round. Looking for 6 with high silhouette score. This will take about 2
00s to run
PCU utilization: 53.6 %
Total time: 136.70 s
```

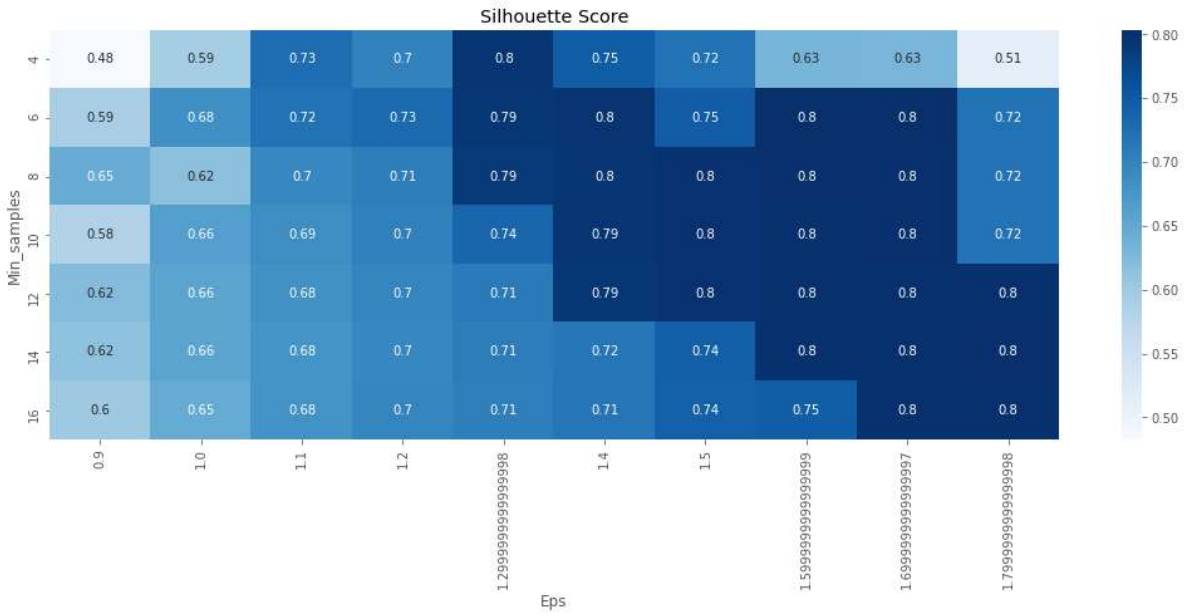
In [28]:

```
#Show clustering matrix with number of clusters, eps and min_samples (x,y).
import matplotlib.ticker as ticker
tmp = pd.DataFrame.from_records(DBSCAN_params, columns =['Eps', 'Min_samples'])
tmp['No_of_clusters'] = no_of_clusters
pivot_1 = pd.pivot_table(tmp, values='No_of_clusters', index='Min_samples', columns='Eps')
fig, ax = plt.subplots(figsize=(12,6))
sns.heatmap(pivot_1, annot=True,annot_kws={"size": 16}, cmap="Blues", ax=ax)
ax.set_title('Number of clusters')
plt.show()
```



In [29]:

```
##Show clustering matrix with silhoutte score, eps and min_samples (x,y).
#Silhouette score indicates how well clusters are separates. Range is -1..1. 1 is the best sc
from matplotlib.ticker import (MultipleLocator,
                               FormatStrFormatter,
                               AutoMinorLocator)
tmp = pd.DataFrame.from_records(DBSCAN_params, columns =['Eps', 'Min_samples'])
tmp['Sil_score'] = sil_score

pivot_1 = pd.pivot_table(tmp, values='Sil_score', index='Min_samples', columns='Eps')

fig, ax = plt.subplots(figsize=(18,6))
sns.heatmap(pivot_1, annot=True, annot_kws={"size": 10}, cmap="Blues", ax=ax)
ax.set_title('Silhouette Score')
plt.show()
```



In [30]:

```
#Final clustering with most optimal eps and min_samples parameters selected from the above.
print('PCU utilization:', psutil.cpu_percent(),'%')
start = time.time()

DBS_clustering = DBSCAN(eps=1.6, min_samples=12).fit(X_data)#1.6&10 goood!
core_samples_mask = np.zeros_like(DBS_clustering.labels_, dtype=bool)
core_samples_mask[DBS_clustering.core_sample_indices_] = True
labels = DBS_clustering.labels_
n_clusters_ = len(set(labels)) - (1 if -1 in labels else 0)
n_noise_ = list(labels).count(-1)
DBSCAN_clustered = pd.DataFrame(X_data.copy())
DBSCAN_clustered.loc[:,'Cluster'] = DBS_clustering.labels_ # append labels to points

end = time.time()
print('PCU utilization:', psutil.cpu_percent(),'%')
print('Total time: %0.2f'%(end-start),'s')
```

```
PCU utilization: 20.5 %
PCU utilization: 42.5 %
Total time: 0.46 s
```

In [31]:

```
#Check number of clusters and amount of samples in each.
DBSCAN_clust_sizes = DBSCAN_clustered.groupby('Cluster').size().to_frame()
DBSCAN_clust_sizes.columns = ["DBSCAN_size"]
DBSCAN_clust_sizes
```

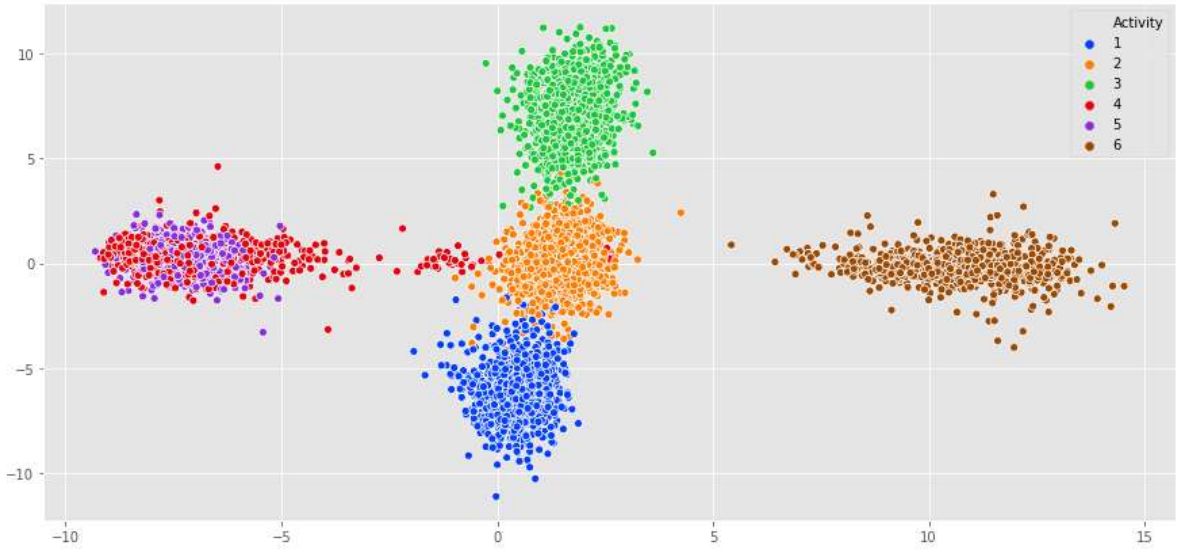
Out[31]:

Cluster	DBSCAN_size
-1	81
0	2643
1	1377
2	1216
3	972
4	1063

In [32]:

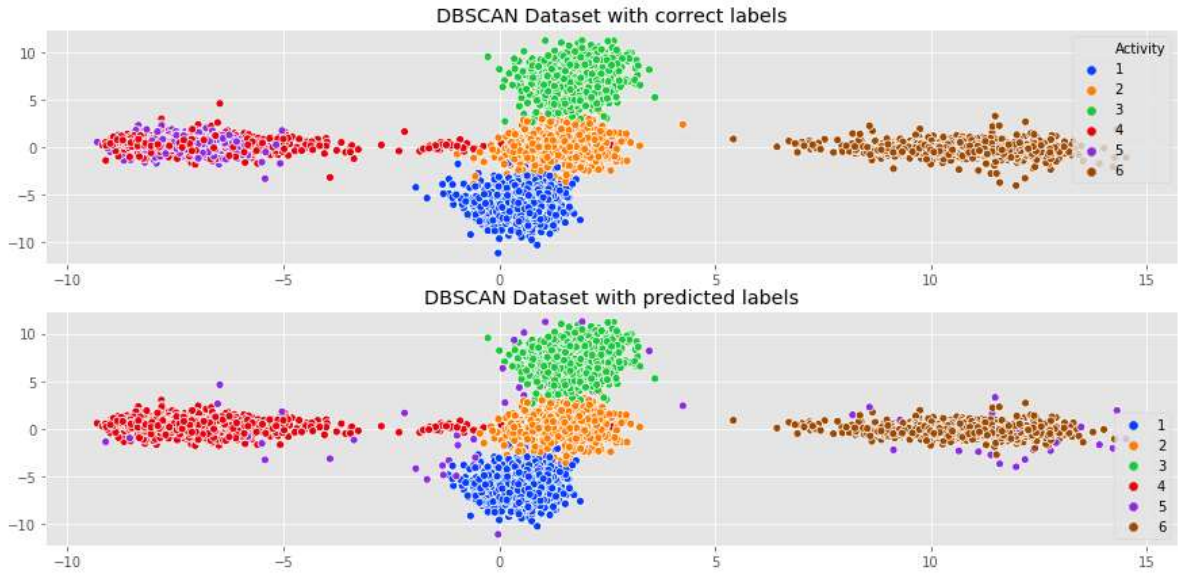
```
#Plot the original cluster assignments using given cluster assignments.
sns.scatterplot(X_data[:,1], X_data[:,2], hue=train_data["Activity"], palette="bright")
```

Out[32]: <matplotlib.axes._subplots.AxesSubplot at 0x231ab81c548>



In [33]:

```
#Plot DBSCAN predicted clusters. Label '5' is outliers. Sitting and standing in same cluster
#Match the colors with original.
DBSCAN_clustered['Cluster'] = DBSCAN_clustered['Cluster'] + 10
#Relabeling to match input data
data_labels = DBSCAN_clustered.Cluster.values
data_labels[data_labels == 10] = 4
data_labels[data_labels == 11] = 6
data_labels[data_labels == 12] = 1
data_labels[data_labels == 13] = 3
data_labels[data_labels == 14] = 2
data_labels[data_labels == 9] = 5

plt.subplot(211)
sns.scatterplot(X_data[:,1], X_data[:,2], hue=train_data["Activity"], palette="bright")
plt.title('DBSCAN Dataset with correct labels')

plt.subplot(212)
sns.scatterplot(X_data[:,1], X_data[:,2], data_labels, palette="bright")
plt.title('DBSCAN Dataset with predicted labels')

plt.show()
#sns.scatterplot(X_data[:,1], X_data[:,2], data_labels, palette="bright")
```



DBSCAN KPI creation.

In [34]:

```
#Print the DBSCAN KPIs.
#Reshape original label arrays to match DBSCAN labeling
label_opt = np.array(np.reshape(label,-1))
label_opt = np.array(np.reshape(label_opt,-1))
print('Estimated number of clusters: %d' % n_clusters_)
print('Estimated number of noise points: %d' % n_noise_)
print("Homogeneity: %0.3f" % metrics.homogeneity_score(label_opt, labels))
print("Completeness: %0.3f" % metrics.completeness_score(label_opt, labels))
print("V-measure: %0.3f" % metrics.v_measure_score(label_opt, labels))
print("Adjusted Rand Index: %0.3f" % metrics.adjusted_rand_score(label_opt, labels))
print("Adjusted Mutual Information: %0.3f" % metrics.adjusted_mutual_info_score(label_opt, la
print("Silhouette Coefficient: %0.3f" % metrics.silhouette_score(X_data, labels))
```

```
Estimated number of clusters: 5
Estimated number of noise points: 81
Homogeneity: 0.850
Completeness: 0.962
V-measure: 0.903
Adjusted Rand Index: 0.787
Adjusted Mutual Information: 0.903
Silhouette Coefficient: 0.800
```

In [35]:
```
#Model accuracy. Cluster assignment matching the original label.
results1 = np.array(train_data["Activity"]) == data_labels
sum(bool(x) for x in results1)/len(data_labels)
```

Out[35]:
```
0.8039989118607181
```

Network Layout

In [36]:
```
DBS_clustering.get_params(deep=True)
```

Out[36]:
```
{'algorithm': 'auto',
 'eps': 1.6,
 'leaf_size': 30,
 'metric': 'euclidean',
 'metric_params': None,
 'min_samples': 12,
 'n_jobs': None,
 'p': None}
```

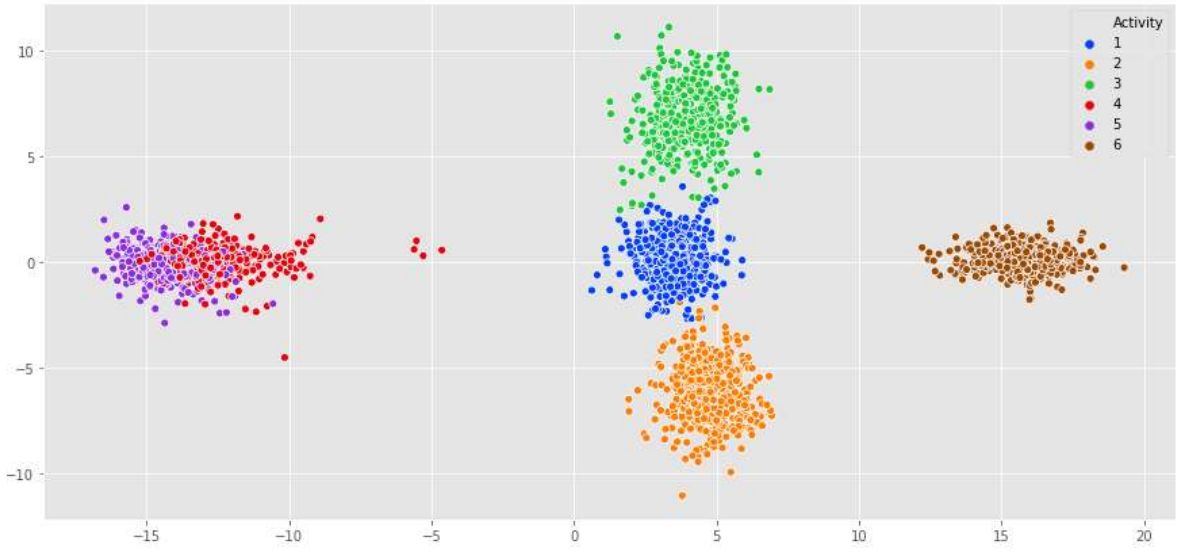
Use test data to verify model performance.

In [37]:
```
#Read the data. 'train_data includes features and label.'
test_data = pd.read_csv("Test_Dataset.csv")
Xt = np.array(pd.read_csv("X_test.csv", header=None))
t_label = pd.read_csv("y_test.csv", header=None)
```

In [38]:
```
lda = LDA(n_components=4)
X_test = lda.fit_transform(Xt, t_label)
sns.scatterplot(X_test[:,1], X_test[:,3], hue=test_data['Activity'], palette='bright')
```

```
C:\Users\marpulli\Anaconda3\lib\site-packages\sklearn\utils\validation.py:760: DataConversionWar
ning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to
(n_samples, ), for example using ravel().
  y = column_or_1d(y, warn=True)
```

Out[38]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x231b2a3dbc8>
```



In [39]:
```
#Final clustering with most optimal eps and min_samples parameters selected from the above.
X_t_data = X_test #No scaling
DBS_clustering = DBSCAN(eps=1.6, min_samples=12).fit(X_t_data)
core_samples_mask = np.zeros_like(DBS_clustering.labels_, dtype=bool)
core_samples_mask[DBS_clustering.core_sample_indices_] = True
labels = DBS_clustering.labels_
n_clusters_ = len(set(labels)) - (1 if -1 in labels else 0)
n_noise_ = list(labels).count(-1)
DBSCAN_clustered = pd.DataFrame(X_t_data.copy())
DBSCAN_clustered.loc[:,'Cluster'] = DBS_clustering.labels_ # append labels to points
```

In [40]:

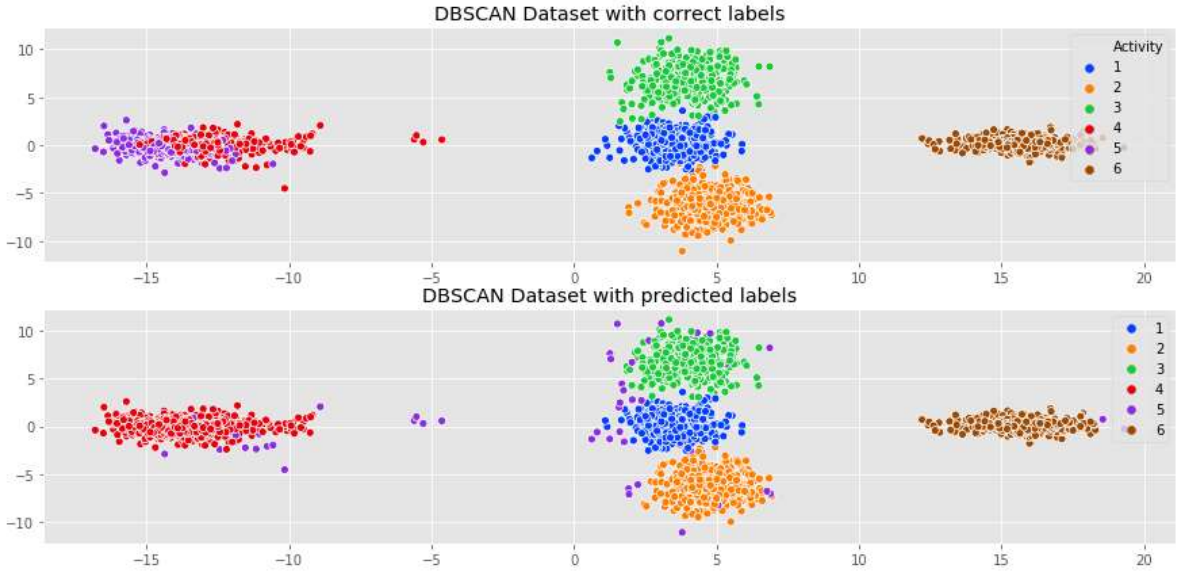
```
DBSCAN_clust_sizes = DBSCAN_clustered.groupby('Cluster').size().to_frame()
DBSCAN_clust_sizes.columns = ["DBSCAN_size"]
DBSCAN_clust_sizes
```

Out[40]:

Cluster	DBSCAN_size
-1	63
0	1001
1	534
2	487
3	399
4	463

In [41]:

```
#Plot DBSCAN predicted clusters. Label '5' is outliers. Sitting and standing in same cluster
#Match the colors with original.
DBSCAN_clustered['Cluster'] = DBSCAN_clustered['Cluster'] + 10
#Relabeling to match input data. Unsupervised learning clustering done correctly but labels n
data_labels = DBSCAN_clustered.Cluster.values
data_labels[data_labels == 10] = 4
data_labels[data_labels == 11] = 6
data_labels[data_labels == 12] = 1
data_labels[data_labels == 13] = 3
data_labels[data_labels == 14] = 2
data_labels[data_labels == 9] = 5
#sns.scatterplot(X_t_data[:,1], X_t_data[:,3], data_labels, palette="bright")

plt.subplot(211)
sns.scatterplot(X_t_data[:,1], X_t_data[:,3], test_data["Activity"], palette="bright")
#sns.scatterplot(X_t_data[:,1], X_t_data[:,3], hue=test_data["Activity"], palette="bright")
plt.title('DBSCAN Dataset with correct labels')

plt.subplot(212)
#sns.scatterplot(X_t_data[:,1], X_t_data[:,3], data_labels, palette="bright")
sns.scatterplot(X_t_data[:,1], X_t_data[:,3], data_labels, palette="bright")
plt.title('DBSCAN Dataset with predicted labels')

plt.show()
```



In [42]:
```
#Print clustering KPIs
label_opt = np.array(np.reshape(t_label,-1))
label_opt = np.array(np.reshape(label_opt,-1))
print('Estimated number of clusters: %d' % n_clusters_)
print('Estimated number of noise points: %d' % n_noise_)
print("Homogeneity: %0.3f" % metrics.homogeneity_score(label_opt, labels))
print("Completeness: %0.3f" % metrics.completeness_score(label_opt, labels))
print("V-measure: %0.3f" % metrics.v_measure_score(label_opt, labels))
print("Adjusted Rand Index: %0.3f" % metrics.adjusted_rand_score(label_opt, labels))
print("Adjusted Mutual Information: %0.3f" % metrics.adjusted_mutual_info_score(label_opt, la
print("Silhouette Coefficient: %0.3f" % metrics.silhouette_score(X_t_data, labels))
```

```
Estimated number of clusters: 5
Estimated number of noise points: 63
Homogeneity: 0.849
Completeness: 0.938
V-measure: 0.891
Adjusted Rand Index: 0.793
Adjusted Mutual Information: 0.891
Silhouette Coefficient: 0.825
```

In [43]:
```
#Model accuracy. Cluster assignment matching the original label. Test accuracy is very close
results1 = np.array(test_data["Activity"]) == data_labels
sum(bool(x) for x in results1)/len(data_labels)
```

Out[43]: 0.8048863250763488

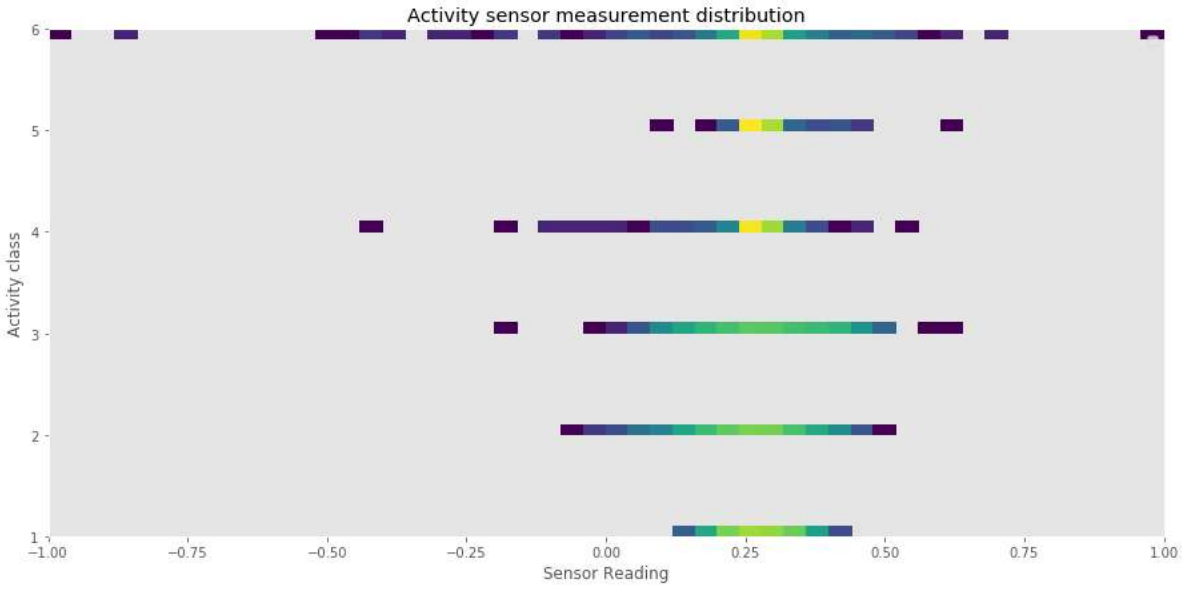
GMM clustering.

In [44]:
```
from sklearn.cluster import KMeans
from sklearn.mixture import GaussianMixture
from matplotlib import colors
```

In [45]:
```
#Let's check the data distribution. Follows normal distribution.
plt.hist2d(train_data['1 tBodyAcc-mean()-X'], train_data['Activity'],bins=(50,50), norm=color
plt.xlabel('Sensor Reading')
plt.ylabel('Activity class')
plt.title('Activity sensor measurement distribution')
plt.legend(loc='upper right')
```

```
No handles with labels found to put in legend.
```

Out[45]: <matplotlib.legend.Legend at 0x231b2587bc8>

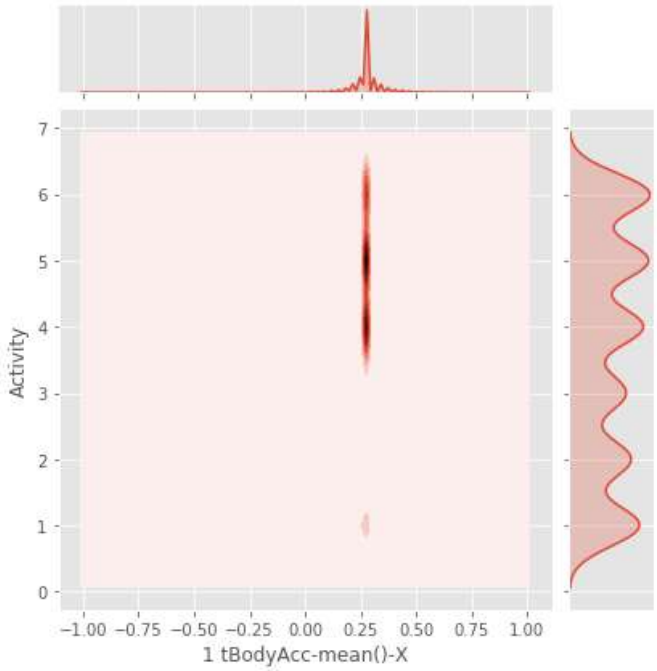


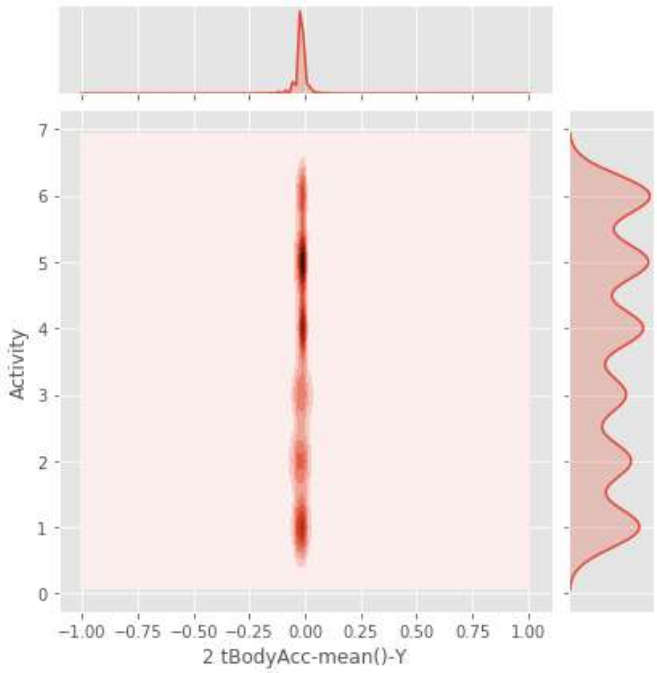
In [46]:

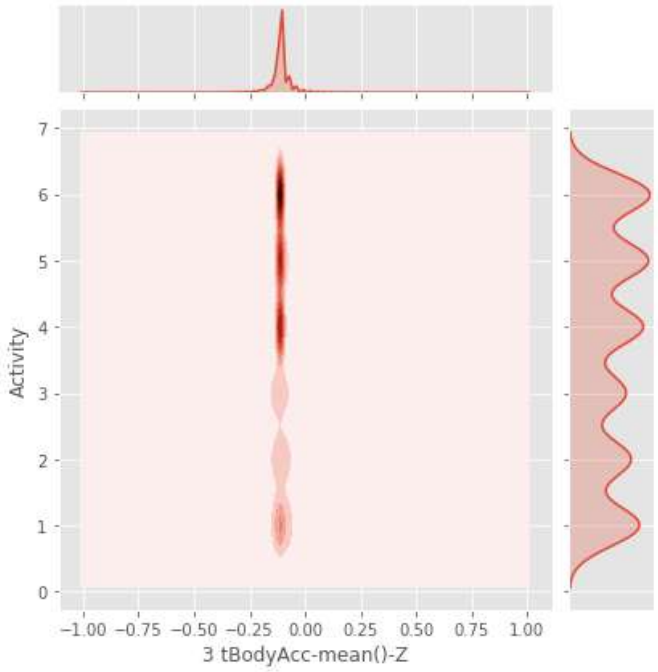
```
#Other way to check data distribution. As seen data follows normal distribution.
sns.jointplot(data=train_data, x="1 tBodyAcc-mean()-X", y="Activity", hue="Activity", kind="k
sns.jointplot(data=train_data, x="2 tBodyAcc-mean()-Y", y="Activity", hue="Activity", kind="k
sns.jointplot(data=train_data, x="3 tBodyAcc-mean()-Z", y="Activity", hue="Activity", kind="k
```

```
C:\Users\marpulli\Anaconda3\lib\site-packages\seaborn\distributions.py:437: UserWarning: The fol
lowing kwargs were not used by contour: 'hue'
  cset = contour_func(xx, yy, z, n_levels, **kwargs)
C:\Users\marpulli\Anaconda3\lib\site-packages\seaborn\distributions.py:437: UserWarning: The fol
lowing kwargs were not used by contour: 'hue'
  cset = contour_func(xx, yy, z, n_levels, **kwargs)
C:\Users\marpulli\Anaconda3\lib\site-packages\seaborn\distributions.py:437: UserWarning: The fol
lowing kwargs were not used by contour: 'hue'
  cset = contour_func(xx, yy, z, n_levels, **kwargs)
```

Out[46]: <seaborn.axisgrid.JointGrid at 0x231b25dce08>



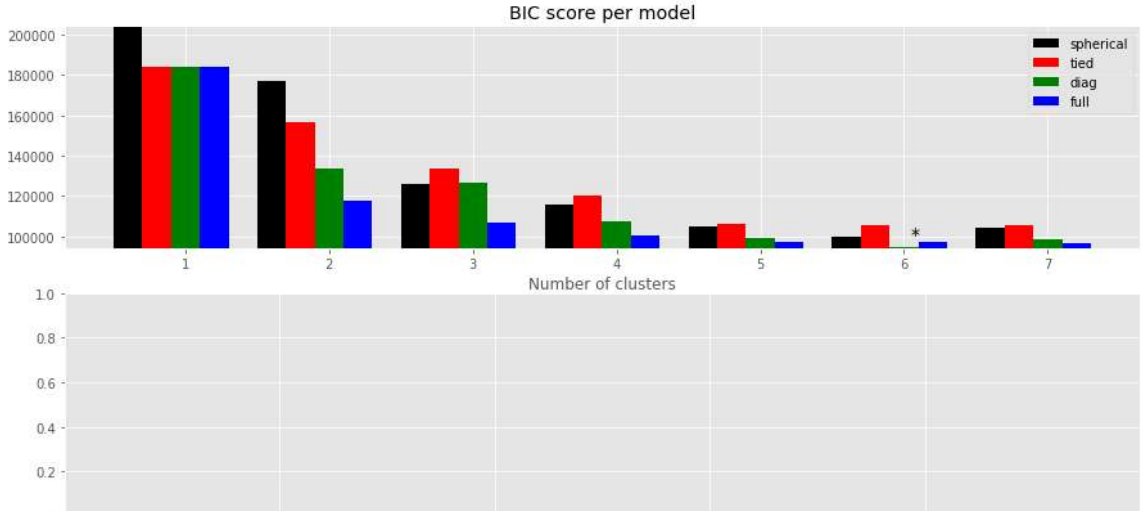



Activity
7
6
5
4
3
2
1
0
−1.00 −0.75 −0.50 −0.25 0.00 0.25 0.50 0.75 1.00
3 tBodyAcc-mean()-Z

In [48]:

```
#from scikit learn

print(__doc__)

import itertools
import matplotlib as mpl
from scipy import linalg
from sklearn import mixture

# Number of samples per component
n_samples = 400

# Generate random sample, two components
#np.random.seed(0)
#C = np.array([[0., -0.1], [1.7, .4]])
X = X_data

lowest_bic = np.infty
bic = []
n_components_range = range(1, 8)
cv_types = ['spherical', 'tied', 'diag', 'full']
for cv_type in cv_types:
    for n_components in n_components_range:
        # Fit a mixture of Gaussians with EM
        gmm = GaussianMixture(n_components=n_components, covariance_type=cv_type)
        gmm.fit(X)
        bic.append(gmm.bic(X))
        if bic[-1] < lowest_bic:
            lowest_bic = bic[-1]
            best_gmm = gmm

bic = np.array(bic)
color_iter = itertools.cycle(['k', 'r', 'g', 'b', 'c', 'm', 'y'])
clf = best_gmm
bars = []

# Plot the BIC scores
spl = plt.subplot(2, 1, 1)
for i, (cv_type, color) in enumerate(zip(cv_types, color_iter)):
    xpos = np.array(n_components_range) + .2 * (i - 2)
    bars.append(plt.bar(xpos, bic[i * len(n_components_range):
                                  (i + 1) * len(n_components_range)],
                        width=.2, color=color))
plt.xticks(n_components_range)
plt.ylim([bic.min() * 1.01 - .01 * bic.max(), bic.max()])
plt.title('BIC score per model')
xpos = np.mod(bic.argmin(), len(n_components_range)) + .65 +\
    .2 * np.floor(bic.argmin() / len(n_components_range))
plt.text(xpos, bic.min() * 0.97 + .03 * bic.max(), '*', fontsize=14)
spl.set_xlabel('Number of clusters')
spl.legend([b[0] for b in bars], cv_types)

# Plot the winner
splot = plt.subplot(2, 1, 2)
Y_ = clf.predict(X)
for i, (mean, covar, color) in enumerate(zip(clf.means_, clf.covariances_,
                                             color_iter)):
    v, w = linalg.eigh(covar)
    #print(v)
    #print(w)
    if not np.any(Y_ == i):
        continue
    plt.scatter(X[Y_ == i, 0], X[Y_ == i, 1], .8, color=color)

    # Plot an ellipse to show the Gaussian component
    angle = np.arctan2(w[0][1], w[0][0])
    angle = 180 * angle / np.pi  # convert to degrees
    v *= 4
    ell = mpl.patches.Ellipse(mean, v[0], v[1], 180 + angle, color=color)
    ell.set_clip_box(splot.bbox)
    ell.set_alpha(.5)
    splot.add_artist(ell)

#plt.xlim(-10, 10)
#plt.ylim(-3, 6)
#plt.xticks(())
```

```
#plt.yticks(())
plt.title('Selected GMM: full model, 6 components')
plt.subplots_adjust(hspace=.35, bottom=.02)
#plt.show()
```



In [49]:
```
#Create model and fit it.
gmm=GaussianMixture(n_components=6, covariance_type='full', max_iter = 600, random_state = 3)
gmm.fit(X_data, label)
```

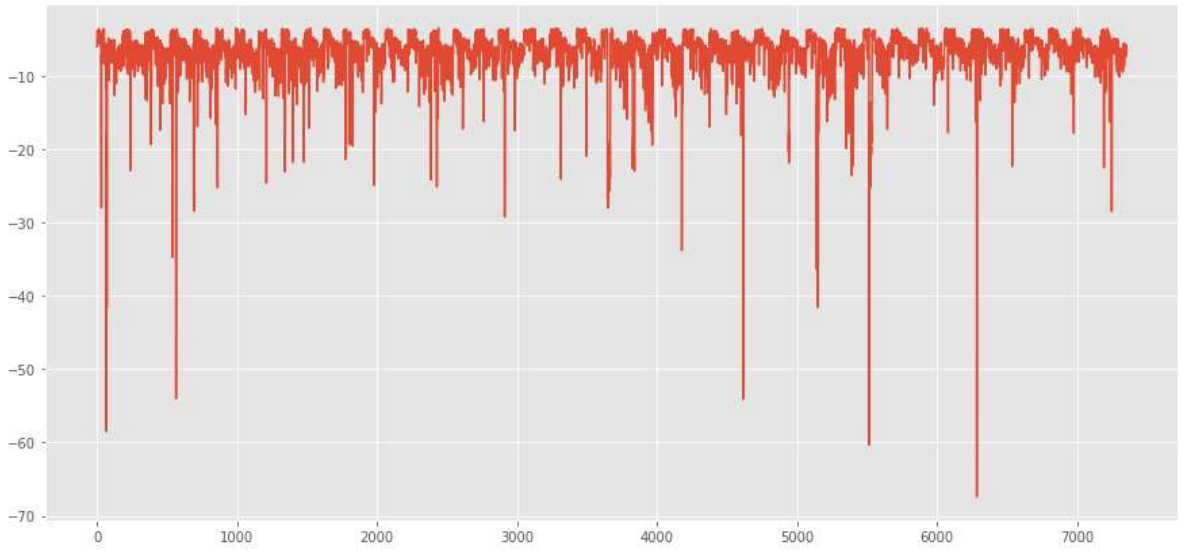
Out[49]:
```
GaussianMixture(covariance_type='full', init_params='kmeans', max_iter=600,
                means_init=None, n_components=6, n_init=1, precisions_init=None,
                random_state=3, reg_covar=1e-06, tol=0.001, verbose=0,
                verbose_interval=10, warm_start=False, weights_init=None)
```

In [50]:
```
#This is log-likelihood score. This does not have much meaning regarding the accuracy except
gmm.score(X_data)
```

Out[50]:
```
-6.550598356220418
```

In [51]:
```
#Make prediction. Graph is log likelihood.
predG=gmm.predict(X_data)
score_S = gmm.score_samples(X_data)
plt.plot(score_S)
```

Out[51]:
```
[<matplotlib.lines.Line2D at 0x231a97cbac8>]
```



In [ ]:

```
#Plot train clusters with given labels.
#sns.scatterplot(X_train[:,2], X_train[:,0], hue=predG, palette='bright')
fig, ax = plt.subplots()
sns.scatterplot(X_data[:,1], X_data[:,3], hue=train_data['Activity'], palette='bright')
#Zoom in to 3&5 border.
ax2 = plt.axes([0.12, -0.2, .3, .2], facecolor='lightgrey')
sns.scatterplot(X_data[:,2], X_data[:,0], hue=train_data['Activity'], palette='bright')
ax2.set_title('Zoom in clusters 3 & 5 border.')
ax2.set_xlim([6,7.75])
ax2.set_ylim([-20,-10])
ax2.legend(loc='upper right')
```

In [ ]:

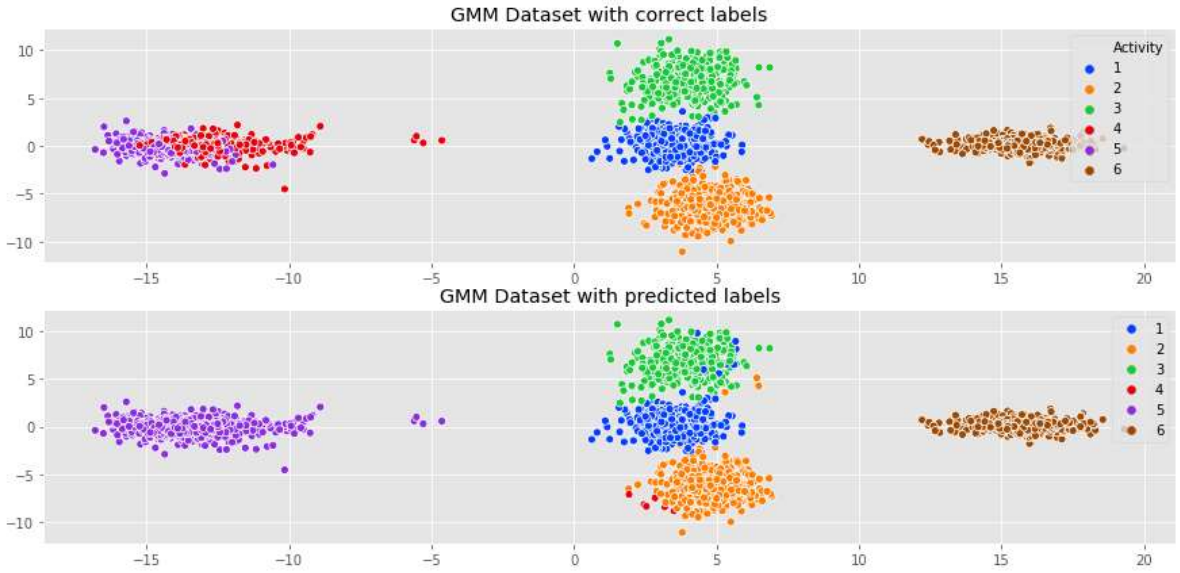
```
#Plot clusters with predicted labels.
#sns.scatterplot(X_train[:,2], X_train[:,0], hue=predG, palette='bright')
fig, ax = plt.subplots()
sns.scatterplot(X_data[:,1], X_data[:,3], hue=predG, palette='bright')
#Zoom in to 3&5 border.
ax2 = plt.axes([0.12, -0.2, .3, .2], facecolor='lightgrey')
sns.scatterplot(X_data[:,1], X_data[:,3], hue=predG, palette='bright')
ax2.set_title('Zoom in clusters 3 & 5 border.')
ax2.set_xlim([6,7.75])
ax2.set_ylim([-20,-10])
ax2.legend(loc='upper right')
```

In [ ]:

```
#Plot DBSCAN predicted clusters. Label '5' is outliers. Sitting and standing in same cluster
#Match the colors with original.
predG10=[]
predG10 = predG + 10
#Relabeling to match input data
data_labels = predG
data_labels[data_labels == 10] = 5
data_labels[data_labels == 11] = 2
data_labels[data_labels == 12] = 6
data_labels[data_labels == 13] = 3
data_labels[data_labels == 14] = 1
data_labels[data_labels == 15] = 4
#sns.scatterplot(X_data[:,1], X_data[:,3], data_labels, palette="bright")
```

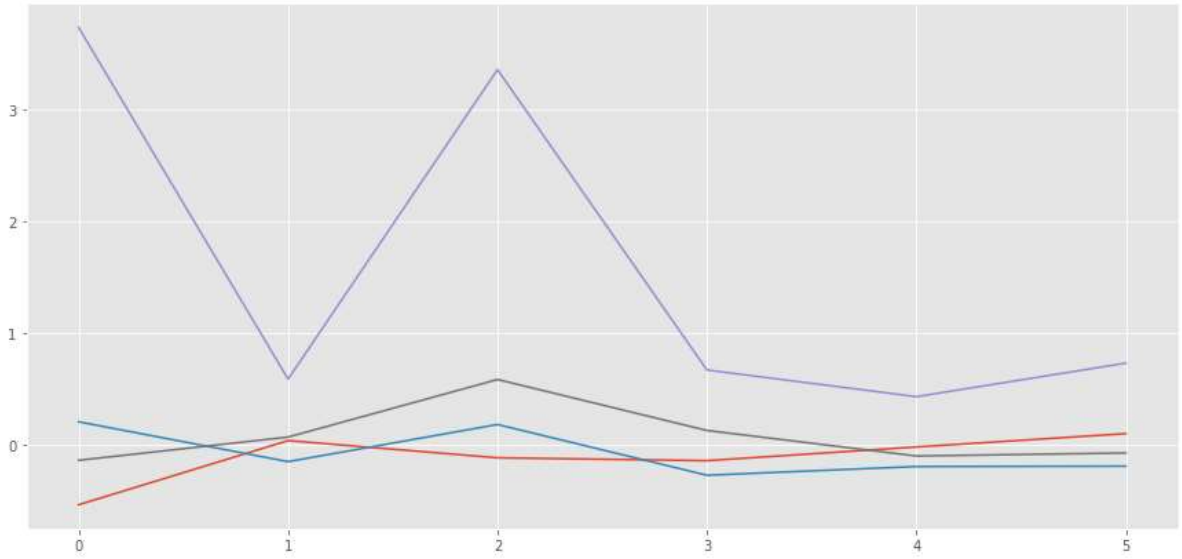
In [52]:

```
#Plot test data clusters and predicted data clusters.
gmm_pred = gmm.predict(X_t_data)

#Map cluster labels.
gmm_pred10 = []
gmm_pred10 = gmm_pred + 10
#Relabeling to match input data
data_labels = gmm_pred10
data_labels[data_labels == 10] = 5
data_labels[data_labels == 11] = 2
data_labels[data_labels == 12] = 6
data_labels[data_labels == 13] = 3
data_labels[data_labels == 14] = 1
data_labels[data_labels == 15] = 4

plt.subplot(211)
sns.scatterplot(X_t_data[:,1], X_t_data[:,3], test_data["Activity"], palette="bright")
plt.title('GMM Dataset with correct labels')

plt.subplot(212)
sns.scatterplot(X_t_data[:,1], X_t_data[:,3], data_labels, palette="bright")
plt.title('GMM Dataset with predicted labels')

plt.show()
```



In [53]:
```
#The precision matrices for each component in the mixture.  A precision matrix is the inverse
#Just one component shown.
plt.plot(gmm.precisions_[:,2])
```

Out[53]:
```
[<matplotlib.lines.Line2D at 0x231b126ac08>,
 <matplotlib.lines.Line2D at 0x231b7179e08>,
 <matplotlib.lines.Line2D at 0x231b119a808>,
 <matplotlib.lines.Line2D at 0x231b119ae48>]
```



In [54]:
```
#Accuracy of model. Cluster assignment matching the original label. True positives (TP).
results1 = np.array(test_data["Activity"]) == data_labels
sum(bool(x) for x in results1)/len(data_labels)
```

Out[54]:
```
0.8262639972853749
```