

## Import the necessary Libraries and dataset

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

```
In [2]: data = pd.read_csv("/content/drive/MyDrive/DSC 630/als_data.csv")
data.head()
```

```
Out[2]:   ID  Age_mean  Albumin_max  Albumin_median  Albumin_min  Albumin_range  ALSFRS_slope  ALSFRS_Total_max  ALSFRS_Total_median  ALSFRS_Total_min
0   1       65        57.0         40.5        38.0      0.066202     -0.965608          30            28.0            22
1   2       48        45.0         41.0        39.0      0.010453     -0.921717          37            33.0            21
2   3       38        50.0         47.0        45.0      0.008929     -0.914787          24            14.0            10
3   4       63        47.0         44.0        41.0      0.012111     -0.598361          30            29.0            24
4   5       63        47.0         45.5        42.0      0.008292     -0.444039          32            27.5            20
```

5 rows × 101 columns

```
In [3]: # Remove ID column
data = data.drop(['ID', 'SubjectID'], axis=1)
```

```
In [4]: # Check the structure of the data
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2223 entries, 0 to 2222
Data columns (total 99 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Age_mean         2223 non-null    int64  
 1   Albumin_max      2223 non-null    float64 
 2   Albumin_median   2223 non-null    float64 
 3   Albumin_min      2223 non-null    float64 
 4   Albumin_range    2223 non-null    float64 
 5   ALSFRS_slope     2223 non-null    float64 
 6   ALSFRS_Total_max 2223 non-null    int64  
 7   ALSFRS_Total_median 2223 non-null    float64 
 8   ALSFRS_Total_min 2223 non-null    int64  
 9   ALSFRS_Total_range 2223 non-null    float64 
 10  ALT.SGPT._max    2223 non-null    float64 
 11  ALT.SGPT._median 2223 non-null    float64 
 12  ALT.SGPT._min    2223 non-null    float64 
 13  ALT.SGPT._range  2223 non-null    float64 
 14  AST.SGOT._max    2223 non-null    int64  
 15  AST.SGOT._median 2223 non-null    float64 
 16  AST.SGOT._min    2223 non-null    float64 
 17  AST.SGOT._range  2223 non-null    float64 
 18  Bicarbonate_max   2223 non-null    float64 
 19  Bicarbonate_median 2223 non-null    float64 
 20  Bicarbonate_min   2223 non-null    float64 
 21  Bicarbonate_range 2223 non-null    float64 
 22  Blood.Urea.Nitrogen..BUN._max 2223 non-null    float64 
 23  Blood.Urea.Nitrogen..BUN._median 2223 non-null    float64 
 24  Blood.Urea.Nitrogen..BUN._min  2223 non-null    float64 
 25  Blood.Urea.Nitrogen..BUN._range 2223 non-null    float64 
 26  bp_diastolic_max  2223 non-null    int64  
 27  bp_diastolic_median 2223 non-null    float64 
 28  bp_diastolic_min   2223 non-null    int64  
 29  bp_diastolic_range 2223 non-null    float64 
 30  bp_systolic_max   2223 non-null    int64  
 31  bp_systolic_median 2223 non-null    float64 
 32  bp_systolic_min   2223 non-null    int64  
 33  bp_systolic_range 2223 non-null    float64 
 34  Calcium_max       2223 non-null    float64 
 35  Calcium_median    2223 non-null    float64 
 36  Calcium_min       2223 non-null    float64 
 37  Calcium_range     2223 non-null    float64 
 38  Chloride_max      2223 non-null    float64 
 39  Chloride_median   2223 non-null    float64 
 40  Chloride_min      2223 non-null    float64 
 41  Chloride_range    2223 non-null    float64 
 42  Creatinine_max    2223 non-null    float64 
 43  Creatinine_median 2223 non-null    float64 
 44  Creatinine_min    2223 non-null    float64 
 45  Creatinine_range   2223 non-null    float64 
 46  Gender_mean       2223 non-null    int64  
 47  Glucose_max       2223 non-null    float64 
 48  Glucose_median    2223 non-null    float64 
 49  Glucose_min       2223 non-null    float64 
 50  Glucose_range     2223 non-null    float64 
 51  hands_max         2223 non-null    int64  
 52  hands_median      2223 non-null    float64 
 53  hands_min         2223 non-null    int64  
 54  hands_range        2223 non-null    float64 
 55  Hematocrit_max    2223 non-null    float64 
 56  Hematocrit_median 2223 non-null    float64 
 57  Hematocrit_min    2223 non-null    float64 
 58  Hematocrit_range   2223 non-null    float64 
 59  Hemoglobin_max    2223 non-null    float64 
 60  Hemoglobin_median 2223 non-null    float64 
 61  Hemoglobin_min    2223 non-null    float64 
 62  Hemoglobin_range   2223 non-null    float64 
 63  leg_max           2223 non-null    int64  
 64  leg_median         2223 non-null    float64 
 65  leg_min           2223 non-null    int64  
 66  leg_range          2223 non-null    float64
```

```

67 mouth_max                2223 non-null    int64
68 mouth_median              2223 non-null    float64
69 mouth_min                 2223 non-null    int64
70 mouth_range                2223 non-null    float64
71 onset_delta_mean           2223 non-null    int64
72 onset_site_mean            2223 non-null    int64
73 Platelets_max              2223 non-null    int64
74 Platelets_median           2223 non-null    float64
75 Platelets_min              2223 non-null    float64
76 Potassium_max              2223 non-null    float64
77 Potassium_median           2223 non-null    float64
78 Potassium_min              2223 non-null    float64
79 Potassium_range             2223 non-null    float64
80 pulse_max                  2223 non-null    int64
81 pulse_median               2223 non-null    float64
82 pulse_min                  2223 non-null    int64
83 pulse_range                 2223 non-null    float64
84 respiratory_max             2223 non-null    int64
85 respiratory_median          2223 non-null    float64
86 respiratory_min             2223 non-null    int64
87 respiratory_range            2223 non-null    float64
88 Sodium_max                  2223 non-null    float64
89 Sodium_median               2223 non-null    float64
90 Sodium_min                  2223 non-null    float64
91 Sodium_range                 2223 non-null    float64
92 trunk_max                  2223 non-null    int64
93 trunk_median                2223 non-null    float64
94 trunk_min                   2223 non-null    int64
95 trunk_range                  2223 non-null    float64
96 Urine.Ph_max                2223 non-null    float64
97 Urine.Ph_median              2223 non-null    float64
98 Urine.Ph_min                 2223 non-null    float64
dtypes: float64(75), int64(24)
memory usage: 1.7 MB

```

The dataset contains 98 columns. We'll adopt randomforest regression for feature selection. From the literature, ALS condition is measured by ALSFRS\_slope.

```
In [5]: # import random forest Libraries

from sklearn.ensemble import RandomForestRegressor
from sklearn.feature_selection import SelectFromModel
```

```
In [6]: # Create the features

X = data.drop('ALSFRLS_slope',axis=1)
y = data['ALSFRLS_slope']
```

```
In [7]: # Create a randomforest regressor

clf = RandomForestRegressor(n_estimators=200,random_state=0,n_jobs=-1)

clf.fit(X,y)

# print the name of and gini importance of each feature

for feature in zip(X.columns,clf.feature_importances_):
    print(feature)
```

```
('Age_mean', 0.0037744688668357403)
('Albumin_max', 0.0019376217608390053)
('Albumin_median', 0.0018192338239591958)
('Albumin_min', 0.0017183887255982123)
('Albumin_range', 0.005264135674859937)
('ALSFRLS_Total_max', 0.0020532032092087688)
('ALSFRLS_Total_median', 0.010889015881257025)
('ALSFRLS_Total_min', 0.0033366382923384922)
('ALSFRLS_Total_range', 0.6939651837415662)
('ALT.SGPT._max', 0.00295319904925661)
('ALT.SGPT._median', 0.0036660291425108862)
('ALT.SGPT._min', 0.003139578367509986)
('ALT.SGPT._range', 0.004751087090298099)
('AST.SGOT._max', 0.002432724048575397)
('AST.SGOT._median', 0.0032721341619729536)
('AST.SGOT._min', 0.002124354823806451)
('AST.SGOT._range', 0.0037533735963918334)
('Bicarbonate_max', 0.0021510402231933907)
('Bicarbonate_median', 0.0027435407955361552)
('Bicarbonate_min', 0.0021067745505395446)
('Bicarbonate_range', 0.0047492099309716556)
('Blood.Urea.Nitrogen..BUN._max', 0.0026961113635823705)
('Blood.Urea.Nitrogen..BUN._median', 0.0032930035472456976)
('Blood.Urea.Nitrogen..BUN._min', 0.0028739993049752555)
('Blood.Urea.Nitrogen..BUN._range', 0.0039664344459234505)
('bp_diastolic_max', 0.0023420990149761395)
('bp_diastolic_median', 0.002726738577044919)
('bp_diastolic_min', 0.0029040783062228683)
('bp_diastolic_range', 0.006009549936135036)
('bp_systolic_max', 0.003281655547487151)
('bp_systolic_median', 0.003194279148484597)
('bp_systolic_min', 0.0016222291502942263)
('bp_systolic_range', 0.004546157460037492)
('Calcium_max', 0.003842454772770578)
('Calcium_median', 0.003832219913324575)
('Calcium_min', 0.004523704904076454)
('Calcium_range', 0.00755071113843114)
('Chloride_max', 0.002122242028121051)
('Chloride_median', 0.003126319569869943)
('Chloride_min', 0.0017390666810308728)
('Chloride_range', 0.00403117069097829)
('Creatinine_max', 0.004362647198038211)
('Creatinine_median', 0.001998213919830301)
('Creatinine_min', 0.002220724330725083)
('Creatinine_range', 0.003438747016236064)
('Gender_mean', 0.00017071045460614168)
('Glucose_max', 0.0027822005158054373)
('Glucose_median', 0.003835075427164478)
```

```
('Glucose_min', 0.0035936180224792136)
('Glucose_range', 0.0038133557410437568)
('hands_max', 0.0016508444766616486)
('hands_median', 0.003182895023346062)
('hands_min', 0.0009487691704029239)
('hands_range', 0.011313916283717002)
('Hematocrit_max', 0.004334419483766233)
('Hematocrit_median', 0.0024247411754134128)
('Hematocrit_min', 0.002364624207826169)
('Hematocrit_range', 0.002971208103657695)
('Hemoglobin_max', 0.003178924398053193)
('Hemoglobin_median', 0.0024527039269567202)
('Hemoglobin_min', 0.0024706885719664087)
('Hemoglobin_range', 0.003699016311182744)
('leg_max', 0.0007491980978650781)
('leg_median', 0.003994358323156322)
('leg_min', 0.0010704859743531627)
('leg_range', 0.005827842783422995)
('mouth_max', 0.0011821914670597994)
('mouth_median', 0.002699246434720386)
('mouth_min', 0.0015252558183068863)
('mouth_range', 0.009582535505828122)
('onset_delta_mean', 0.005944568629152332)
('onset_site_mean', 0.0003483322355555323)
('Platelets_max', 0.0032408888378353726)
('Platelets_median', 0.0030886501705636882)
('Platelets_min', 0.0029510453373391738)
('Potassium_max', 0.0022071866642747683)
('Potassium_median', 0.0032916545719424892)
('Potassium_min', 0.001884817224567828)
('Potassium_range', 0.004468731566231369)
('pulse_max', 0.0023282463562429375)
('pulse_median', 0.0035788196596888665)
('pulse_min', 0.0020645805877248903)
('pulse_range', 0.003644296754251333)
('respiratory_max', 0.00014079330156300239)
('respiratory_median', 0.0010243732421574847)
('respiratory_min', 0.0010046476800021657)
('respiratory_range', 0.010141287509838174)
('Sodium_max', 0.001824542348036824)
('Sodium_median', 0.0014565683457035544)
('Sodium_min', 0.0015975117448724337)
('Sodium_range', 0.003863864564495714)
('trunk_max', 0.0012038502370728525)
('trunk_median', 0.0038080348142703235)
('trunk_min', 0.0011710330365869936)
('trunk_range', 0.005156980371164798)
('Urine.Ph_max', 0.0011348931662468827)
('Urine.Ph_median', 0.001330407814205934)
('Urine.Ph_min', 0.00023876141966601707)
```

In [8]: # Identify and select the most important features

```
sfm = SelectFromModel(clf, threshold=0.0035)
sfm.fit(X,y)
```

Out[8]: SelectFromModel(estimator=RandomForestRegressor(n\_estimators=200, n\_jobs=-1, random\_state=0), threshold=0.0035)

In [9]: for feature\_list in sfm.get\_support(indices=True):
 feat\_names = X.columns[feature\_list]
 print(feat\_names)

```
Age_mean
Albumin_range
ALFRS_Total_median
ALFRS_Total_range
ALT.SGPT._median
ALT.SGPT._range
AST.SGOT._range
Bicarbonate_range
Blood.Urea.Nitrogen..BUN._range
bp_diastolic_range
bp_systolic_range
Calcium_max
Calcium_median
Calcium_min
Calcium_range
Chloride_range
Creatinine_max
Glucose_median
Glucose_min
Glucose_range
hands_range
Hematocrit_max
Hemoglobin_range
leg_median
leg_range
mouth_range
onset_delta_mean
Potassium_range
pulse_median
pulse_range
respiratory_range
Sodium_range
trunk_median
trunk_range
```

We have reduced 98 features to 33 most important features. Clustering will be done with these features.

## Create a dataframe of important features

In [10]:

```
df = data[['Age_mean','Albumin_range','ALFRS_Total_median','ALFRS_Total_range','ALT.SGPT._median','ALT.SGPT._range','AST.SGOT._range',
           'Bicarbonate_range','Blood.Urea.Nitrogen..BUN._range','bp_diastolic_range','bp_systolic_range','Calcium_max','Calcium_median',
           'Calcium_min','Calcium_range','Chloride_range','Creatinine_max','Glucose_median','Glucose_min','Glucose_range','hands_range',
           'Hemoglobin_range','leg_median','leg_range','mouth_range','onset_delta_mean','Potassium_range','pulse_median','pulse_range',
           'Sodium_range','trunk_median','trunk_range']]
```

```
In [11]: df.head()
```

```
Out[11]:   Age_mean  Albumin_range  ALSFRS_Total_median  ALSFRS_Total_range  ALT.SGPT._median  ALT.SGPT._range  AST.SGOT._range  Bicarbonate_range  Blood.Ure
0         65      0.066202          28.0        0.021164          22.0       0.020906       0.027875      0.017422
1         48      0.010453          33.0        0.028725          13.0       0.029617       0.029617      0.012195
2         38      0.008929          14.0        0.025000          20.0       0.019643       0.010714      0.019643
3         63      0.012111          29.0        0.014963          60.0       0.052369       0.032419      0.007481
4         63      0.008292          27.5        0.020374          26.5       0.026534       0.024876      0.014925
```

5 rows × 34 columns

```
In [12]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2223 entries, 0 to 2222
Data columns (total 34 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Age_mean         2223 non-null    int64  
 1   Albumin_range    2223 non-null    float64 
 2   ALSFRS_Total_median 2223 non-null    float64 
 3   ALSFRS_Total_range 2223 non-null    float64 
 4   ALT.SGPT._median 2223 non-null    float64 
 5   ALT.SGPT._range   2223 non-null    float64 
 6   AST.SGOT._range   2223 non-null    float64 
 7   Bicarbonate_range 2223 non-null    float64 
 8   Blood.Urea.Nitrogen..BUN._range 2223 non-null    float64 
 9   bp_diastolic_range 2223 non-null    float64 
 10  bp_systolic_range 2223 non-null    float64 
 11  Calcium_max      2223 non-null    float64 
 12  Calcium_median    2223 non-null    float64 
 13  Calcium_min      2223 non-null    float64 
 14  Calcium_range     2223 non-null    float64 
 15  Chloride_range    2223 non-null    float64 
 16  Creatinine_max    2223 non-null    float64 
 17  Glucose_median    2223 non-null    float64 
 18  Glucose_min      2223 non-null    float64 
 19  Glucose_range     2223 non-null    float64 
 20  hands_range       2223 non-null    float64 
 21  Hematocrit_max    2223 non-null    float64 
 22  Hemoglobin_range  2223 non-null    float64 
 23  leg_median        2223 non-null    float64 
 24  leg_range         2223 non-null    float64 
 25  mouth_range       2223 non-null    float64 
 26  onset_delta_mean  2223 non-null    int64  
 27  Potassium_range   2223 non-null    float64 
 28  pulse_median      2223 non-null    float64 
 29  pulse_range       2223 non-null    float64 
 30  respiratory_range 2223 non-null    float64 
 31  Sodium_range      2223 non-null    float64 
 32  trunk_median      2223 non-null    float64 
 33  trunk_range       2223 non-null    float64 
dtypes: float64(32), int64(2)
memory usage: 590.6 KB
```

## Apply a Standard Scalar to the data

```
In [13]: from sklearn.preprocessing import MinMaxScaler
from sklearn import cluster
from sklearn import metrics
```

```
In [14]: cols = df.columns
ms = MinMaxScaler()
df = ms.fit_transform(df)
```

```
In [15]: df = pd.DataFrame(df,columns=cols)
df.head()
```

```
Out[15]:   Age_mean  Albumin_range  ALSFRS_Total_median  ALSFRS_Total_range  ALT.SGPT._median  ALT.SGPT._range  AST.SGOT._range  Bicarbonate_range  Blood.Ure
0         0.746032      0.271429          0.680000          0.179894          0.075676       0.007629       0.014543      0.081301
1         0.476190      0.042857          0.813333          0.244165          0.027027       0.011288       0.015452      0.056911
2         0.317460      0.036607          0.306667          0.212500          0.064865       0.007098       0.005590      0.091667
3         0.714286      0.049656          0.706667          0.127182          0.281081       0.020846       0.016914      0.034913
4         0.714286      0.033997          0.666667          0.173175          0.100000       0.009993       0.012979      0.069652
```

5 rows × 34 columns

## Create a Plot the cluster Silhouette score versus the number of clusters in a K-means cluster

```
In [16]: krange = list(range(2,11))
avg_silhouettes = []
for n in krange:
    model = cluster.KMeans(n_clusters=n, random_state=10)
    cluster_assignments = model.fit_predict(df)
    silhouette_avg = metrics.silhouette_score(df, cluster_assignments)
    avg_silhouettes.append(silhouette_avg)
```

/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al

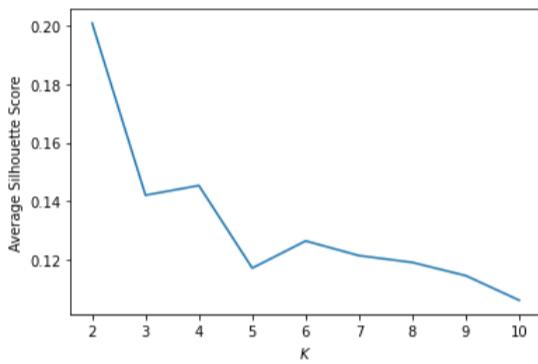
```

1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,

```

## Plot the result of krangle against avg\_silhouette

```
In [17]: plt.plot(krange,avg_silhouettes)
plt.xlabel("$K$")
plt.ylabel("Average Silhouette Score")
plt.show()
```



The above plot seem to suggest k = 2. since the highest average silhouette score was at its highest (0.20) when k =2.

## Fit a K-means model to the data with k = 2

```
In [19]: from sklearn.cluster import KMeans
km_2 = KMeans(n_clusters=2,random_state=42)
km_2.fit(df)

/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
```

```
Out[19]: KMeans(n_clusters=2, random_state=42)
```

```
In [27]: df['cluster'] = km_2.labels_
km2 = pd.DataFrame(km_2.labels_,columns=['cluster'])
km2.head()
```

```
Out[27]: cluster
0    0
1    0
2    1
3    0
4    1
```

## Fitting a PCA

```
In [24]: from sklearn.decomposition import PCA
```

```
In [30]: pca = PCA(n_components=2).fit(df)
pca_trans = pca.transform(df)
pca_trans_df = pd.DataFrame(pca_trans,columns=['pca1','pca2'])

# concatenate km2 with pca_trans_df

km2 = pd.concat([km2,pca_trans_df],axis=1)
km2.head()
```

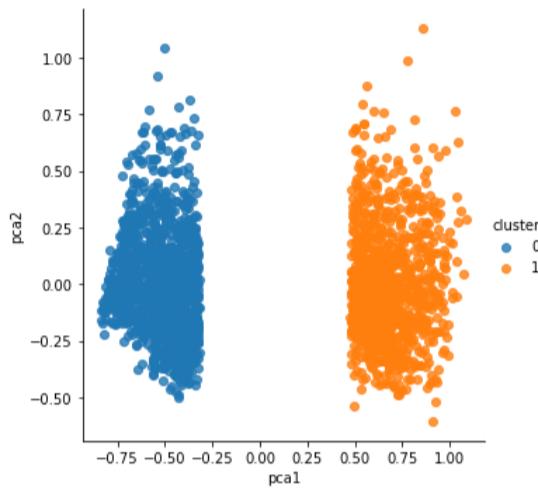
```
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:1692: FutureWarning: Feature names only support names that are al
1 strings. Got feature names with dtypes: ['tuple']. An error will be raised in 1.2.
  FutureWarning,
```

```
Out[30]: cluster    pca1    pca2
```

	cluster	pca1	pca2
0	0	-0.560863	0.162707
1	0	-0.646207	0.207739
2	1	0.820034	-0.100761
3	0	-0.382765	-0.217366
4	1	0.576030	-0.288326

## Plot the PCA

```
In [31]: fig = sns.lmplot(x='pca1',y='pca2',data=km2,hue='cluster',fit_reg=False)
plt.show()
```



## Summary of Results

This project utilized the Silhouette chart to select the number of optimal clusters in our dataframe. The dataframe consists of 101 features but 30 of the features were selected based on random forest regressor selection method with a threshold of 0.003.

Using the PCA to compress the dimension of the data, 2 clear groups were observed from the PCA visualization.

```
In [ ]:
```