Análisis de Datos y Aprendizaje Máquina con Tensorflow 2.0: Clustering y reducción de dimensionalidad

2019/09/30

1 K-means

Objetivo: Entender el concepto de clustering y aplicarlo en un dataset.

- Documentación: https://scikit-learn.org/stable/modules/clustering.html#k-means

K-means es un método de agrupamiento, cada observación pertenece al grupo donde la distancia a la media es menor, el objetivo es asignar un conjunto de n observaciones a k grupos, esto también es conocido como aprendizaje no supervisado.

- **Inicialización**
  - elegir k posiciones aleatorias
  - asignar los centroides $C = \{c_1, \ldots, c_k\}$ a esas posiciones
- **Iteraración**
  - asignar cada x_i al cluster que tenga la distancia mínima

$$\min_{c_k \in C} ||x_i - c_k||^2 \tag{1}$$

  - actualizar centroides, moviando el centroide a la media de los puntos del cluster, donde n_k es el número de elementos en el cluster k :

$$c_k = \frac{1}{n_k} \sum_{i=1}^{n_k} x_i \tag{2}$$

  - hasta que exista convergencia

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

```
In [2]: df = pd.read_csv('iris.csv')
        df.head(10)
```

Out[2]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.1	3.5	1.4	0.2	setosa
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa
5	5.4	3.9	1.7	0.4	setosa
6	4.6	3.4	1.4	0.3	setosa
7	5.0	3.4	1.5	0.2	setosa
8	4.4	2.9	1.4	0.2	setosa
9	4.9	3.1	1.5	0.1	setosa

```
In [3]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
sepal_length    150 non-null float64
sepal_width     150 non-null float64
petal_length    150 non-null float64
petal_width     150 non-null float64
species         150 non-null object
dtypes: float64(4), object(1)
memory usage: 6.0+ KB
```

```
In [4]: df = df.replace({'setosa':0, 'virginica':1, 'versicolor':2})
        df.tail()
```

Out[4]:

	sepal_length	sepal_width	petal_length	petal_width	species
145	6.7	3.0	5.2	2.3	1
146	6.3	2.5	5.0	1.9	1
147	6.5	3.0	5.2	2.0	1
148	6.2	3.4	5.4	2.3	1
149	5.9	3.0	5.1	1.8	1

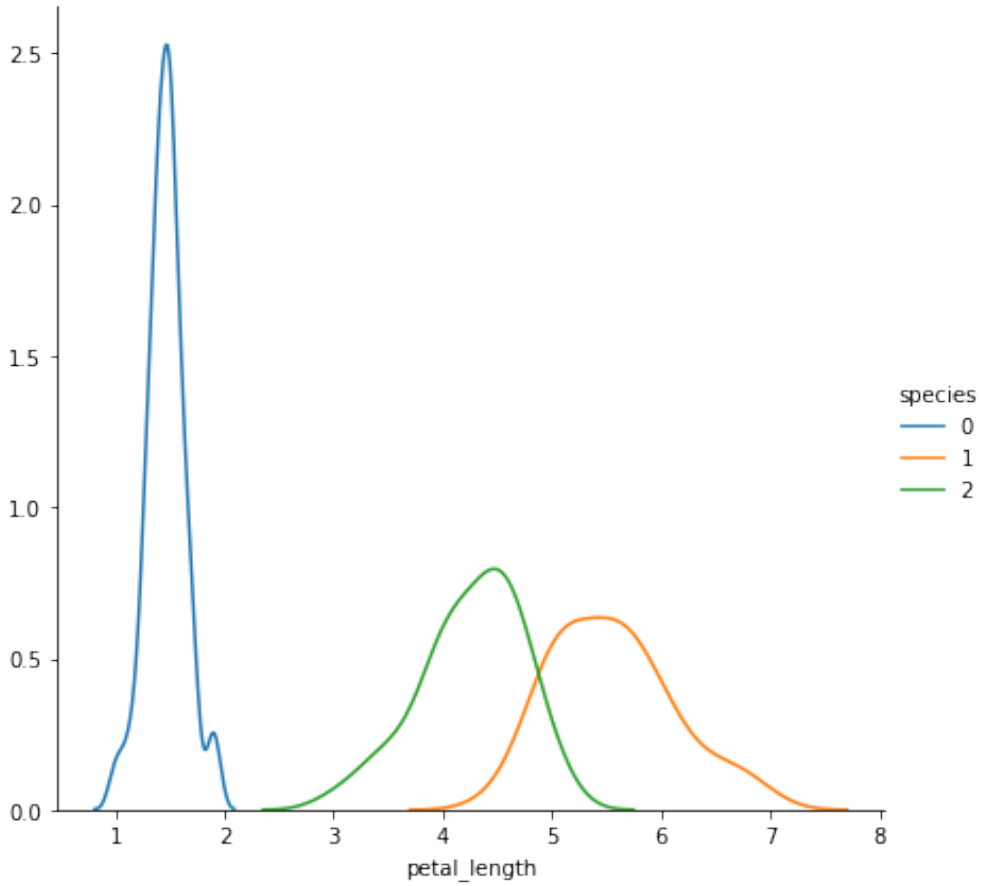
```
In [5]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
sepal_length    150 non-null float64
sepal_width     150 non-null float64
petal_length    150 non-null float64
petal_width     150 non-null float64
species         150 non-null int64
dtypes: float64(4), int64(1)
memory usage: 6.0 KB
```

1.1 Viisualizar separación de clases por variables

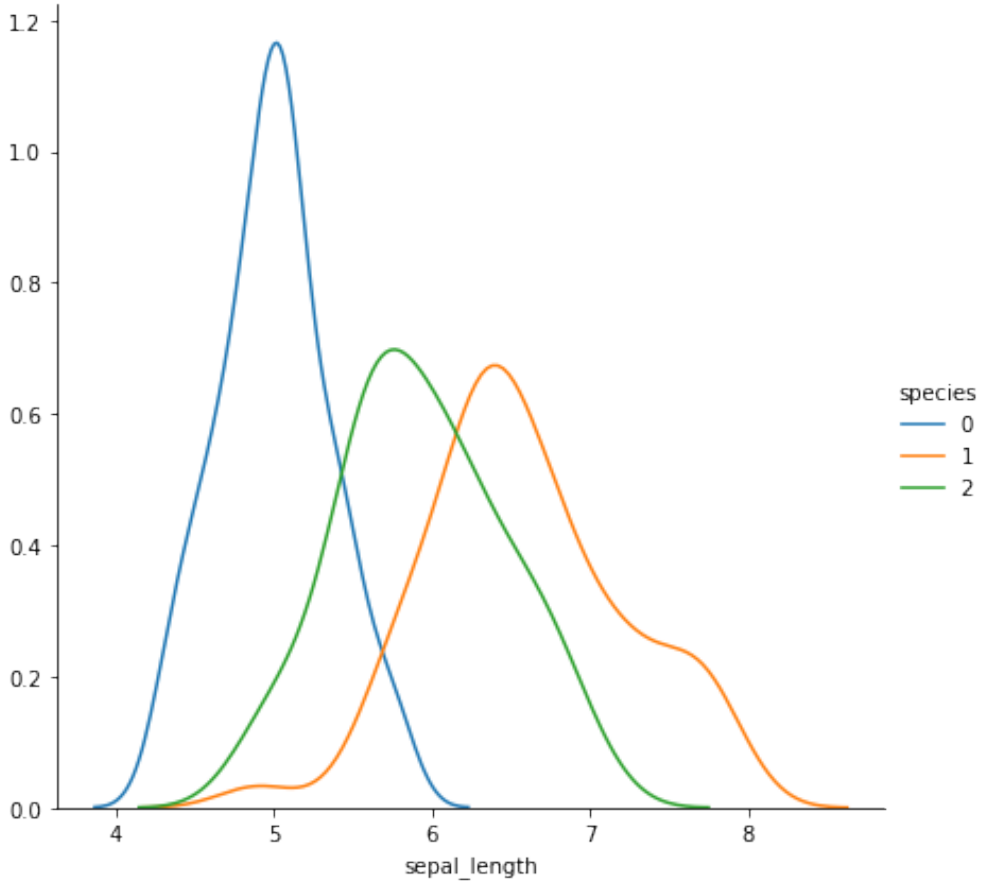
```
In [6]: sns.FacetGrid(df, hue="species", height=6) \
            .map(sns.kdeplot, "petal_length") \
            .add_legend()
```

```
Out[6]: <seaborn.axisgrid.FacetGrid at 0x7fc4db7c9b10>
```



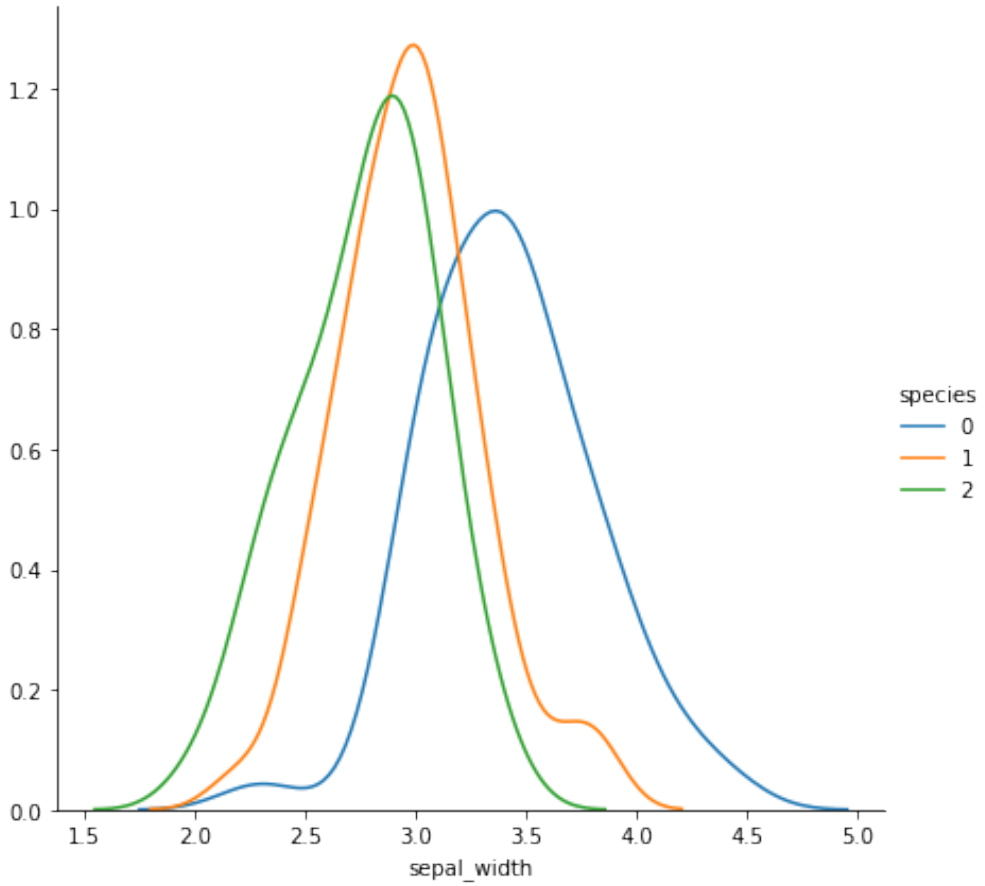

```
In [7]: sns.FacetGrid(df, hue="species", height=6) \
            .map(sns.kdeplot, "sepal_length") \
            .add_legend()
```

```
Out[7]: <seaborn.axisgrid.FacetGrid at 0x7fc4db4c2290>
```



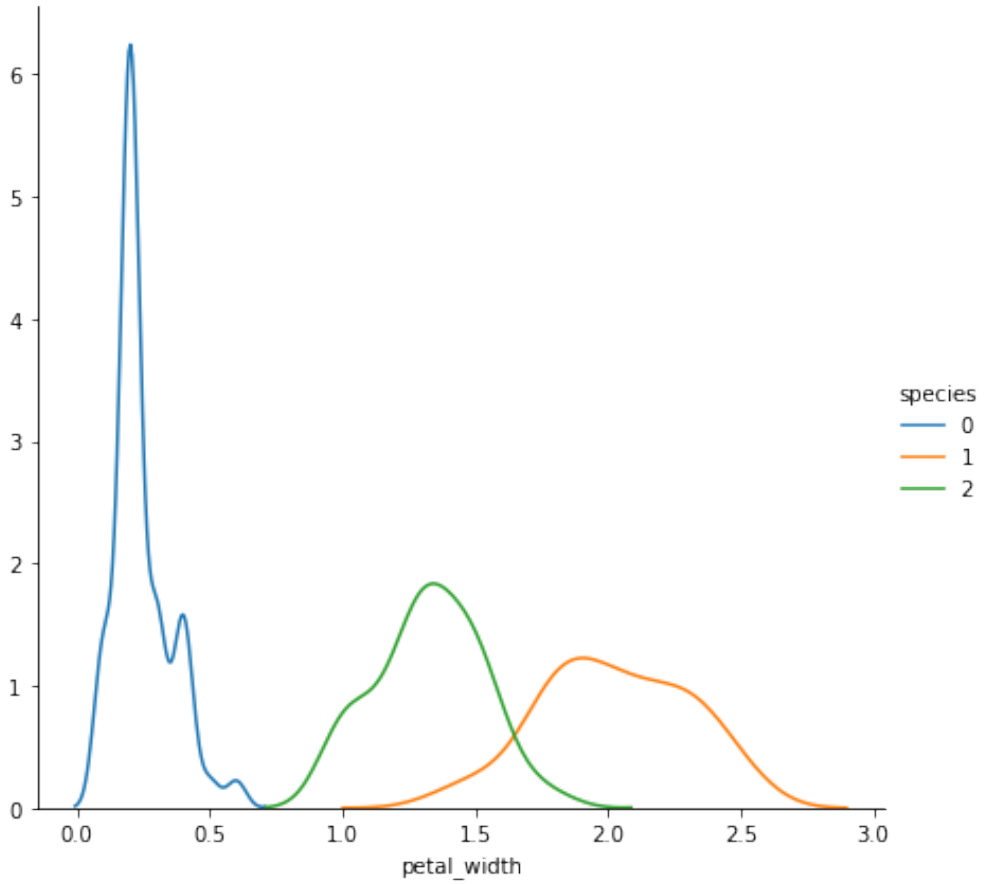

```
In [8]: sns.FacetGrid(df, hue="species", height=6) \
            .map(sns.kdeplot, "sepal_width") \
            .add_legend()
```

```
Out[8]: <seaborn.axisgrid.FacetGrid at 0x7fc4db398250>
```




```
In [9]: sns.FacetGrid(df, hue="species", height=6) \
            .map(sns.kdeplot, "petal_width") \
            .add_legend()
```

```
Out[9]: <seaborn.axisgrid.FacetGrid at 0x7fc4db36ecd0>
```



1.2 K Means

- Se asigna el parámetro 'K' que indica el número de clusters. También se puede asignar el número de iteraciones

```
In [10]: from sklearn.cluster import KMeans

In [11]: kmeans = KMeans(n_clusters=3,verbose=0,tol=1e-3,max_iter=300,n_init=20,random_state=14)

In [12]: kmeans.fit(df.drop('species',axis=1))

Out[12]: KMeans(algorithm='auto', copy_x=True, init='k-means++', max_iter=300,
                n_clusters=3, n_init=20, n_jobs=None, precompute_distances='auto',
                random_state=14, tol=0.001, verbose=0)

In [13]: clus_cent=kmeans.cluster_centers_
         clus_cent
```

```
Out[13]: array([[6.85      , 3.07368421, 5.74210526, 2.07105263],
                [5.006     , 3.418     , 1.464     , 0.244     ],
                [5.9016129 , 2.7483871 , 4.39354839, 1.43387097]])
```

```
In [14]: print(kmeans.labels_)
```

```
[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 1 1 1 1 1 1 1 1 1 1 1 1 2 2 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 2 2 2 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 0 2 0 0 0 0 2 0 0 0 0
 0 0 2 2 0 0 0 0 2 0 2 0 2 0 0 2 2 0 0 0 0 0 2 0 0 0 0 2 0 0 0 0 2 0 0 0 2 0
 0 2]
```

```
In [15]: df['species'].values
```

```
Out[15]: array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
                2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
                2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1])
```

1.2.1 Adaptar para 'kmeans.labels_'

```
In [16]: labels = df.replace({0:1, 1:0})
         labels.species.values
```

```
Out[16]: array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
                1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
                2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
                2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0])
```

1.3 Comportamiento de etiquetas 'K-means'

- Se obtienen las predicciones, informe de clasificación y matriz de confusión.

```
In [17]: from sklearn.metrics import classification_report,confusion_matrix
         print("Predicciones:\n")
         print(kmeans.labels_)
         print("\nReporte de clasificación:\n")
         print(classification_report(kmeans.labels_,labels.species.values))
```

```
Predicciones:

[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 1 1 1 1 1 1 1 1 1 1 1 1 2 2 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 2 2 2 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 0 2 0 0 0 0 2 0 0 0 0
```

```
 0 0 2 2 0 0 0 0 2 0 2 0 2 0 0 2 2 0 0 0 0 0 2 0 0 0 0 2 0 0 0 2 0 0 0 2 0
 0 2]

Reporte de clasificación:

              precision    recall  f1-score   support

           0       0.72      0.95      0.82        38
           1       1.00      1.00      1.00        50
           2       0.96      0.77      0.86        62

    accuracy                           0.89       150
   macro avg       0.89      0.91      0.89       150
weighted avg       0.91      0.89      0.89       150
```

```
In [18]: print("Confusion matrix")
         confusion_matrix(kmeans.labels_,labels.species.values)
```

```
Confusion matrix
```

```
Out[18]: array([[36,  0,  2],
                [ 0, 50,  0],
                [14,  0, 48]])
```

1.4 Utilizando PCA para visualizar la clasificación de K-means

```
In [19]: from sklearn.decomposition import PCA
         pca = PCA(n_components=2).fit(df.drop('species',axis=1))
         y = kmeans.labels_
         X_pca = pca.transform(df.drop('species',axis=1))
         clus_cent=kmeans.cluster_centers_
         cent = pca.transform(clus_cent)
```

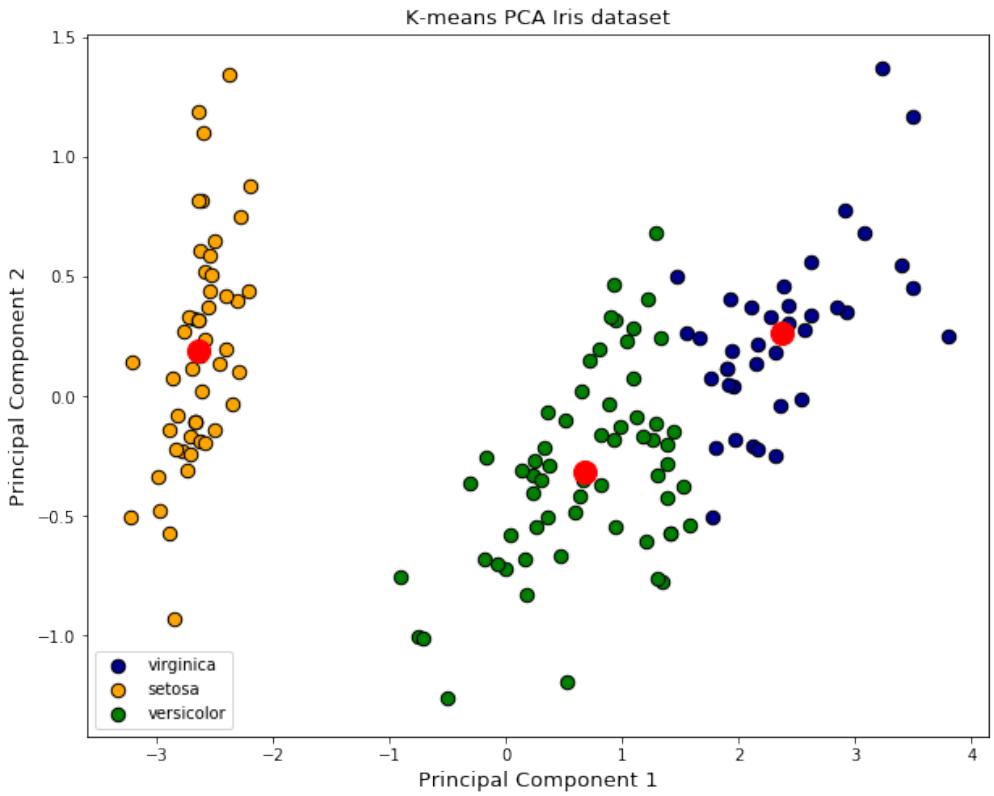
1.5 Ploteando centroides

```
In [20]: plt.figure(figsize=(10,6))
         target_ids = np.unique(df.values[:,-1])
         colors = ['darkblue','orange','green']
         target_names = ['virginica', 'setosa','versicolor']


         plt.figure(figsize=(10,8))
         for i, c, label in zip(target_ids, colors, target_names):
             plt.scatter(X_pca[i == y,0], X_pca[i == y,1], c = c,  edgecolors='black', s=285,labe
         plt.legend()
         plt.scatter(cent[:,0], cent[:,1], s=200, color = 'red')
         plt.title("K-means PCA Iris dataset",fontsize=13)
```

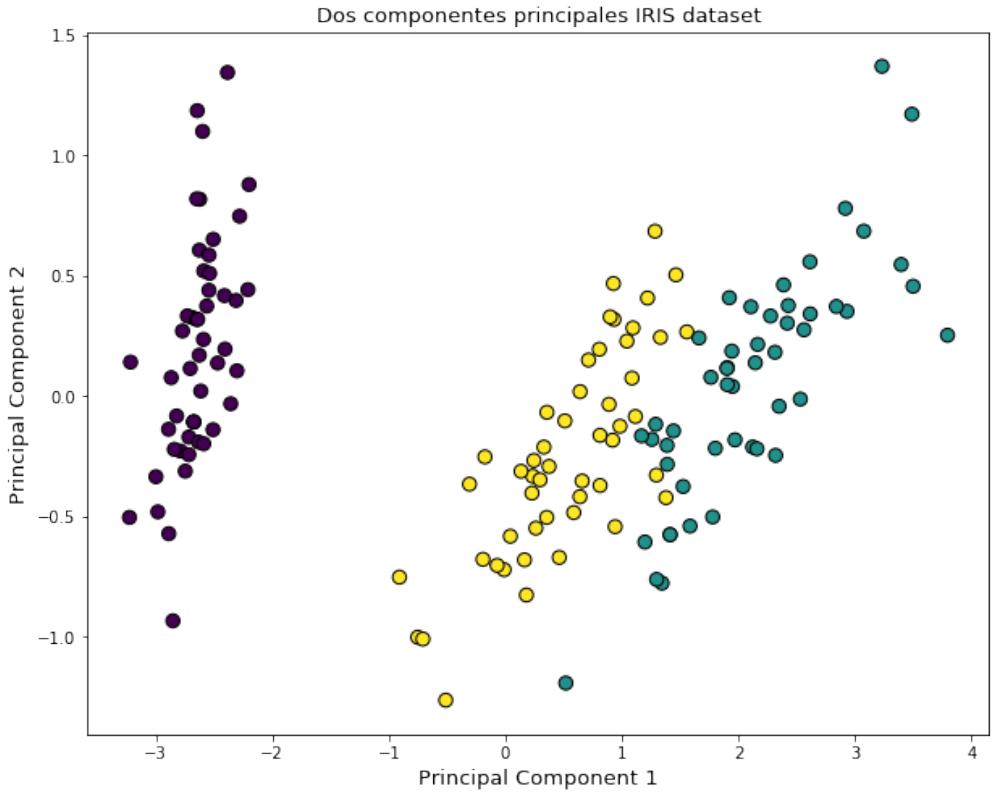
```
        plt.xlabel("Principal Component 1",fontsize=13)
        plt.ylabel("Principal Component 2",fontsize=13)
        plt.show()
```

```
<Figure size 720x432 with 0 Axes>
```



2 Etiquetas originales

```
In [21]: plt.figure(figsize=(10,8))
         plt.scatter(X_pca[:,0],X_pca[:,1],c=df['species'],edgecolors='black', s=285, marker = '.
         plt.title("Dos componentes principales IRIS dataset",fontsize=13)
         plt.xlabel("Principal Component 1",fontsize=13)
         plt.ylabel("Principal Component 2",fontsize=13)
         plt.show()
```



2.1 K-means con dataset de los ejercicios de clasificación

- Visualizar dataset de clasificación
- Se crean dos grupos para tratar de separar de manera no-supervisada y visualizar el comportamiento del algoritmo
- Se escalan los datos con 'StandardScaler'

```
In [22]: from sklearn.preprocessing import StandardScaler
         scaler = StandardScaler()

In [23]: df = pd.read_csv("data-breast.csv",index_col=0)
         df = df.replace({'B':0, 'M':1})
         df.head()
         df.head(10)
```

Out[23]:

id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
842302	1	17.99	10.38	122.80	1001.0	
842517	1	20.57	17.77	132.90	1326.0	
84300903	1	19.69	21.25	130.00	1203.0	
84348301	1	11.42	20.38	77.58	386.1	

```
84358402         1        20.29         14.34          135.10     1297.0
843786           1        12.45         15.70           82.57      477.1
844359           1        18.25         19.98          119.60     1040.0
84458202         1        13.71         20.83           90.20      577.9
844981           1        13.00         21.82           87.50      519.8
84501001         1        12.46         24.04           83.97      475.9

          smoothness_mean  compactness_mean  concavity_mean  \
id
842302            0.11840           0.27760         0.30010
842517            0.08474           0.07864         0.08690
84300903          0.10960           0.15990         0.19740
84348301          0.14250           0.28390         0.24140
84358402          0.10030           0.13280         0.19800
843786            0.12780           0.17000         0.15780
844359            0.09463           0.10900         0.11270
84458202          0.11890           0.16450         0.09366
844981            0.12730           0.19320         0.18590
84501001          0.11860           0.23960         0.22730

          concave points_mean  symmetry_mean  ...  texture_worst  \
id                                            ...
842302                0.14710         0.2419  ...          17.33
842517                0.07017         0.1812  ...          23.41
84300903              0.12790         0.2069  ...          25.53
84348301              0.10520         0.2597  ...          26.50
84358402              0.10430         0.1809  ...          16.67
843786                0.08089         0.2087  ...          23.75
844359                0.07400         0.1794  ...          27.66
84458202              0.05985         0.2196  ...          28.14
844981                0.09353         0.2350  ...          30.73
84501001              0.08543         0.2030  ...          40.68

          perimeter_worst  area_worst  smoothness_worst  compactness_worst  \
id
842302             184.60      2019.0            0.1622             0.6656
842517             158.80      1956.0            0.1238             0.1866
84300903           152.50      1709.0            0.1444             0.4245
84348301            98.87       567.7            0.2098             0.8663
84358402           152.20      1575.0            0.1374             0.2050
843786             103.40       741.6            0.1791             0.5249
844359             153.20      1606.0            0.1442             0.2576
84458202           110.60       897.0            0.1654             0.3682
844981             106.20       739.3            0.1703             0.5401
84501001            97.65       711.4            0.1853             1.0580

          concavity_worst  concave points_worst  symmetry_worst  \
id
842302             0.7119                0.2654          0.4601
```

```
842517            0.2416                0.1860          0.2750
84300903          0.4504                0.2430          0.3613
84348301          0.6869                0.2575          0.6638
84358402          0.4000                0.1625          0.2364
843786            0.5355                0.1741          0.3985
844359            0.3784                0.1932          0.3063
84458202          0.2678                0.1556          0.3196
844981            0.5390                0.2060          0.4378
84501001          1.1050                0.2210          0.4366

          fractal_dimension_worst  Unnamed: 32
id
842302                    0.11890          NaN
842517                    0.08902          NaN
84300903                  0.08758          NaN
84348301                  0.17300          NaN
84358402                  0.07678          NaN
843786                    0.12440          NaN
844359                    0.08368          NaN
84458202                  0.11510          NaN
844981                    0.10720          NaN
84501001                  0.20750          NaN

[10 rows x 32 columns]
```

In [24]:
```
y_true = df['diagnosis']
X = df.drop(['diagnosis','Unnamed: 32'],axis=1)
X = scaler.fit_transform(X)
dfx = pd.DataFrame(data=X,columns=df.columns[1:31])

dfx.tail()
```

Out[24]:
```
     radius_mean  texture_mean  perimeter_mean  area_mean  smoothness_mean  \
564     2.110995      0.721473        2.060786   2.343856         1.041842
565     1.704854      2.085134        1.615931   1.723842         0.102458
566     0.702284      2.045574        0.672676   0.577953        -0.840484
567     1.838341      2.336457        1.982524   1.735218         1.525767
568    -1.808401      1.221792       -1.814389  -1.347789        -3.112085

     compactness_mean  concavity_mean  concave points_mean  symmetry_mean  \
564          0.219060        1.947285             2.320965      -0.312589
565         -0.017833        0.693043             1.263669      -0.217664
566         -0.038680        0.046588             0.105777      -0.809117
567          3.272144        3.296944             2.658866       2.137194
568         -1.150752       -1.114873            -1.261820      -0.820070

     fractal_dimension_mean  ...  radius_worst  texture_worst  \
564               -0.931027  ...      1.901185       0.117700
565               -1.058611  ...      1.536720       2.047399
566               -0.895587  ...      0.561361       1.374854
```

```
567                1.043695  ...       1.961239       2.237926
568               -0.561032  ...      -1.410893       0.764190

     perimeter_worst  area_worst  smoothness_worst  compactness_worst  \
564         1.752563    2.015301          0.378365          -0.273318
565         1.421940    1.494959         -0.691230          -0.394820
566         0.579001    0.427906         -0.809587           0.350735
567         2.303601    1.653171          1.430427           3.904848
568        -1.432735   -1.075813         -1.859019          -1.207552

     concavity_worst  concave points_worst  symmetry_worst  \
564         0.664512              1.629151       -1.360158
565         0.236573              0.733827       -0.531855
566         0.326767              0.414069       -1.104549
567         3.197605              2.289985        1.919083
568        -1.305831             -1.745063       -0.048138

     fractal_dimension_worst
564                -0.709091
565                -0.973978
566                -0.318409
567                 2.219635
568                -0.751207

[5 rows x 30 columns]
```

In [25]:
```
kmeans = KMeans(n_clusters=2,max_iter=300,n_init=20, random_state=110)
kmeans.fit(dfx)
y = kmeans.labels_
pca = PCA(n_components=2).fit(dfx)
clus_cent_breast=kmeans.cluster_centers_
cent = pca.transform(clus_cent_breast)
```

In [26]:
```
pca = PCA(n_components=2)
X_pca = pca.fit_transform(dfx)
```

In [27]:
```
df['diagnosis'].values
```

Out[27]:
```
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
       1, 1, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 1, 1,
       0, 0, 0, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 0, 0, 1, 1, 0, 1, 1, 1,
       0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0,
       0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 0, 1, 0, 1,
       1, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0,
       0, 1, 0, 0, 1, 1, 1, 0, 1, 0, 1, 0, 0, 0, 1, 0, 0, 1, 1, 0, 1, 1,
       1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1, 0, 0, 1, 1,
       0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0,
       0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
```

```
1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1, 0, 0, 1, 0, 1, 1, 0, 0,
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0,
0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 1,
1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1,
1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 1, 1, 0, 1, 1,
0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0,
0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1,
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 1, 0, 0, 0, 0,
0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 1,
0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0,
0, 0, 0, 1, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 1, 0, 0,
0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0,
0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 0])
```

2.2 Comportamiento de etiquetas 'K-means'

```
In [28]: print("Predicciones:\n")
         print(kmeans.labels_)
         print("\nReporte de clasificación:\n")
         print(classification_report(kmeans.labels_,df.diagnosis.values))
```

```
Predicciones:

[1 1 1 1 1 1 1 1 1 1 0 1 1 0 1 1 0 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 0 0 0 0 0 1 0 0 1 0 1 0 0 0 0 0 1 0 0 1 1 0 0 0 0 1 0 1 1 0 0 1 0 1 0 1 0
 0 1 0 1 1 0 0 1 1 1 0 1 0 1 0 1 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0
 0 1 0 0 0 0 1 1 0 0 1 1 0 0 0 0 1 1 1 1 0 1 1 0 1 0 0 0 1 0 0 1 0 0 0 0 1 0
 0 0 0 0 1 0 0 0 1 0 0 0 0 1 1 0 1 0 0 1 1 0 0 0 1 0 0 0 0 1 0 0 1 1 0 0 0
 0 0 0 0 0 1 0 0 1 1 0 1 1 1 1 0 1 1 1 0 0 0 0 0 0 1 0 1 1 1 1 0 0 1 1 0 0
 0 1 0 0 0 0 0 1 1 0 0 1 0 0 1 1 0 1 0 0 1 0 1 0 0 0 0 0 1 0 1 1 1 0 1 1 1
 1 1 0 1 0 1 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 1 1 0 0 0 0 0 0 1 0 0 0 0 0
 0 0 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 1 0 1 0 0 0 0 1 1 1 0 0
 0 0 1 0 1 0 1 0 0 0 1 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 1 1 0 1 1
 1 0 1 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 1 1 0 0 0 0 0 0 1 0 0 0 0 0 0
 0 1 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 1 0 1 1 0 0 0 0 0 0 0 1 0 0
 0 0 1 0 0 1 0 1 0 0 0 0 0 0 0 0 1 1 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0
 0 0 0 0 1 0 1 0 0 0 0 1 0 0 0 0 0 1 1 0 1 0 1 1 0 0 0 0 1 0 0 1 0 0 0 1 1
 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 1 1 1 1 1 1 0]

Reporte de clasificación:

              precision    recall  f1-score   support

           0       0.96      0.90      0.93       380
           1       0.83      0.93      0.87       189

    accuracy                           0.91       569
   macro avg       0.89      0.91      0.90       569
```

```
weighted avg       0.92      0.91      0.91       569
```

```
In [29]: print("Confusion matrix")
         confusion_matrix(kmeans.labels_,df.diagnosis.values)
```

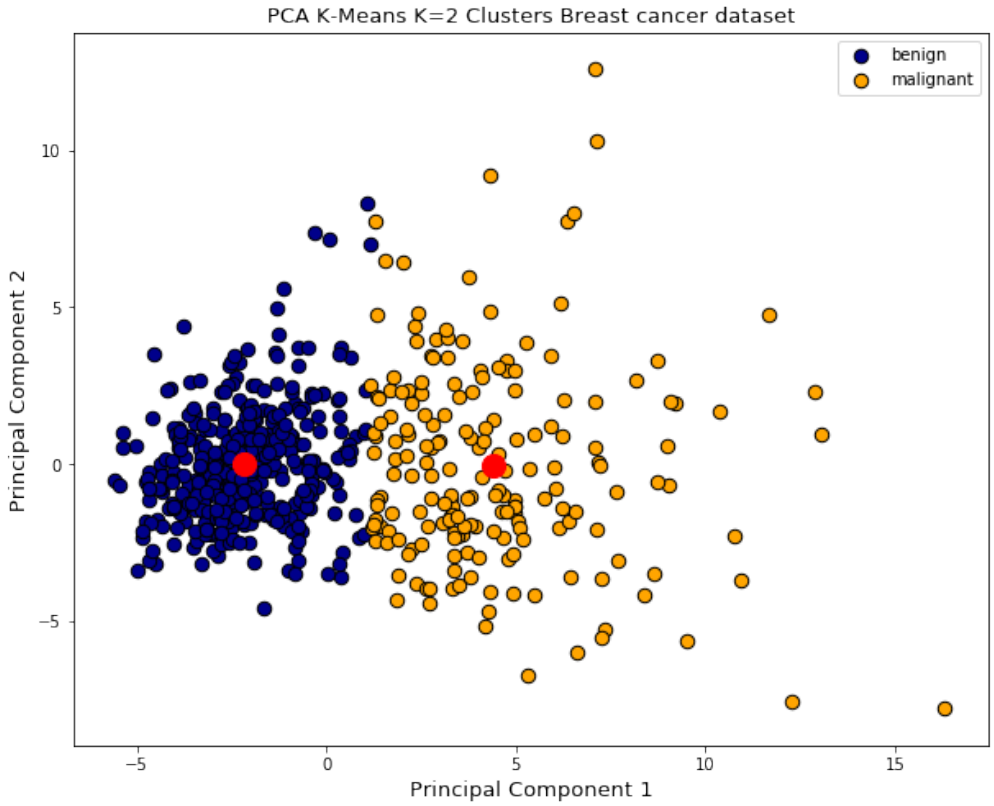
```
Confusion matrix
```

```
Out[29]: array([[343,  37],
                [ 14, 175]])
```

2.3 K-means con PCA

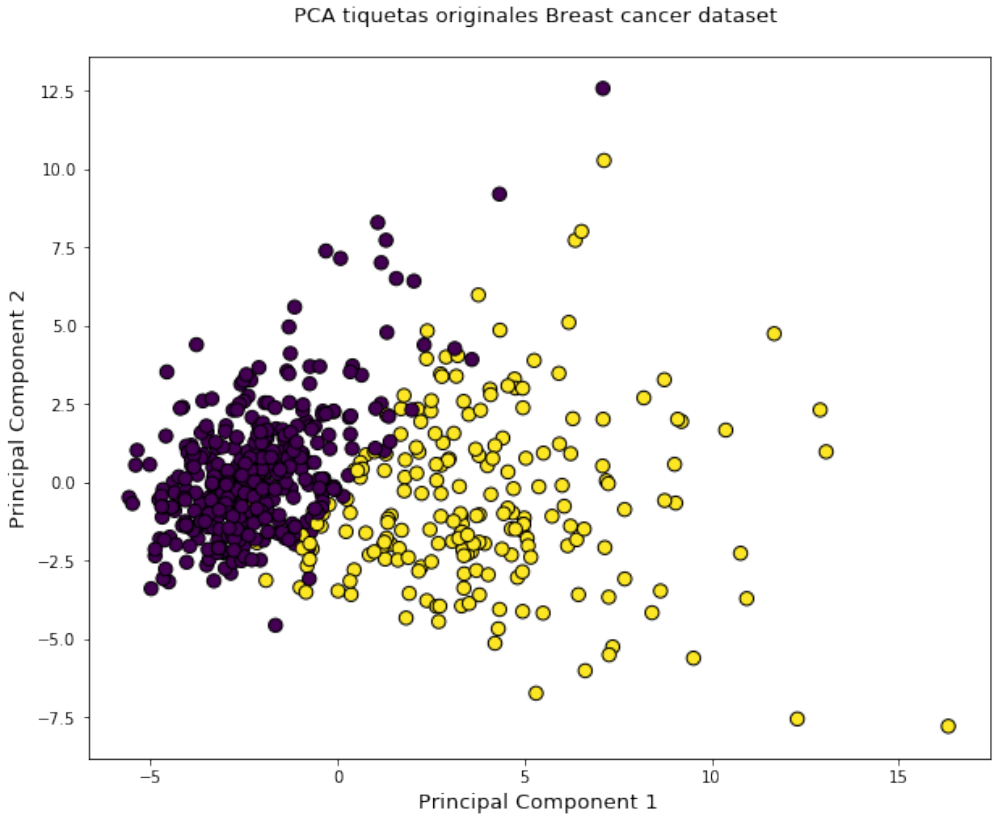
```
In [30]: target_ids = np.unique(y)
         plt.figure(figsize=(10,8))
         colors = ['darkblue', 'orange']
         target_names = ['benign','malignant']
         for i, c, label in zip(target_ids, colors, target_names):
             plt.scatter(X_pca[i == y,0], X_pca[i == y,1], c = c,  edgecolors='black', s=285,labe
         plt.legend()
         plt.scatter(cent[:,0], cent[:,1], s=200, color = 'red')
         plt.title('PCA K-Means K=2 Clusters Breast cancer dataset',fontsize=13)
         plt.xlabel("Principal Component 1",fontsize=13)
         plt.ylabel("Principal Component 2",fontsize=13)

         plt.show()
```



2.4 Etiquetas originales

```
In [31]: plt.figure(figsize=(10,8))
         plt.scatter(X_pca[:,0],X_pca[:,1],c=y_true, edgecolors='black', s=285,label=label, marke
         plt.title("PCA tiquetas originales Breast cancer dataset \n",fontsize=13)
         plt.xlabel("Principal Component 1",fontsize=13)
         plt.ylabel("Principal Component 2",fontsize=13)
         plt.show()
```



2.5 K = 3

- Ahora se crean 3 clases

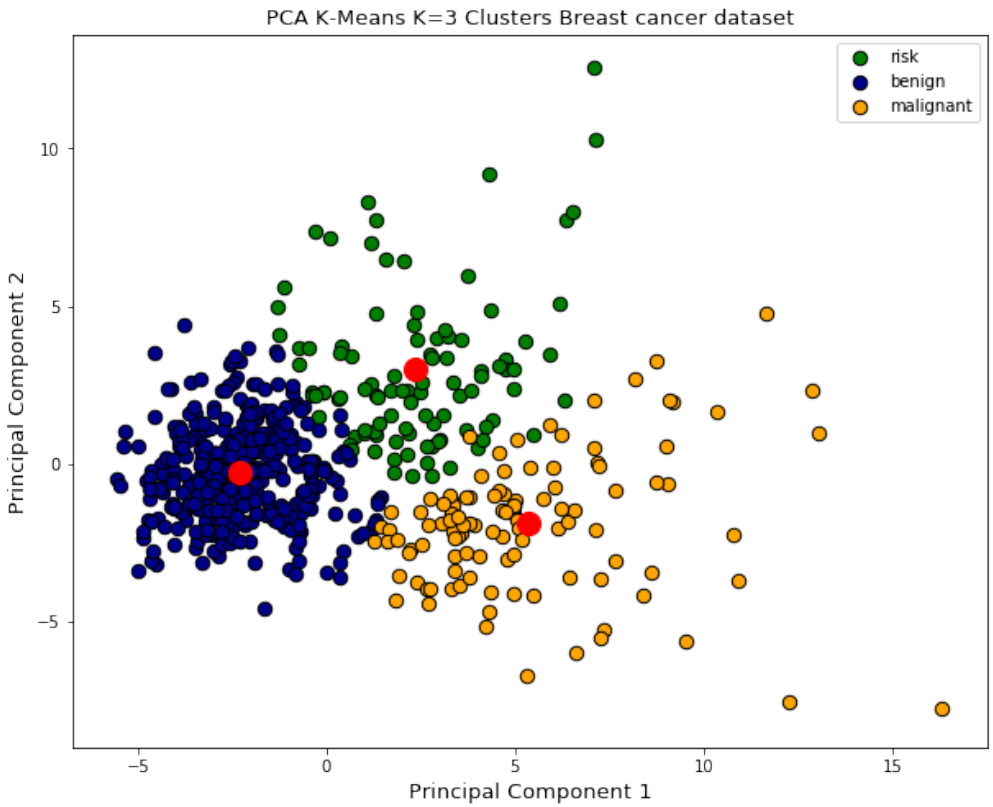
```
In [32]: kmeans = KMeans(n_clusters=3,max_iter=300,n_init=20, random_state=1221)
         kmeans.fit(dfx)
         y = kmeans.labels_
         pca = PCA(n_components=2).fit(dfx)
         clus_cent_breast=kmeans.cluster_centers_
         cent = pca.transform(clus_cent_breast)

In [33]: pca = PCA(n_components=2)
         X_pca = pca.fit_transform(dfx)

In [34]: target_ids = np.unique(y)
         plt.figure(figsize=(10,8))
         colors = ['green','darkblue','orange']
         target_names = ['risk','benign','malignant']
         for i, c, label in zip(target_ids, colors, target_names):
             plt.scatter(X_pca[i == y,0], X_pca[i == y,1], c = c,  edgecolors='black', s=285,labe
```

```
plt.legend()
plt.scatter(cent[:,0], cent[:,1], s=200, color = 'red')
plt.title('PCA K-Means K=3 Clusters Breast cancer dataset',fontsize=13)
plt.xlabel("Principal Component 1",fontsize=13)
plt.ylabel("Principal Component 2",fontsize=13)

plt.show()
```



- Probar K-means con un diferente dataset
- Crear diferentes clusters