

Trabalho1

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UNIVERSIDADE ESTADUAL DE CAMPINAS

INSTITUTE OF COMPUTING

Machine Learning

MC886A/MO444A

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1 1. Introduction

Clustering allows us to be able to group a set of objects into subsets of objects called clusters, each cluster is made up of a collection of objects that are similar to each other, but that are different from the objects of other clusters. It can be used for the diagnosis of diseases through images, in the monitoring of social networks, marketing. Clustering is part of unsupervised learning, there are some clustering methods such as k-means, hierarchical clustering, K-medoids, DBSCAN, Hierarchical Clustering, etc.

2 2. Clustering Methods

2.1 2.1 K-Means

The K-means algorithm is an iterative algorithm that attempts to divide the data set into K distinct non-overlapping predefined subgroups called clusters, where each data point belongs to a single group. Trying to make the intra-cluster data points as similar as possible while keeping the clusters as different as possible.

```
[1]: def kmeans(k,x,y):  
  
    # Find min and max values  
    x_min=np.min(x)  
    x_max=np.max(x)  
    y_min=np.min(y)  
    y_max=np.max(y)  
  
    # Select K Random Points  
    punto_x=np.random.uniform(low=x_min,high=x_max,size=k)  
    punto_y=np.random.uniform(low=y_min,high=y_max,size=k)
```

```

# Setting a huge distortion
# Used to stop algorithm
old_distortion = np.inf

for it in range(20):
    # Create distance matrix
    matriz_distancias = np.zeros((len(x),k))
    for k_i in range(k):
        # Euclidean distance
        x_h=(x-punto_x[k_i])**2
        y_h=(y-punto_y[k_i])**2
        dist= np.sqrt(x_h+y_h)
        matriz_distancias[:,k_i]=dist

    # Find the minimum distance. Creation of mask matrix
    min=np.argmin(matriz_distancias,axis=1)
    matriz_clusters=np.zeros(matriz_distancias.shape)
    i=0
    for min_i in min:
        matriz_clusters[i][min_i]=1
        i+=1

    # Column matrix transformation
    x_r=x.reshape(-1,1)
    y_r=y.reshape(-1,1)

    # Sum of cluster values
    matriz_clusters_x=x_r*matriz_clusters
    matriz_clusters_y=y_r*matriz_clusters

    total=matriz_clusters.sum(axis=0)

    total_x=matriz_clusters_x.sum(axis=0)
    total_y=matriz_clusters_y.sum(axis=0)

    # Update point with mean total_x
    punto_x=(total_x/ (total+0.0000000001) )
    punto_y=(total_y/ (total+0.0000000001) )

    # Cluster list
    clusters = np.argmax(matriz_clusters,axis=1)
    centroides_x = np.matmul(matriz_clusters,punto_x)
    centroides_y = np.matmul(matriz_clusters,punto_y)

    distortion = Distortion(x,y,centroides_x,centroides_y)

```

```

# Distortion - Condition
if ( abs( old_distortion - distortion ) <= 0.001 ):
    break
else: old_distortion = distortion

print ( "\n \n DISTORTION =",distortion, "Clusters=", k)
plt.scatter(x,y,marker="o",c=clusters)
plt.scatter(punto_x,punto_y,marker="*",c="red")
plt.show()

return punto_x,punto_y,matriz_clusters,distortion

```

2.2 DBSCAN

The Density-Based Noisy Applications Spatial Clustering Algorithm (DBSCAN) is an algorithm used for density-based clustering. Being able to discover groups of different shapes and sizes from a large amount of data that contains noise and outliers. The DBSCAN algorithm uses two parameters: the minimum number of points (threshold) grouped for a region to be considered dense, and an average distance that will be used to locate the points in the vicinity of any point.

```

[2]: def dbscan(x,y, radio, M ):
    marcas = np.zeros( x.shape )

    # Repeat until all points are visited
    while( True ):

        por_procesar = np.where( marcas == 0)
        if ( len ( por_procesar[0] ) == 0): break

        # Choose a point not visited
        p_index = por_procesar[0][0]
        punto_x = x[p_index]
        punto_y = y[p_index]

        # Get Distances
        distancias = np.sqrt ( ( x - punto_x )**2 + ( y - punto_y )**2 )

        # Select points that are neighbors from the choose point

        n_vecinos = len ( distancias[ distancias < radio ] )

        # Classify
        # 0 No worked
        # 1 Core Point
        # 2 Border

```

```

# 3 Outlier

if n_vecinos >= M:
    marcas[p_index] = 1
elif n_vecinos > 0 :
    marcas[p_index] = 2
else:
    marcas[p_index] = 3

# -1 : No cluster
clusters = -1 * np.ones ( marcas.shape )

visitados = np.zeros ( marcas.shape , dtype=bool)

core_points = np.where(marcas == 1)[0]
n_cluster = 0

# Repeat until all core points have been visited
while ( True ):
    if ( len(core_points) == 0 ) : break
    if len( np.where ( ( ~ visitados ) & ( clusters != -1 ) & ( marcas_
→ == 1 ) ) [0] ) == 0:

        #
        c_p_x = x[core_points[0]]
        c_p_y = y[core_points[0]]
        visitados[ core_points[0] ] = 1
        distancias = np.sqrt ( ( x - c_p_x )**2 + ( y - c_p_y )**2 )
        clusters[ np.where(distancias < radio) ] = n_cluster
        core_points = core_points[ 1 : ]
        n_cluster += 1
    else:
        #
        core_points_nuevos = np.where ( ( ~ visitados ) & ( clusters != -1
→ ) & ( marcas == 1 ) ) [0]
        c_p_x = x[core_points_nuevos[0]]
        c_p_y = y[core_points_nuevos[0]]
        visitados[ core_points_nuevos[0] ] = 1
        distancias = np.sqrt ( ( x - c_p_x )**2 + ( y - c_p_y )**2 )
        clusters[ np.where(distancias < radio) ] = clusters[
→ core_points_nuevos[0] ]
        core_points = np.delete(core_points, np.where( core_points ==
→ core_points_nuevos[0] ))

print("\n \nBorders and Core Points")
plt.scatter(x,y,c=marcas)

```

```

plt.show()

## Getting centroides
matrix_clusters = pd.get_dummies(clusters).to_numpy()

sumas = matrix_clusters.sum(axis=0)

x_matrix = x.reshape(-1,1)*matrix_clusters
y_matrix = y.reshape(-1,1)*matrix_clusters

x_centro = (x_matrix.sum(axis=0)/sumas)

y_centro = (y_matrix.sum(axis=0)/sumas)

# centroides_x = np.matmul(x_centro,matrix_clusters.T)
# centroides_y = np.matmul(y_centro,matrix_clusters.T)

# ( 1, 3 ) x ( 760 , 3 )

print("Final Clusters formed")
plt.scatter(x,y,c=clusters,s=3)
plt.show()

return x_centro,y_centro,matrix_clusters,matrix_clusters.shape[1]

```

3 3. Evaluation Metrics

3.1 3.1 Distortion

The sum of all squared errors (SSE). The error is the difference between the coordinates of each data point and the coordinates of the centroid.

$$SSE = \sum_{i=1}^m (y_i - \hat{y}_i)^2$$

```

[3]: def Distortion(x,y,centroides_x,centroides_y):
      distortion = ( ( x - centroides_x )**2 + ( y - centroides_y )**2 ).sum()
      return distortion

```

3.2 3.2 RMSSTD

Root mean squared error standard deviation (RMSSTD), is a frequently used measure of the differences between the values predicted by a model and the observed values

- Root mean squared error standard deviation (RMSSTD)

$$RMSSTD = \sqrt{\frac{\sum_i \sum_{x \in c_i} \|x - c_i\|^2}{p \cdot \sum_i (n_i - 1)}}$$

```
[4]: def RMSSTD(x,y,punto_x,punto_y,matriz_clusters,k):
      centroides_x = np.matmul(matriz_clusters,punto_x)
      centroides_y = np.matmul(matriz_clusters,punto_y)
      distortion = Distortion(x,y,centroides_x,centroides_y)
      number_attributes = 2 * ( len(x) - k )
      return np.sqrt(distortion/number_attributes)
```

4 4. Dataset 1: clusters.dat

4.1 4.1 Load Datasets

```
[5]: import matplotlib.pyplot as plt
      import pandas as pd
      import numpy as np

      df = pd.read_table("cluster.dat",header=None, sep="\s+")
      datos = pd.DataFrame(df)
      datos
```

```
[5]:
```

	0	1
0	1555.0	28.65
1	1490.0	27.55
2	1445.0	28.35
3	1415.0	28.80
4	1375.0	28.05
..
568	3420.0	27.95
569	3465.0	26.85
570	3525.0	26.00
571	3570.0	26.15
572	3440.0	25.60

[573 rows x 2 columns]

- Transforming the dataset to a numpy array

```
[6]: datos=datos.to_numpy()
      datos
```

```
[6]: array([[1555. , 28.65],
          [1490. , 27.55],
```

```

[1445. , 28.35],
...,
[3525. , 26. ],
[3570. , 26.15],
[3440. , 25.6 ]]

```

4.2 4.2 Split Dataset (Train/test)

```

[7]: #Shuffle data
np.random.shuffle(datos)
datos

```

```

[7]: array([[3575. , 21.3 ],
[3155. , 25.2 ],
[1170. , 26.35],
...,
[3125. , 27.85],
[ 740. , 25.45],
[1235. , 21.6 ]])

```

```

[8]: #Split data in training/test sets (90/10)
datos_train = datos[:int(0.9*len(datos))]
datos_test = datos[int(0.9*len(datos)):]

x_train = datos_train[:,0]
y_train = datos_train[:,1]

x_test = datos_test[:,0]
y_test = datos_test[:,1]

```

4.3 4.3 Pre-processing

- Normalization (Min Max Scaler)

$$x_{scaled} = \frac{(x - x_{min})}{(x_{max} - x_{min})}$$

$$y_{scaled} = \frac{(y - y_{min})}{(y_{max} - y_{min})}$$

```

[9]: def norm(x,y,x_max,x_min,y_max,y_min):
    x=(x-x_min)/(x_max-x_min)
    y=(y-y_min)/(y_max-y_min)
    return x,y

# It's important to save original parameters

x_max_train = x_train.max()

```

```

x_min_train= x_train.min()
y_max_train = y_train.max()
y_min_train = y_train.min()

x_max_test = x_test.max()
x_min_test = x_test.min()
y_max_test = y_test.max()
y_min_test = y_test.min()

x_n_train, y_n_train = □
    ↪norm(x_train,y_train,x_max_train,x_min_train,y_max_train,y_min_train)
x_n_test, y_n_test = □
    ↪norm(x_test,y_test,x_max_test,x_min_test,y_max_test,y_min_test)

```

4.4 4.4 K-means Clustering

```

[10]: def elbow_method(k_max, x_n_train , y_n_train ):
        list_distortions = []
        list_rmmstds = []
        for k in range(1,k_max+1):
            centroe_x , centroe_y , matriz_clusters , distortion = □
            ↪kmeans(k,x_n_train,y_n_train)
            rmmstd = RMSSTD(x_n_train,y_n_train,centroe_x,centroe_y,□
            ↪matriz_clusters, k)
            list_distortions.append(distortion)
            list_rmmstds.append(rmmstd)

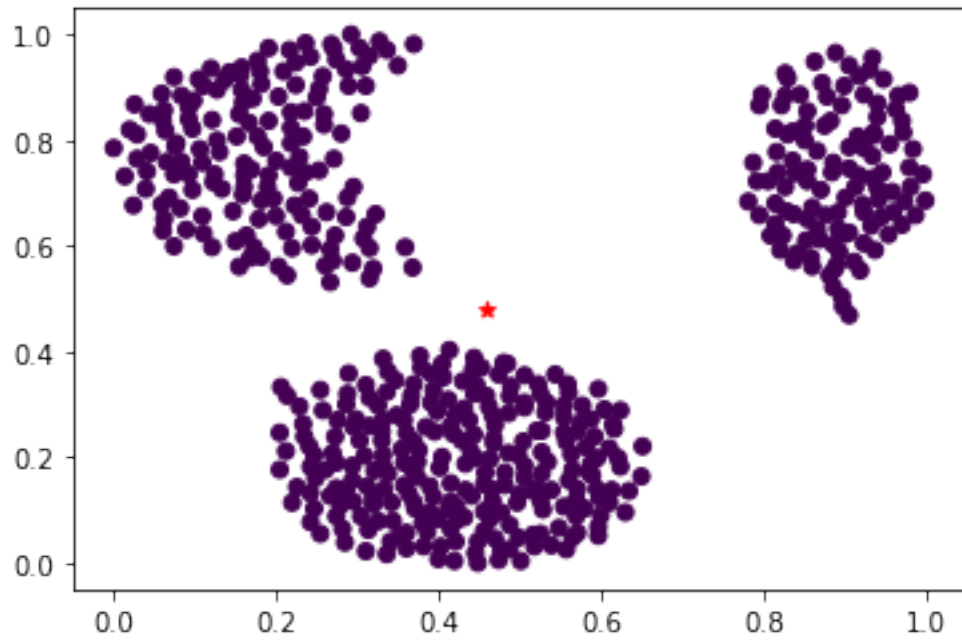
        print("\n \n Distortion")
        plt.plot(range(1,k_max+1),list_distortions,marker="*")
        plt.show()

        print("Root Mean Squared Standard Deviation")
        plt.plot(range(1,k_max+1),list_rmmstds,marker="o")
        plt.show()

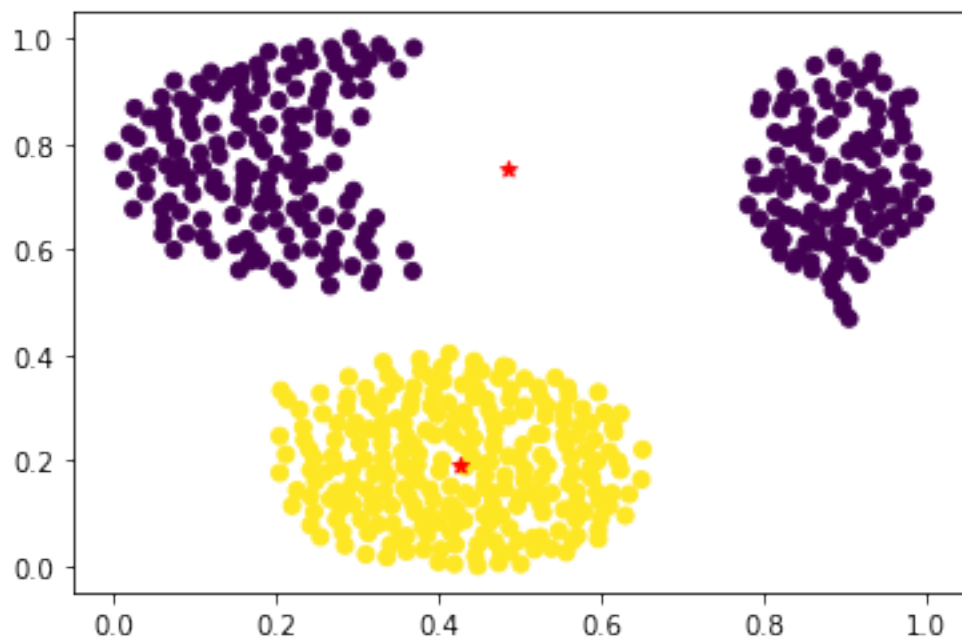
# Execute with until 10 Clusters
elbow_method(10,x_n_train,y_n_train)

```

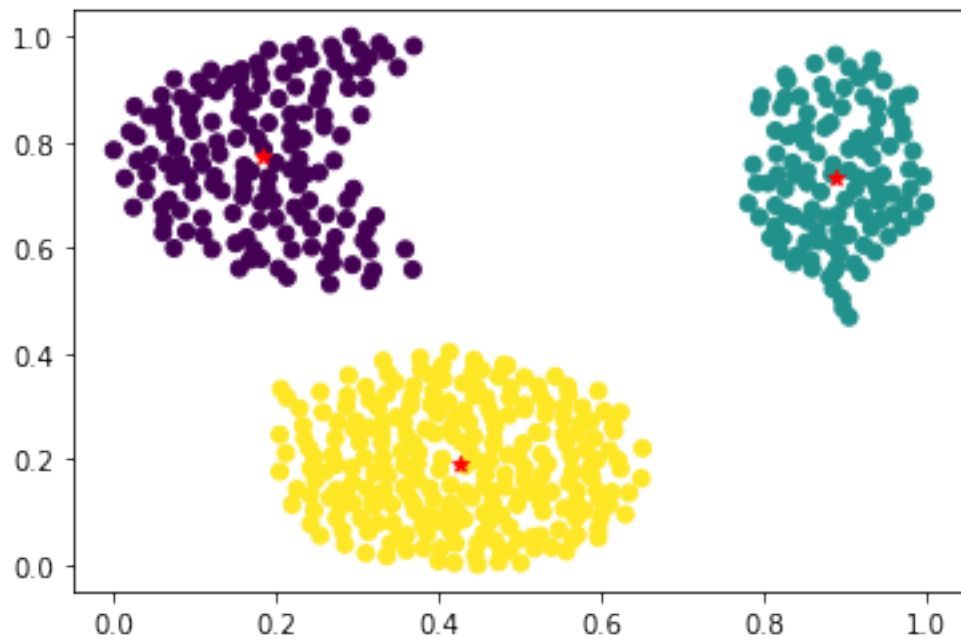
DISTORTION = 85.66036940262198 Clusters= 1



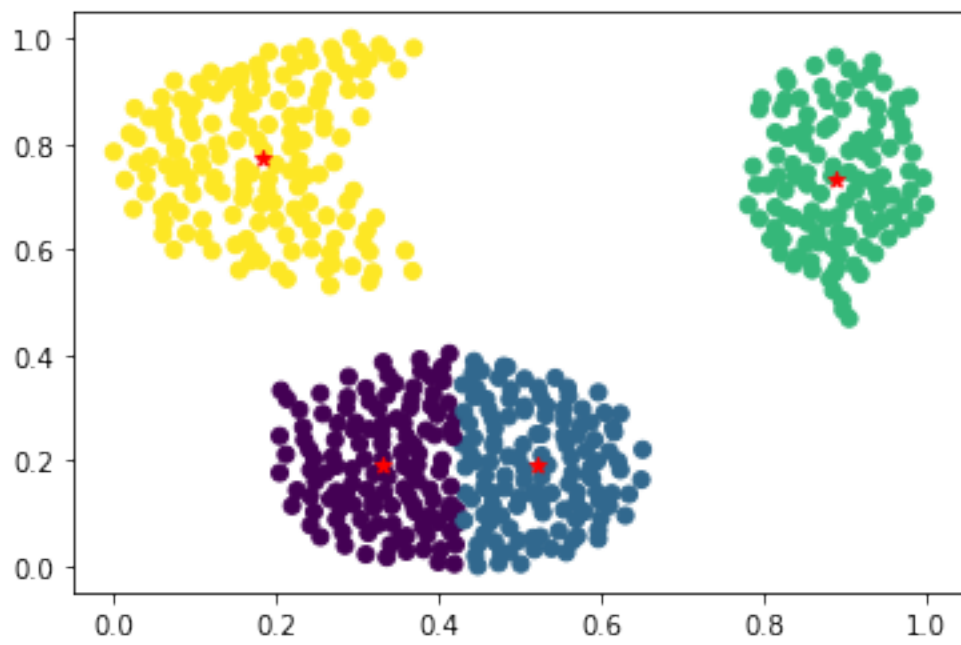
DISTORTION = 44.207895485149606 Clusters= 2



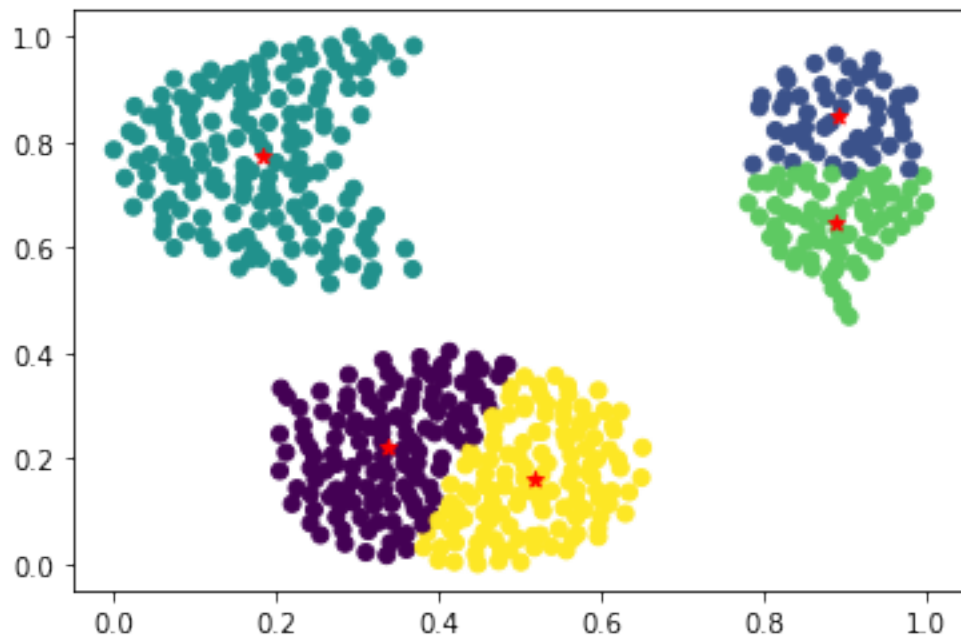
DISTORTION = 11.456342520965901 Clusters= 3



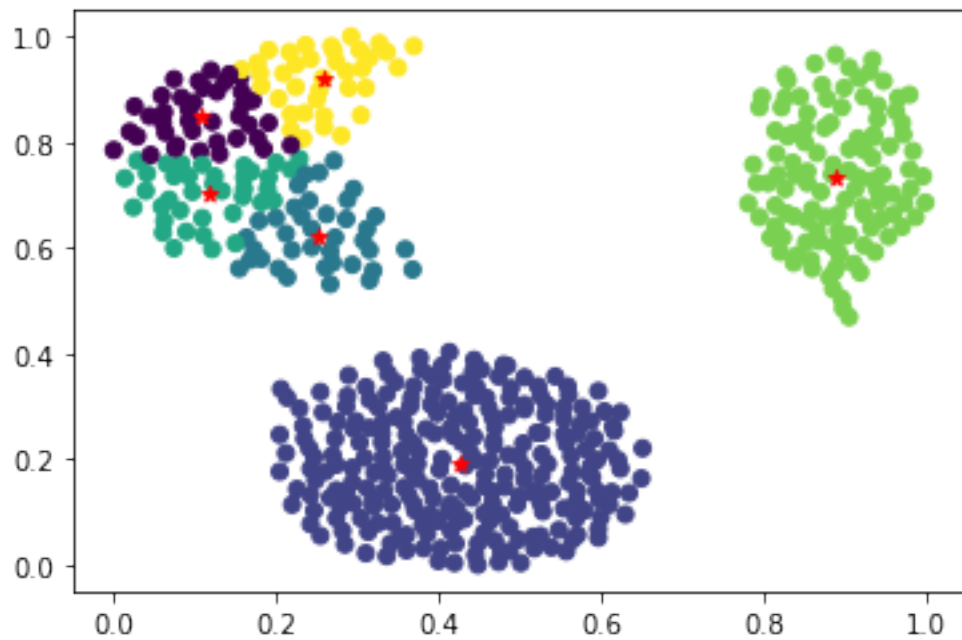
DISTORTION = 9.187854899679449 Clusters= 4



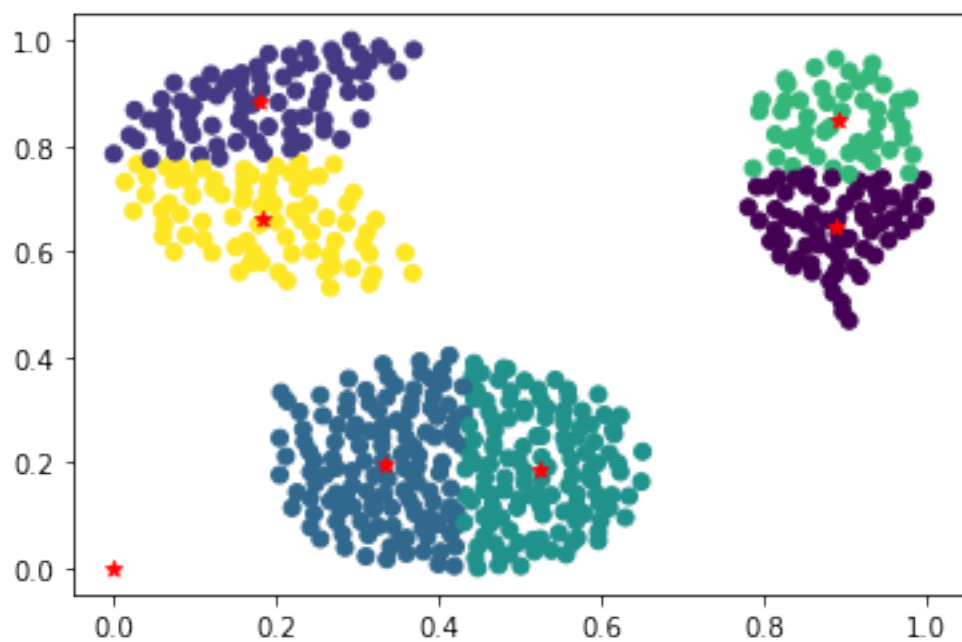
DISTORTION = 8.034799988955351 Clusters= 5



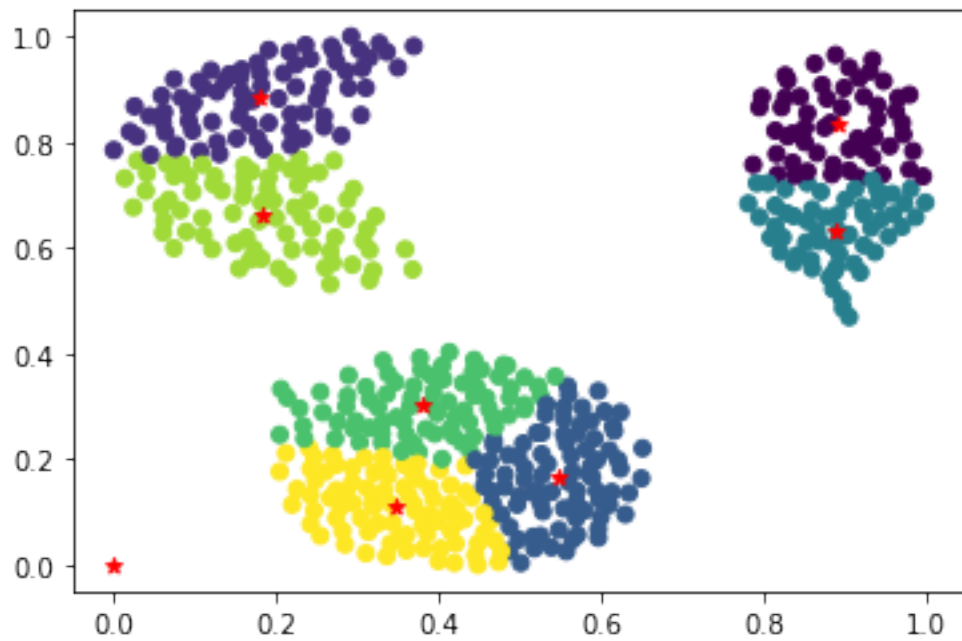
DISTORTION = 8.621122007055924 Clusters= 6



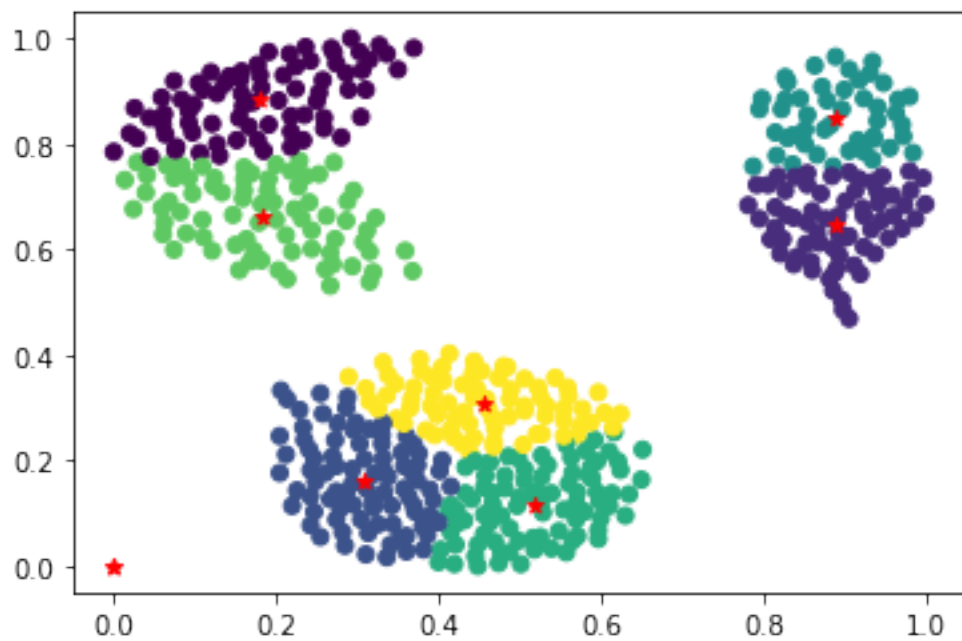
DISTORTION = 6.204174224496712 Clusters= 7



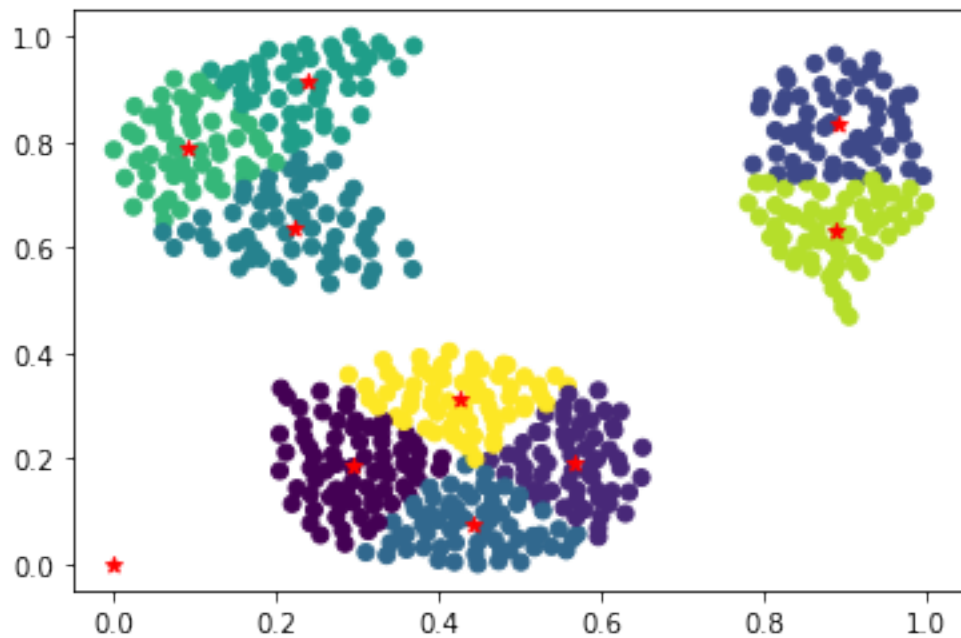
DISTORTION = 4.941833706918952 Clusters= 8



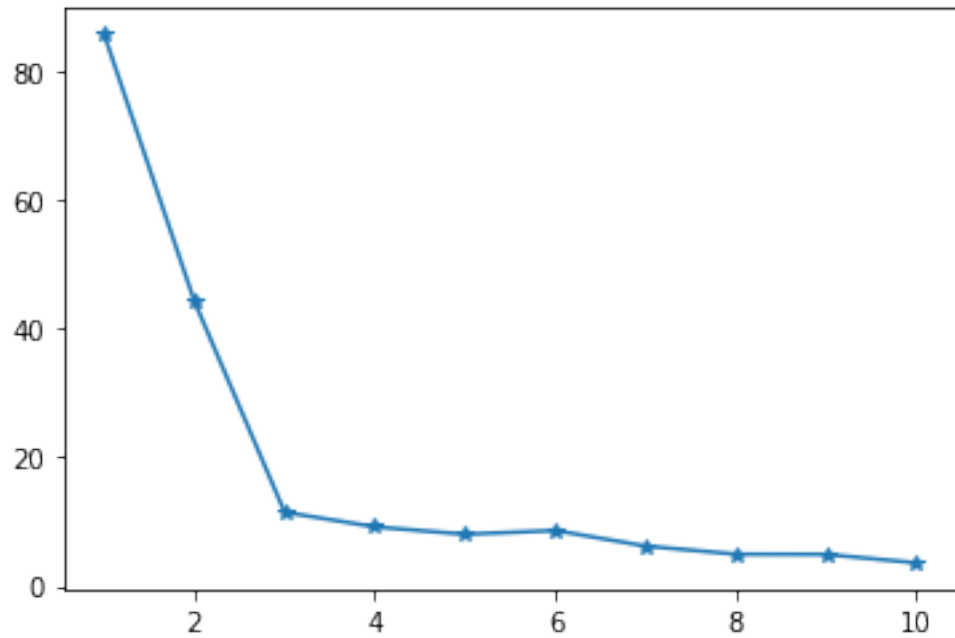
DISTORTION = 4.916213132159976 Clusters= 9



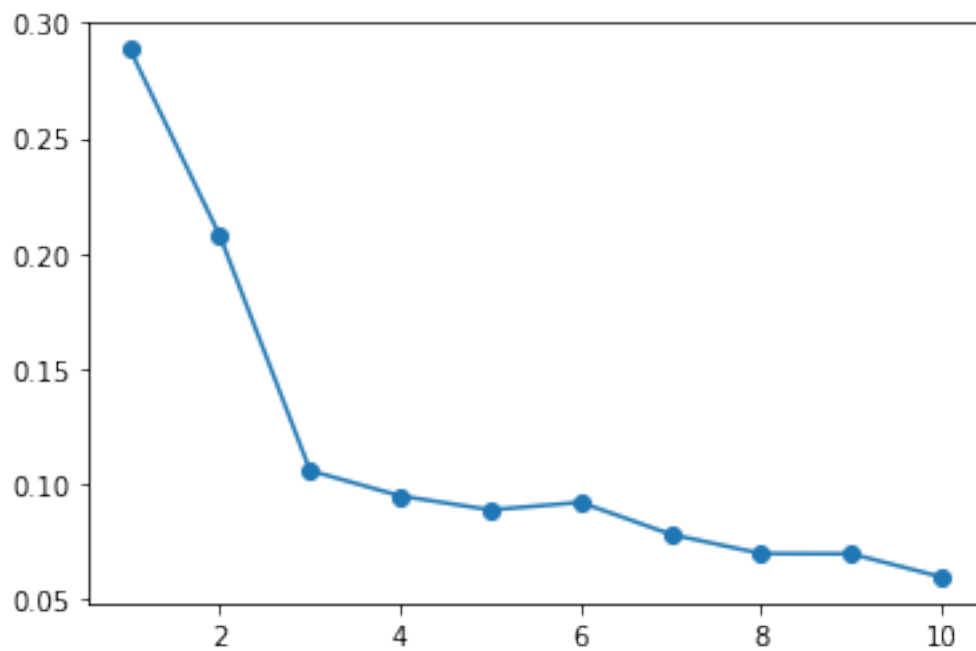
DISTORTION = 3.5937835187307803 Clusters= 10



Distortion



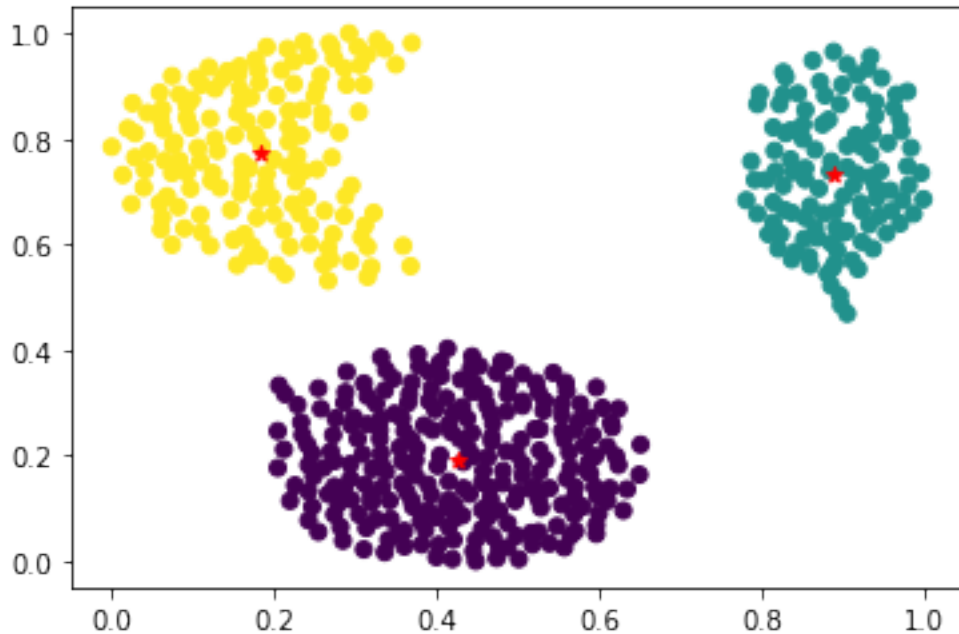
Root Mean Squared Standard Deviation



Observing the last graphic (Elbow Method), Distortion and RMSSD. We choose **k=3**

```
[11]: # k = 3
centroide_x , centroide_y , matriz_clusters , distortion = ↳ kmeans(3,x_n_train,y_n_train)
rmmstd = RMSSTD(x_n_train,y_n_train,centroide_x,centroide_y, matriz_clusters, 3)
print( "ERROR TRAIN:", rmmstd )
```

DISTORTION = 11.456342520965901 Clusters= 3



ERROR TRAIN: 0.10577256020883093

4.4.1 Dataset Test

```
[12]: def get_clusters(x,y,centroide_x,centroide_y,k):
    matriz_distancias = np.zeros((len(x),k))
    for k_i in range(k):
        # Euclidean distance
        x_h=(x-centroide_x[k_i])**2
        y_h=(y-centroide_y[k_i])**2
        dist= np.sqrt(x_h+y_h)
        matriz_distancias[:,k_i]=dist

    # Find the minimum distance. Creation of mask matrix
    min=np.argmin(matriz_distancias,axis=1)
    matriz_clusters=np.zeros(matriz_distancias.shape)
```



```

i=0
for min_i in min:
    matriz_clusters[i][min_i]=1
    i+=1
return matriz_clusters

```

```

[13]: matriz_clusters_test = get_clusters(x_n_test,y_n_test,centroide_x,centroide_y,3)
rmmstd = RMSSTD(x_n_test,y_n_test,centroide_x,centroide_y, matriz_clusters_test,
↪, 3)
print( "ERROR TEST:", rmmstd )

```

ERROR TEST: 0.1160384298684702

4.5 DBSCAN Clustering

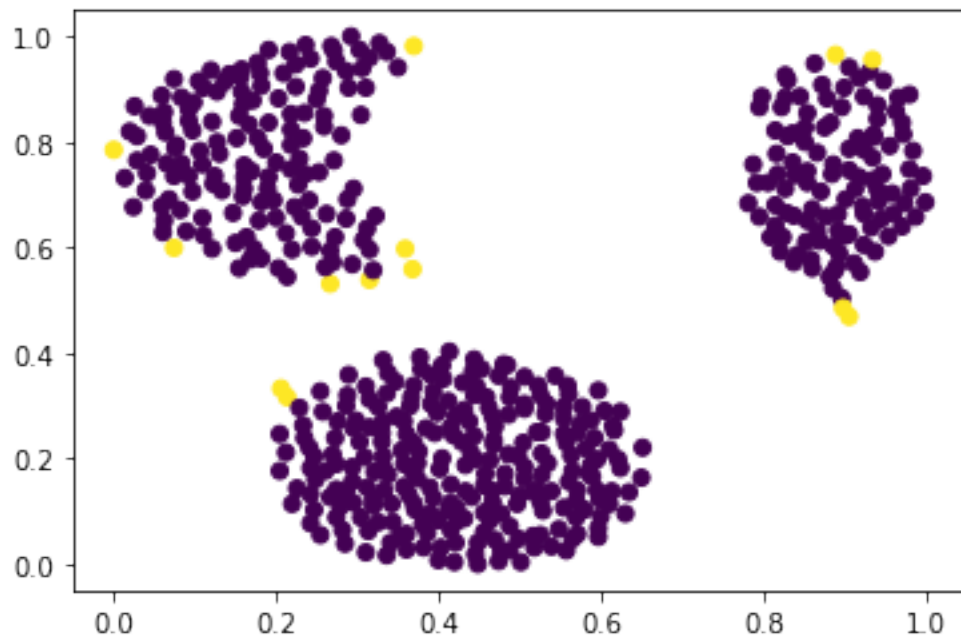
```

[14]: centroide_x , centroide_y , matriz_clusters , k = dbscan(x_n_train, y_n_train,
↪0.07 , 9 )
rmmstd_train = RMSSTD(x_n_train,y_n_train,centroide_x,centroide_y,
↪matriz_clusters, k)

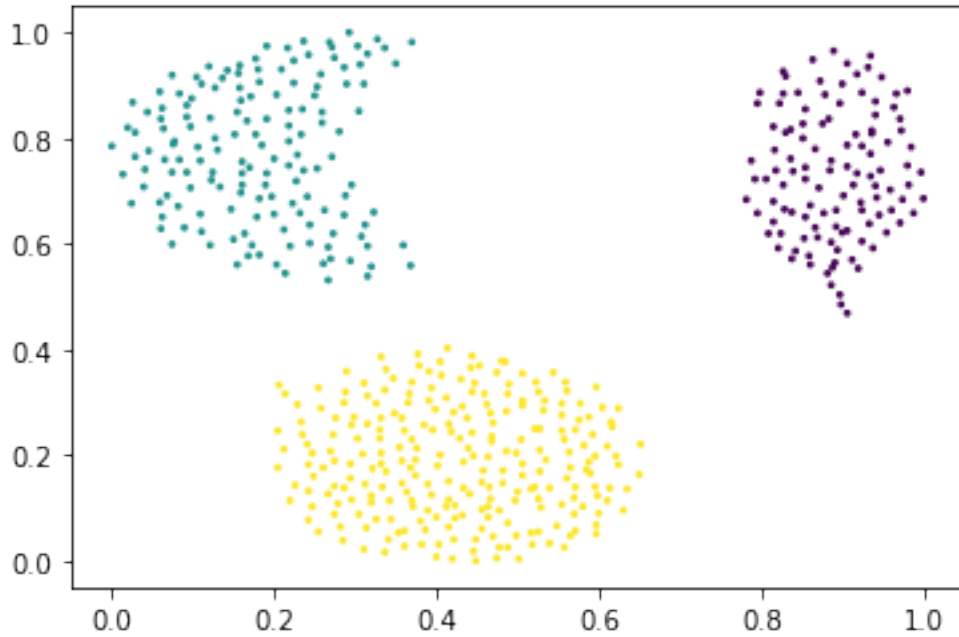
print( "ERROR TRAIN:", rmmstd_train )

```

Borders and Core Points



Final Clusters formed



ERROR TRAIN: 0.10577256020883093

4.5.1 Dataset Test

```
[15]: matriz_clusters_test = get_clusters(x_n_test,y_n_test,centroide_x,centroide_y,k)
      rmmstd = RMSSTD(x_n_test,y_n_test,centroide_x,centroide_y, matriz_clusters_test,
      ↪,k)
      print( "ERROR TEST:", rmmstd )
```

ERROR TEST: 0.11603842986843832

Comparing both RMSSTD's methods

	Kmeans	DBSCAN
Train	0.1055	0.1055
Test	0.1105	0.1105

We could conclude that DBSCAN and KMEANS obtain similar results.

5 5. Dataset: Vehicles Silhouettes

The features were extracted from the silhouettes by the HIPS (Hierarchical Image Processing System) extension BINATTS, which extracts a combination of scale independent features utilising both classical moments based measures such as scaled variance, skewness and kurtosis about the

major/minor axes and heuristic measures such as hollows, circularity, rectangularity and compactness.

ATTRIBUTES - COMPACTNESS (average perim)²/area - CIRCULARITY (average radius)²/area - DISTANCE CIRCULARITY area/(av.distance from border)² - RADIUS RATIO (max.rad-min.rad)/av.radius - PR.AXIS ASPECT RATIO (minor axis)/(major axis) - MAX.LENGTH ASPECT RATIO (length perp. max length)/(max length) - SCATTER RATIO (inertia about minor axis)/(inertia about major axis) - ELONGATEDNESS area/(shrink width)² - PR.AXIS RECTANGULARITY area/(pr.axis lengthpr.axis width) - MAX.LENGTH RECTANGULARITY area/(max.lengthlength perp. to this) - SCALED VARIANCE (2nd order moment about minor axis)/area ALONG MAJOR AXIS - SCALED VARIANCE (2nd order moment about major axis)/area ALONG MINOR AXIS - SCALED RADIUS OF GYRATION (mavar+mivar)/area - SKEWNESS ABOUT (3rd order moment about major axis)/sigma_min³ MAJOR AXIS - SKEWNESS ABOUT (3rd order moment about minor axis)/sigma_maj³ MINOR AXIS - KURTOSIS ABOUT (4th order moment about major axis)/sigma_min⁴ MINOR AXIS - KURTOSIS ABOUT (4th order moment about minor axis)/sigma_maj⁴ MAJOR AXIS - HOLLOWS RATIO (area of hollows)/(area of bounding polygon)

5.0.1 Features

- Number of atributes: 18
- Number of samples: 946

```
[16]: d = pd.read_table("merge-data",delimiter=" ",header=None)

# Clean data
del d[19]
datos = pd.DataFrame(d).dropna()
datos = datos.to_numpy()
print("Filas, columnas",datos.shape)

colores = datos[ : , 18 ]
datos = datos[ : , : 18 ]
```

Filas, columnas (846, 19)

5.1 5.2 Pre-processing (Dimensionality Reduction)

```
[17]: from sklearn.decomposition import PCA
pca = PCA(n_components=2)
datos_pca = pca.fit_transform( datos )
```

5.2 5.2 Split Dataset Train/Test

```
[18]: # Shuffe data
np.random.shuffle(datos_pca)
```

5.3 5.3 Pre-processing (Normalization)

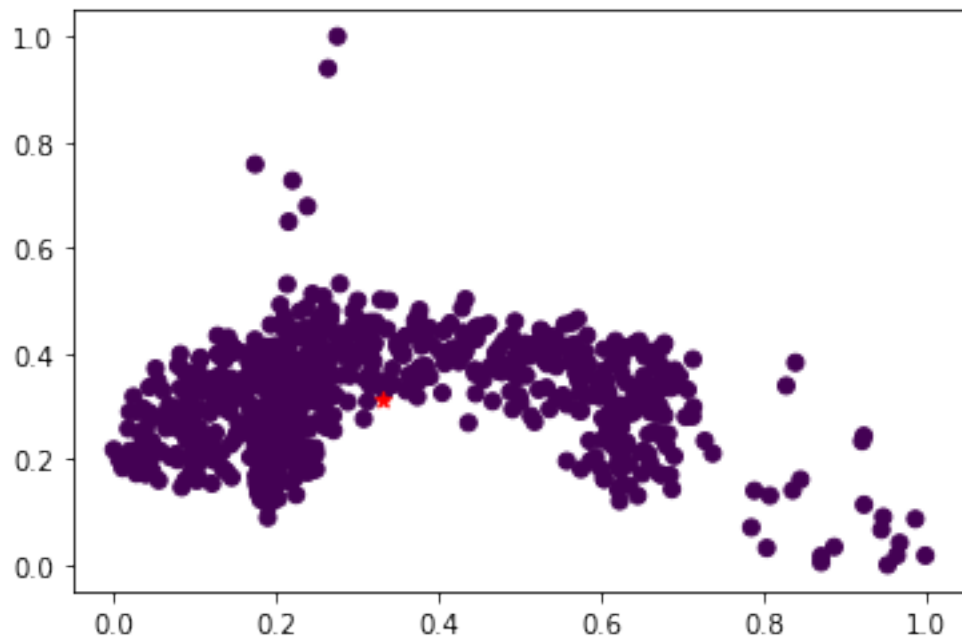
```
[19]: datos_train = datos_pca[:int(0.9*len(datos))]  
      datos_test = datos_pca[int(0.9*len(datos)):]  
  
      x_train = datos_train[:,0]  
      y_train = datos_train[:,1]  
  
      x_test = datos_test[:,0]  
      y_test = datos_test[:,1]  
  
      x_max_train = x_train.max()  
      x_min_train= x_train.min()  
      y_max_train = y_train.max()  
      y_min_train = y_train.min()  
  
      x_max_test = x_test.max()  
      x_min_test = x_test.min()  
      y_max_test = y_test.max()  
      y_min_test = y_test.min()  
  
      x_n_train, y_n_train =  
          ↪norm(x_train,y_train,x_max_train,x_min_train,y_max_train,y_min_train)  
      x_n_test, y_n_test =  
          ↪norm(x_test,y_test,x_max_test,x_min_test,y_max_test,y_min_test)
```

5.4 5.4 KMEANS

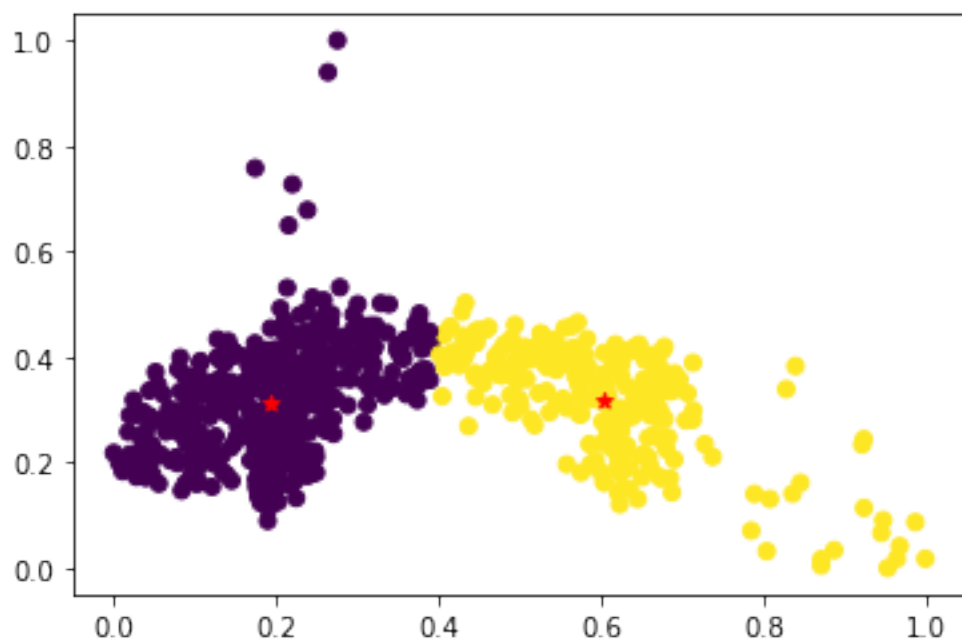
Choose the best k

```
[20]: elbow_method(10,x_n_train,y_n_train)
```

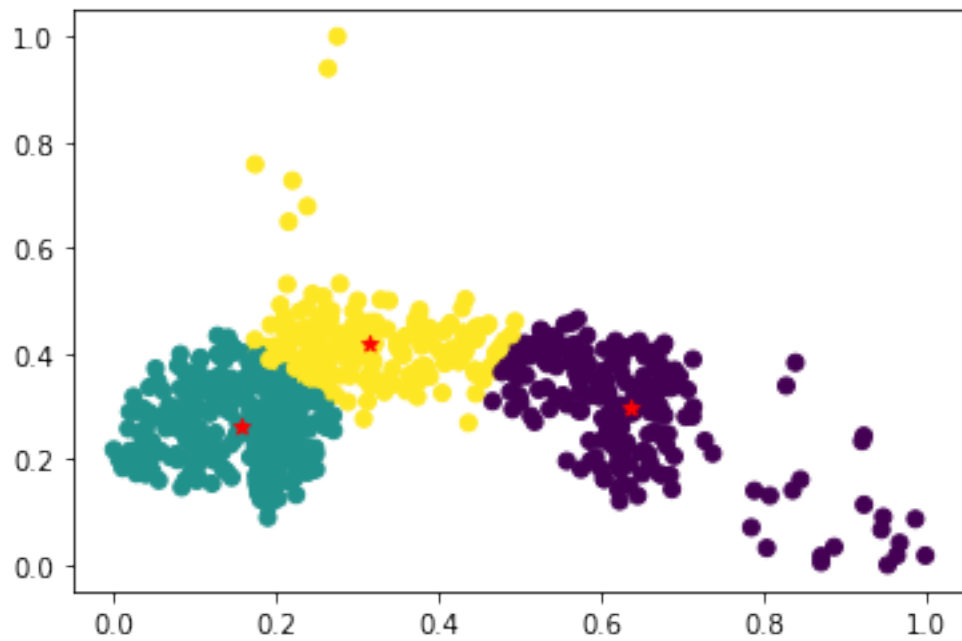
DISTORTION = 44.38821470575579 Clusters= 1



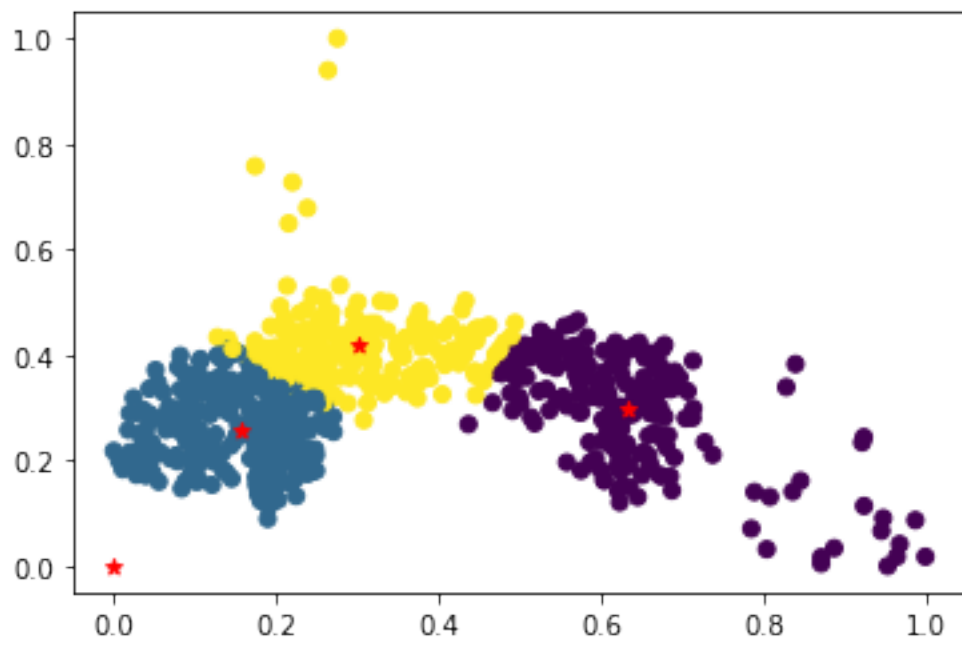
DISTORTION = 15.908904266106568 Clusters= 2



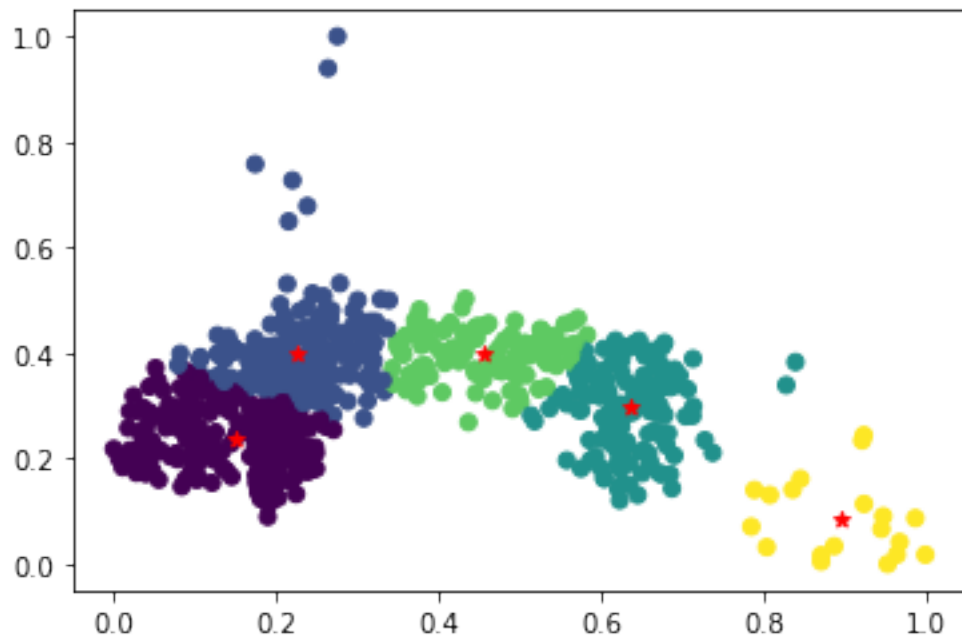
DISTORTION = 10.723865665143528 Clusters= 3



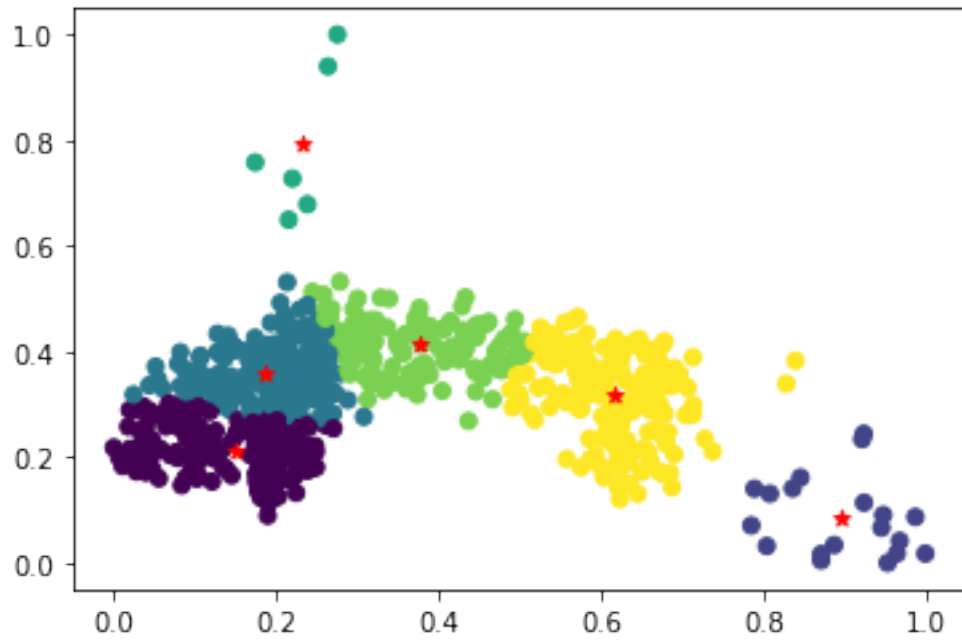
DISTORTION = 10.75255906047223 Clusters= 4



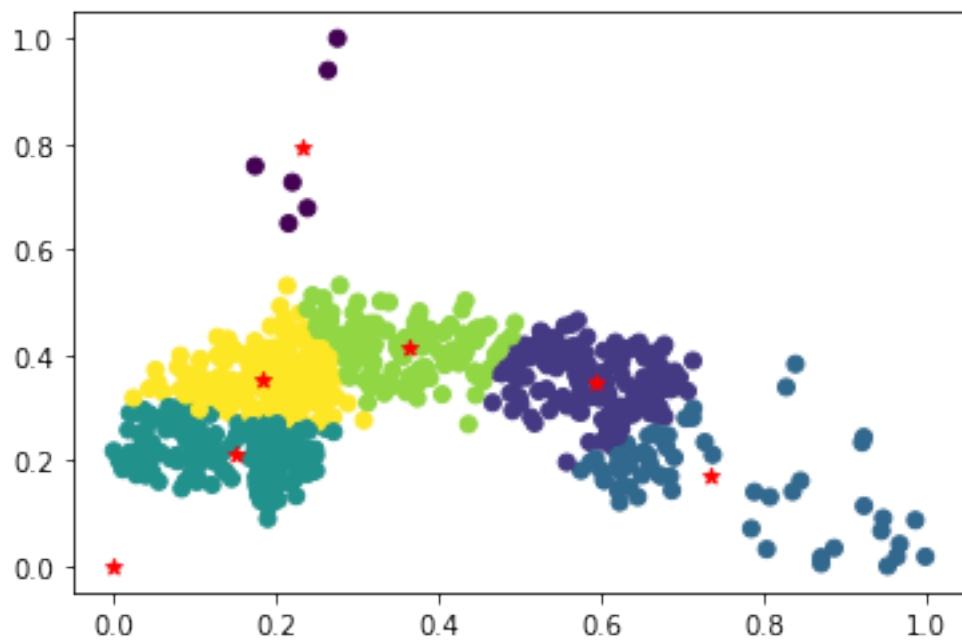
DISTORTION = 6.471851740824892 Clusters= 5



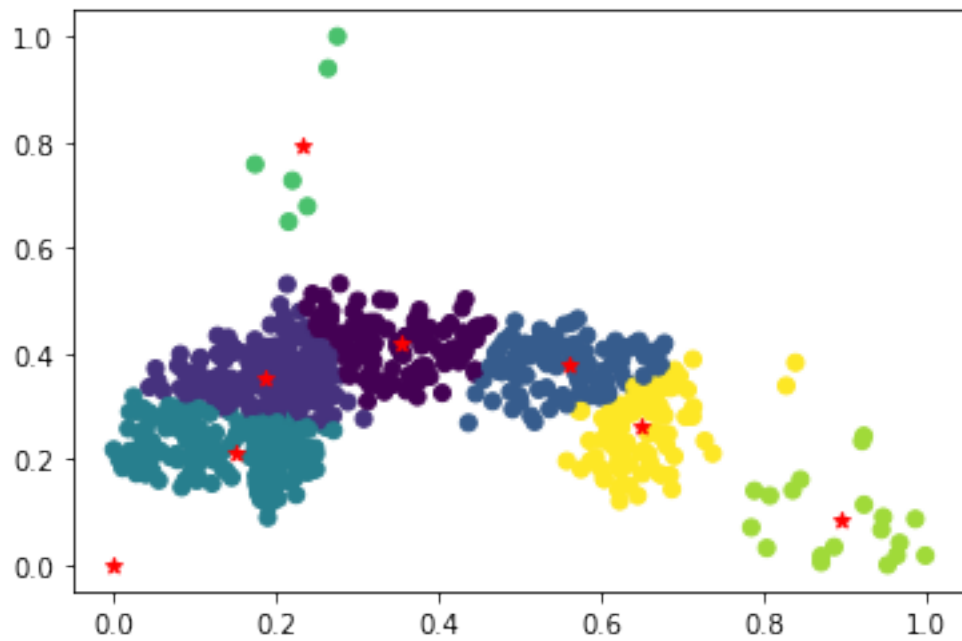
DISTORTION = 5.620418391248892 Clusters= 6



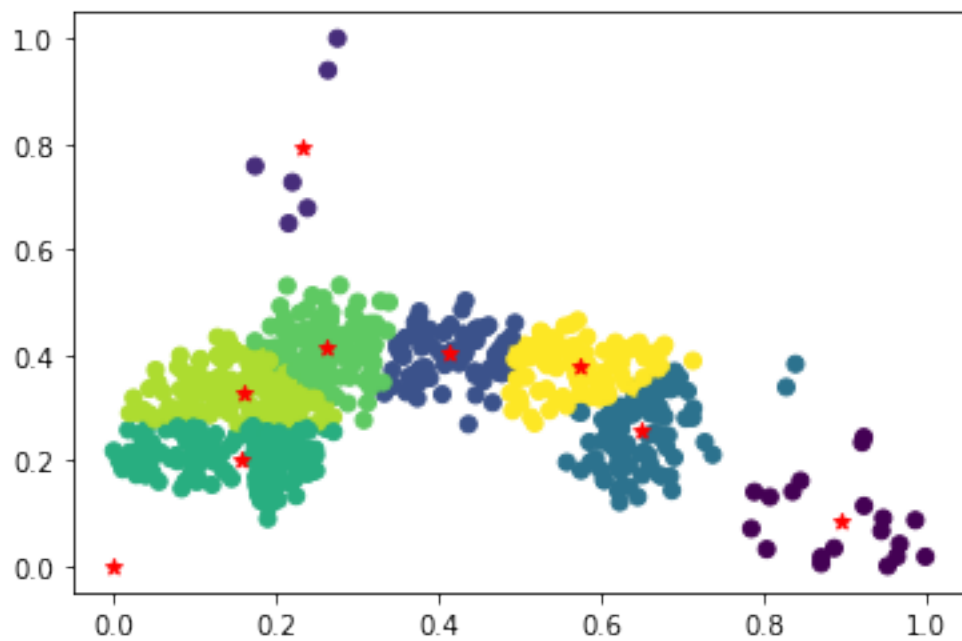
DISTORTION = 5.798964326519122 Clusters= 7



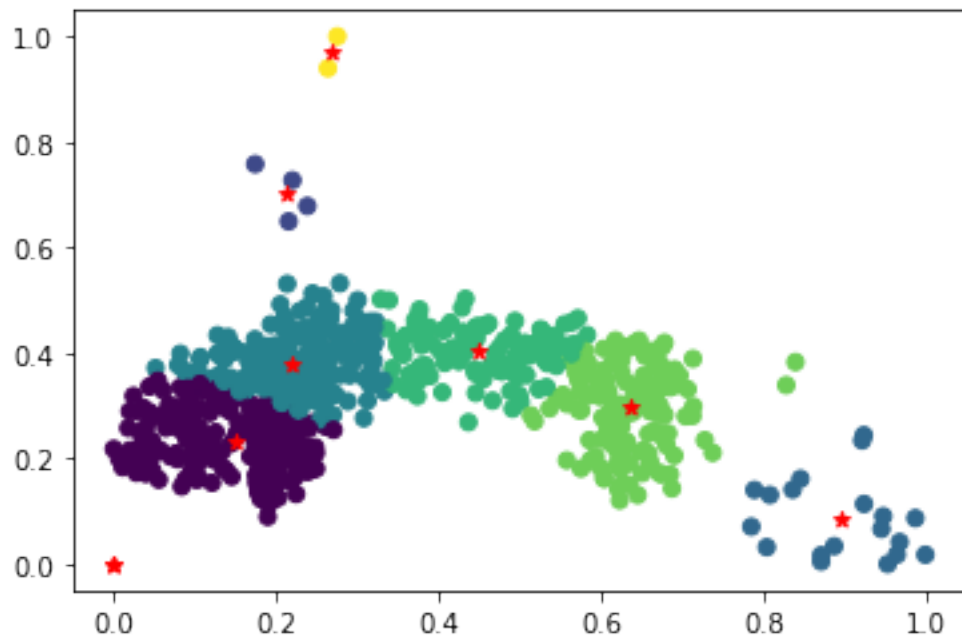
DISTORTION = 4.6404134789136595 Clusters= 8



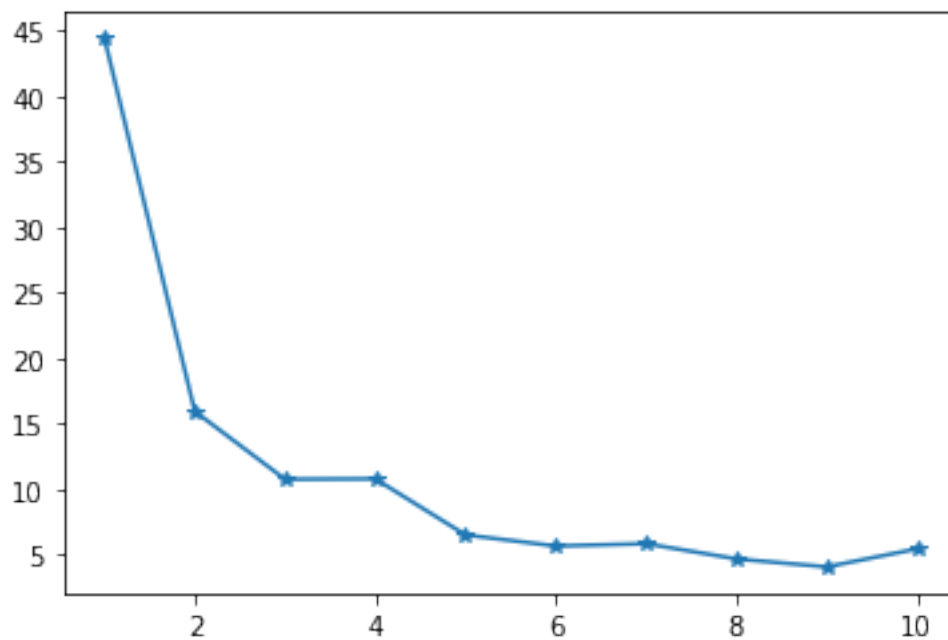
DISTORTION = 4.027662056260145 Clusters= 9



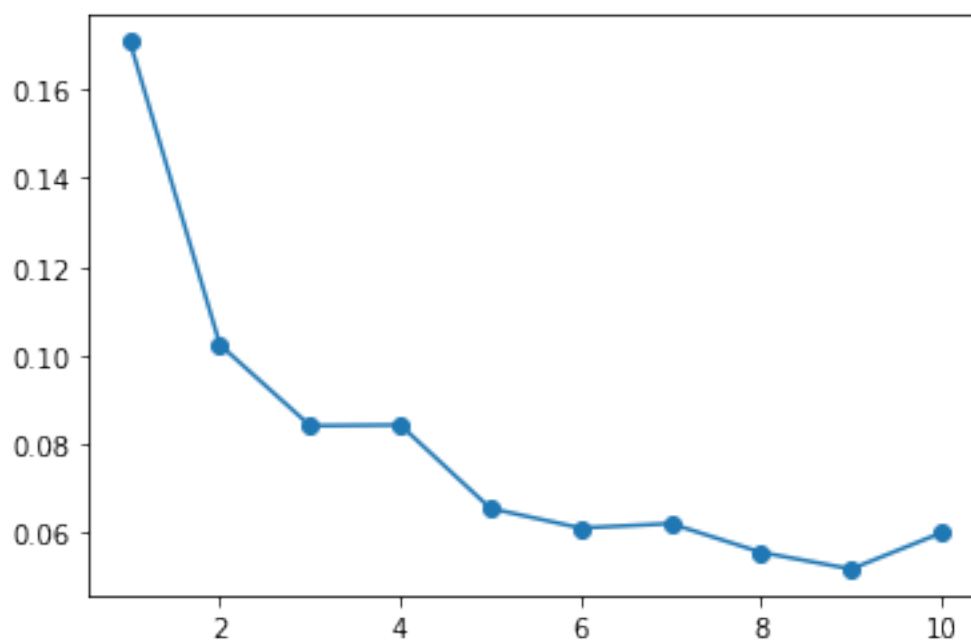
DISTORTION = 5.39590473246261 Clusters= 10



Distortion



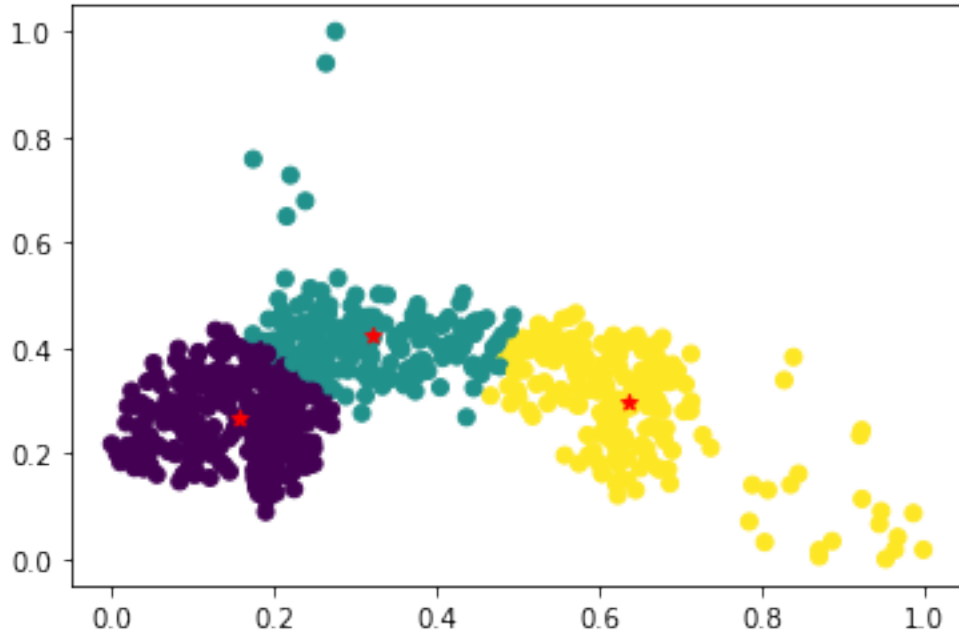
Root Mean Squared Standard Deviation



By observation we could choose $k = 3$

```
[21]: # k = 3
centroide_x , centroide_y , matriz_clusters , distortion =
↳ kmeans(3,x_n_train,y_n_train)
rmmstd = RMSSTD(x_n_train,y_n_train,centroide_x,centroide_y, matriz_clusters, 3)
print( "ERROR TRAIN:", rmmstd )
```

DISTORTION = 10.723264121452793 Clusters= 3



ERROR TRAIN: 0.08410346734799742

5.4.1 Dataset Test

```
[22]: matriz_clusters_test = get_clusters(x_n_test,y_n_test,centroide_x,centroide_y,3)
rmmstd = RMSSTD(x_n_test,y_n_test,centroide_x,centroide_y, matriz_clusters_test,
↳ , 3)
print( "ERROR TEST:", rmmstd )
```

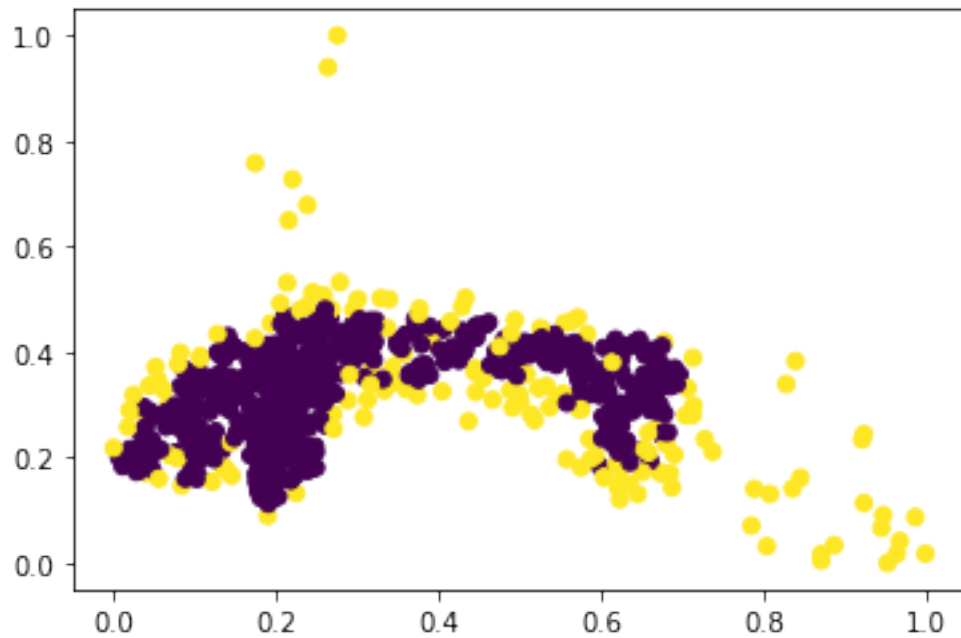
ERROR TEST: 0.09913234799660305

5.5 DBSCAN

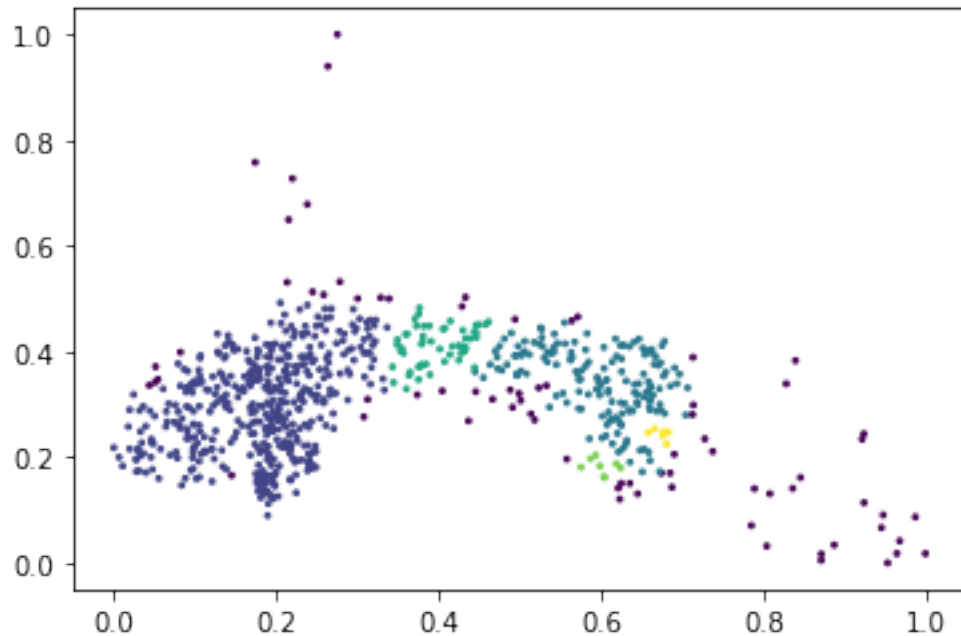
```
[23]: centroide_x , centroide_y , matriz_clusters , k = dbscan(x_n_train, y_n_train,
↳ 0.026 , 6 )
```

```
rmmstd_train = RMSSTD(x_n_train,y_n_train,centroide_x,centroide_y,↵  
↵matriz_clusters, k)  
  
print( "ERROR TRAIN:", rmmstd_train )
```

Borders and Core Points



Final Clusters formed



ERROR TRAIN: 0.10397073920056393

5.5.1 Dataset Test

```
[24]: matriz_clusters_test = get_clusters(x_n_test,y_n_test,centroide_x,centroide_y,k)
      rmmstd = RMSSTD(x_n_test,y_n_test,centroide_x,centroide_y, matriz_clusters_test,
      ↪,k)
      print( "ERROR TEST:", rmmstd )
```

ERROR TEST: 0.10196276795546559

Comparing both RMSSTD's methods

	Kmeans	DBSCAN
Train	0.0841	0.1039
Test	0.0991	0.1019

In this case, Kmeans is superior. But it doesn't mean, the clusters are better. It could be interpreted in several ways.

5.5.2 Contributions

Luis Bernal: - KMeans Implementation - DBScan - Plotting

Jarol Butron - Error Metrics - Elbow method - PCA Dims. Reduction

5.6 6. Bibliography

- Turing Institute Research Memorandum TIRM-87-018 “Vehicle Recognition Using Rule Based Methods” by Siebert,JP (March 1987)