Part II: Practical applications

2.1 K-means clustering

In Python you can use the function KMeans() from the module sklearn.cluster to perform K-means clustering. To begin you will perform K-means with simulated data. Follow the steps:

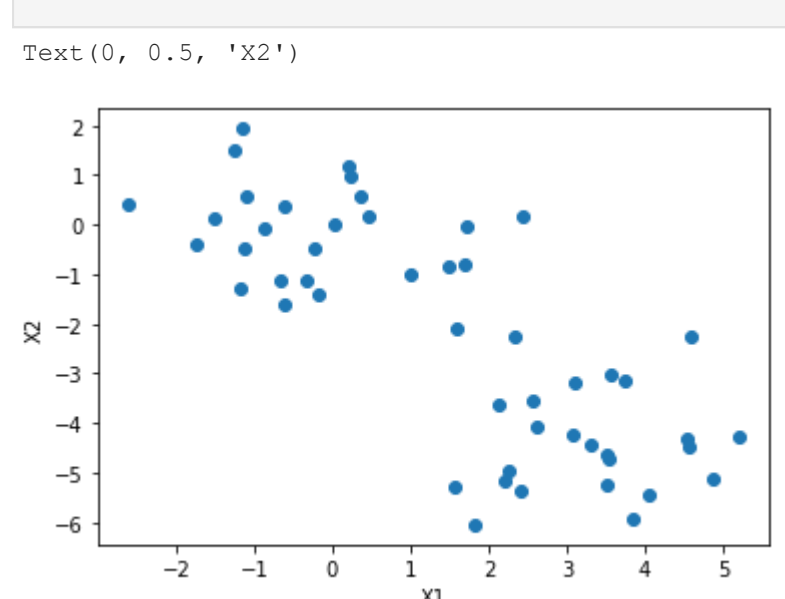
(a) The simulated data will consist in 50 observations described by two normal-distributed variables. In order to define classes in the data the first 25 observations have a mean shift relative to the next 25 observations.

In [21]:
```
import numpy   as   np
X  =  np.random.randn(50,2)
X[0:25, 0]  =  X[0:25, 0] + 3
X[0:25, 1]  =  X[0:25, 1] - 4
```

You can plot the observations and notice that there are two well separated clusters :

In [22]:
```
import matplotlib.pyplot as plt
plt.plot(X[:, 0], X[:,1], "o")
plt.xlabel("X1")
plt.ylabel("X2")
```

Out[22]:
```
Text(0, 0.5, 'X2')
```



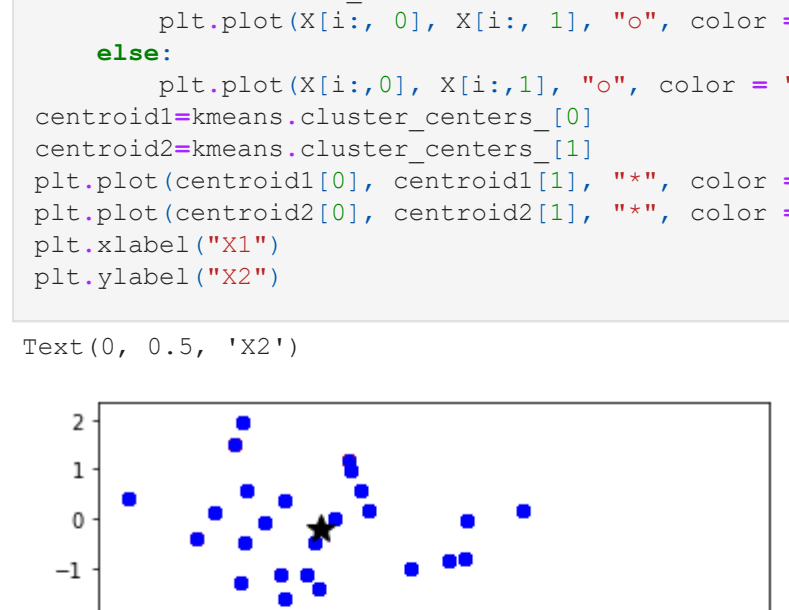
(b) Performs K-means clustering with K=2. Use the following command:

In [23]:
```
from sklearn.cluster import KMeans
kmeans = KMeans(n_clusters = 2, random_state = 100).fit(X)
```

Then, the cluster assignments can be obtained by running print(kmeans.labels_). The final clusters centroids can be known using the command print(kmeans.cluster*centers*). In addition, you can plot the observations using a different color per cluster by running the following code:

In [24]:
```
for i in range(0, X.shape[0]):
    if kmeans.labels_[i]==0:
        plt.plot(X[i:, 0], X[i:, 1], "o", color = "red")
    else:
        plt.plot(X[i:,0], X[i:,1], "o", color = "blue")
centroid1=kmeans.cluster_centers_[0]
centroid2=kmeans.cluster_centers_[1]
plt.plot(centroid1[0], centroid1[1], "*", color = "black", markersize = 15)
plt.plot(centroid2[0], centroid2[1], "*", color = "black", markersize = 15)
plt.xlabel("X1")
plt.ylabel("X2")
```

Out[24]:
```
Text(0, 0.5, 'X2')
```



(c)Now, you are going to perform K−means with real data. The fileHCVdata.csv contains laboratory values of blood donors and Hepatitis C patients and demographic values like age. There are 12 variables, features 4-12 concern laboratory data (ALB, ALT, AST, BIL,CHE, CHOL, CREA, GGT and PROT). Import the data set and get familiar with the data. Answer the following questions :

1. How many observations are there ? There are 567 observations.
2. How many variables are there ? There are 13 variables.
3. What type of variables (numeric, categorical) ? For each categorical variable (if any)give the number of levels and categories. You will denote the resulting dataframe objectdfHVC.

Let's read the data from the csv file and see the variables' data types.

In [25]:
```
import pandas as pd
dfHVC = pd.read_csv('HCVdata.csv', sep=';')
dfHVC.columns.tolist()
```

Out[25]:
```
['Unnamed: 0',
 'Category',
 'Sex',
 'Age',
 'ALB',
 'ALT',
 'AST',
 'BIL',
 'CHE',
 'CHOL',
 'CREA',
 'GGT',
 'PROT']
```

In [26]:
```
dfHVC.head(20)
```

Out[26]:

	Unnamed: 0	Category	Sex	Age	ALB	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
0	1	0=Blood Donor	m	32	38.5	7.7	22.1	7.5	6.93	3.23	106.0	12.1	69.0
1	2	0=Blood Donor	m	32	38.5	18.0	24.7	3.9	11.17	4.80	74.0	15.6	76.5
2	3	0=Blood Donor	m	32	46.9	36.2	52.6	6.1	8.84	5.20	86.0	33.2	79.3
3	4	0=Blood Donor	m	32	43.2	30.6	22.6	18.9	7.33	4.74	80.0	33.8	75.7
4	5	0=Blood Donor	m	32	39.2	32.6	24.8	9.6	9.15	4.32	76.0	29.9	68.7
5	7	0=Blood Donor	m	32	46.3	17.5	17.8	8.5	7.01	4.79	70.0	16.9	74.5
6	8	0=Blood Donor	m	32	42.2	35.8	31.1	16.1	5.82	4.60	109.0	21.5	67.1
7	9	0=Blood Donor	m	32	50.9	23.2	21.2	6.9	8.69	4.10	83.0	13.7	71.3
8	10	0=Blood Donor	m	32	42.4	20.3	20.0	35.2	5.46	4.45	81.0	15.9	69.9
9	11	0=Blood Donor	m	32	44.3	21.7	22.4	17.2	4.15	3.57	78.0	24.1	75.4
10	12	0=Blood Donor	m	33	46.4	10.3	20.0	5.7	7.36	4.30	79.0	18.7	68.6
11	13	0=Blood Donor	m	33	36.3	23.6	22.0	7.0	8.56	5.38	78.0	19.4	68.7
12	14	0=Blood Donor	m	33	39.0	15.9	24.0	6.8	6.46	3.38	65.0	7.0	70.4
13	15	0=Blood Donor	m	33	38.7	22.5	23.0	4.1	4.63	4.97	63.0	15.2	71.9
14	16	0=Blood Donor	m	33	41.8	33.1	38.0	6.6	8.83	4.43	71.0	24.0	72.7
15	17	0=Blood Donor	m	33	40.9	17.2	22.9	10.0	6.98	5.22	90.0	14.7	72.4
16	18	0=Blood Donor	m	33	45.2	32.4	31.2	10.1	9.78	5.51	102.0	48.5	76.5
17	19	0=Blood Donor	m	33	36.6	38.9	40.3	24.9	9.62	5.50	112.0	27.6	69.3
18	20	0=Blood Donor	m	33	42.0	32.6	34.9	11.2	7.01	4.05	105.0	19.1	68.1
19	21	0=Blood Donor	m	33	44.3	32.1	21.6	13.1	7.44	5.59	103.0	30.2	74.0

In [27]:
```
dfHVC.tail(20)
```

Out[27]:

	Unnamed: 0	Category	Sex	Age	ALB	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
547	595	3=Cirrhosis	m	51	33.0	4.5	66.6	91.0	4.02	4.08	75.9	28.5	62.3
548	596	3=Cirrhosis	m	56	27.0	17.0	319.8	37.0	1.42	3.54	66.9	93.7	65.3
549	597	3=Cirrhosis	m	56	23.0	5.1	123.0	43.0	1.80	2.40	62.7	35.9	62.8
550	598	3=Cirrhosis	m	56	30.0	0.9	80.3	119.0	1.88	1.43	79.3	17.6	54.2
551	599	3=Cirrhosis	m	58	31.0	7.0	181.8	58.0	3.29	3.92	66.4	273.7	78.1
552	600	3=Cirrhosis	m	59	36.0	5.2	110.1	37.0	2.29	3.68	118.2	56.9	74.8
553	601	3=Cirrhosis	m	59	27.0	4.0	65.2	209.0	2.47	3.61	71.7	28.5	60.6
554	602	3=Cirrhosis	m	59	31.0	5.4	95.4	117.0	1.57	3.51	60.5	53.6	68.5
555	603	3=Cirrhosis	m	61	39.0	27.3	143.2	15.0	5.38	4.88	72.3	400.3	73.4
556	605	3=Cirrhosis	m	74	23.0	2.1	90.4	22.0	2.50	3.29	51.0	46.8	57.1
557	606	3=Cirrhosis	f	42	33.0	3.7	55.7	200.0	1.72	5.16	89.1	146.3	69.9
558	607	3=Cirrhosis	f	49	33.0	1.2	36.3	7.0	6.92	3.82	485.9	112.0	58.5
559	608	3=Cirrhosis	f	52	39.0	1.3	30.4	21.0	6.33	3.78	158.2	142.5	82.7
560	609	3=Cirrhosis	f	58	34.0	15.0	150.0	8.0	6.26	3.98	56.0	49.7	80.6
561	610	3=Cirrhosis	f	59	39.0	19.6	285.8	40.0	5.77	4.51	136.1	101.1	70.5
562	611	3=Cirrhosis	f	62	32.0	5.9	110.3	50.0	5.57	6.30	55.7	650.9	68.5
563	612	3=Cirrhosis	f	64	24.0	2.9	44.4	20.0	1.54	3.02	63.0	35.9	71.3
564	613	3=Cirrhosis	f	64	29.0	3.5	99.0	48.0	1.66	3.63	66.7	64.2	82.0
565	614	3=Cirrhosis	f	46	33.0	39.0	62.0	20.0	3.56	4.20	52.0	50.0	71.0
566	615	3=Cirrhosis	f	59	36.0	100.0	80.0	12.0	9.07	5.30	67.0	34.0	68.0

In [28]:
```
dfHVC.dtypes
```

Out[28]:
```
Unnamed: 0       int64
Category        object
Sex             object
Age              int64
ALB            float64
ALT            float64
AST            float64
BIL            float64
CHE            float64
CHOL           float64
CREA           float64
GGT            float64
PROT           float64
dtype: object
```

In [29]:
```
dfHVC['Sex'] = dfHVC['Sex'].astype('category');
dfHVC['Category'] = dfHVC['Category'].astype('category');
dfHVC.dtypes
```

Out[29]:
```
Unnamed: 0        int64
Category       category
Sex            category
Age               int64
ALB             float64
ALT             float64
AST             float64
BIL             float64
CHE             float64
CHOL            float64
CREA            float64
GGT             float64
PROT            float64
dtype: object
```

The Category variable can be simplifies, so that there can be only numbers. For '0=Blood Donors' the value would be '0', for '1=Hepatitis' the value would be '1', and for '2=Fibrosis' would be '2', then for the '3=Cirrhosis' the value would be '3'.

In [30]:
```
dfHVC["Category"].replace({"0=Blood Donor": "0",
                           "1=Hepatitis": "1",
                           "2=Fibrosis": "2",
                           "3=Cirrhosis":"3"},
                           inplace=True)

dfHVC.tail(30)
```

Out[30]:

	Unnamed: 0	Category	Sex	Age	ALB	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
537	583	2	f	51	37.0	164.0	70.0	9.0	3.99	4.20	67.0	43.0	72.0
538	584	2	f	56	39.0	42.0	34.0	10.0	7.75	5.00	80.0	84.0	78.0
539	586	3	m	38	44.0	94.0	60.0	12.0	4.37	3.20	61.0	99.0	77.0
540	587	3	m	39	34.0	4.8	35.6	9.0	3.65	4.82	519.0	133.4	57.5
541	588	3	m	41	31.0	4.8	60.2	200.0	1.80	5.34	106.4	151.0	71.8
542	589	3	m	42	36.0	14.9	263.1	40.0	3.61	3.93	49.6	61.0	68.6
543	590	3	m	45	29.0	7.1	101.9	31.0	1.73	3.71	76.7	65.6	70.0
544	592	3	m	46	35.0	2.3	19.2	11.0	7.10	4.10	1079.1	105.6	69.1
545	593	3	m	47	42.0	159.0	102.0	11.0	6.29	5.50	58.0	201.0	79.0
546	594	3	m	51	39.0	29.6	185.0	19.0	2.00	3.60	58.3	399.5	79.4
547	595	3	m	51	33.0	4.5	66.6	91.0	4.02	4.08	75.9	28.5	62.3
548	596	3	m	56	27.0	17.0	319.8	37.0	1.42	3.54	66.9	93.7	65.3
549	597	3	m	56	23.0	5.1	123.0	43.0	1.80	2.40	62.7	35.9	62.8
550	598	3	m	56	30.0	0.9	80.3	119.0	1.88	1.43	79.3	17.6	54.2
551	599	3	m	58	31.0	7.0	181.8	58.0	3.29	3.92	66.4	273.7	78.1
552	600	3	m	59	36.0	5.2	110.1	37.0	2.29	3.68	118.2	56.9	74.8
553	601	3	m	59	27.0	4.0	65.2	209.0	2.47	3.61	71.7	28.5	60.6
554	602	3	m	59	31.0	5.4	95.4	117.0	1.57	3.51	60.5	53.6	68.5
555	603	3	m	61	39.0	27.3	143.2	15.0	5.38	4.88	72.3	400.3	73.4
556	605	3	m	74	23.0	2.1	90.4	22.0	2.50	3.29	51.0	46.8	57.1
557	606	3	f	42	33.0	3.7	55.7	200.0	1.72	5.16	89.1	146.3	69.9
558	607	3	f	49	33.0	1.2	36.3	7.0	6.92	3.82	485.9	112.0	58.5
559	608	3	f	52	39.0	1.3	30.4	21.0	6.33	3.78	158.2	142.5	82.7
560	609	3	f	58	34.0	15.0	150.0	8.0	6.26	3.98	56.0	49.7	80.6
561	610	3	f	59	39.0	19.6	285.8	40.0	5.77	4.51	136.1	101.1	70.5
562	611	3	f	62	32.0	5.9	110.3	50.0	5.57	6.30	55.7	650.9	68.5
563	612	3	f	64	24.0	2.9	44.4	20.0	1.54	3.02	63.0	35.9	71.3
564	613	3	f	64	29.0	3.5	99.0	48.0	1.66	3.63	66.7	64.2	82.0
565	614	3	f	46	33.0	39.0	62.0	20.0	3.56	4.20	52.0	50.0	71.0
566	615	3	f	59	36.0	100.0	80.0	12.0	9.07	5.30	67.0	34.0	68.0

In [31]:
```
dfHVC =  dfHVC.drop(columns=['Unnamed: 0'])
dfHVC.head(20)
```

Out[31]:

	Category	Sex	Age	ALB	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
0	0	m	32	38.5	7.7	22.1	7.5	6.93	3.23	106.0	12.1	69.0
1	0	m	32	38.5	18.0	24.7	3.9	11.17	4.80	74.0	15.6	76.5
2	0	m	32	46.9	36.2	52.6	6.1	8.84	5.20	86.0	33.2	79.3
3	0	m	32	43.2	30.6	22.6	18.9	7.33	4.74	80.0	33.8	75.7
4	0	m	32	39.2	32.6	24.8	9.6	9.15	4.32	76.0	29.9	68.7
5	0	m	32	46.3	17.5	17.8	8.5	7.01	4.79	70.0	16.9	74.5
6	0	m	32	42.2	35.8	31.1	16.1	5.82	4.60	109.0	21.5	67.1
7	0	m	32	50.9	23.2	21.2	6.9	8.69	4.10	83.0	13.7	71.3
8	0	m	32	42.4	20.3	20.0	35.2	5.46	4.45	81.0	15.9	69.9
9	0	m	32	44.3	21.7	22.4	17.2	4.15	3.57	78.0	24.1	75.4
10	0	m	33	46.4	10.3	20.0	5.7	7.36	4.30	79.0	18.7	68.6
11	0	m	33	36.3	23.6	22.0	7.0	8.56	5.38	78.0	19.4	68.7
12	0	m	33	39.0	15.9	24.0	6.8	6.46	3.38	65.0	7.0	70.4
13	0	m	33	38.7	22.5	23.0	4.1	4.63	4.97	63.0	15.2	71.9
14	0	m	33	41.8	33.1	38.0	6.6	8.83	4.43	71.0	24.0	72.7
15	0	m	33	40.9	17.2	22.9	10.0	6.98	5.22	90.0	14.7	72.4
16	0	m	33	45.2	32.4	31.2	10.1	9.78	5.51	102.0	48.5	76.5
17	0	m	33	36.6	38.9	40.3	24.9	9.62	5.50	112.0	27.6	69.3
18	0	m	33	42.0	32.6	34.9	11.2	7.01	4.05	105.0	19.1	68.1
19	0	m	33	44.3	32.1	21.6	13.1	7.44	5.59	103.0	30.2	74.0

Let for the 'Sex' variable 0 is female, and 1 is male.

In [32]:
```
dfHVC["Sex"].replace({"m": "1",
                      "f": "0"},
                       inplace=True)

dfHVC.tail(40)
```

Out[32]:

	Category	Sex	Age	ALB	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
527	2	1	54	41.0	41.5	187.9	21.0	8.59	5.85	91.0	104.9	79.1
528	2	1	57	47.0	10.2	55.9	12.0	6.60	4.64	70.9	69.6	80.9
529	2	1	59	44.0	8.9	74.5	6.0	9.45	4.45	65.0	95.3	69.7
530	2	1	64	38.0	7.1	41.3	13.0	7.10	4.52	70.0	53.0	66.8
531	2	1	71	37.0	130.0	90.0	15.0	9.92	4.70	79.0	77.0	76.0
532	2	0	36	46.0	67.1	161.9	13.0	9.24	4.81	65.3	60.0	73.9
533	2	0	38	40.0	14.9	68.9	11.0	8.55	4.31	60.5	40.1	76.5
534	2	0	57	43.0	8.3	35.8	18.0	8.61	6.19	71.4	27.9	82.0
535	2	0	68	43.0	5.0	42.1	12.0	7.29	4.89	80.9	11.9	76.1
536	2	0	49	39.0	46.0	39.0	9.0	10.21	3.10	89.0	53.0	79.0
537	2	0	51	37.0	164.0	70.0	9.0	3.99	4.20	67.0	43.0	72.0
538	2	0	56	39.0	42.0	34.0	10.0	7.75	5.00	80.0	84.0	78.0
539	3	1	38	44.0	94.0	60.0	12.0	4.37	3.20	61.0	99.0	77.0
540	3	1	39	34.0	4.8	35.6	9.0	3.65	4.82	519.0	133.4	57.5
541	3	1	41	31.0	4.8	60.2	200.0	1.80	5.34	106.4	151.0	71.8
542	3	1	42	36.0	14.9	263.1	40.0	3.61	3.93	49.6	61.0	68.6
543	3	1	45	29.0	7.1	101.9	31.0	1.73	3.71	76.7	65.6	70.0
544	3	1	46	35.0	2.3	19.2	11.0	7.10	4.10	1079.1	105.6	69.1
545	3	1	47	42.0	159.0	102.0	11.0	6.29	5.50	58.0	201.0	79.0
546	3	1	51	39.0	29.6	185.0	19.0	2.00	3.60	58.3	399.5	79.4
547	3	1	51	33.0	4.5	66.6	91.0	4.02	4.08	75.9	28.5	62.3
548	3	1	56	27.0	17.0	319.8	37.0	1.42	3.54	66.9	93.7	65.3
549	3	1	56	23.0	5.1	123.0	43.0	1.80	2.40	62.7	35.9	62.8
550	3	1	56	30.0	0.9	80.3	119.0	1.88	1.43	79.3	17.6	54.2
551	3	1	58	31.0	7.0	181.8	58.0	3.29	3.92	66.4	273.7	78.1
552	3	1	59	36.0	5.2	110.1	37.0	2.29	3.68	118.2	56.9	74.8
553	3	1	59	27.0	4.0	65.2	209.0	2.47	3.61	71.7	28.5	60.6
554	3	1	59	31.0	5.4	95.4	117.0	1.57	3.51	60.5	53.6	68.5
555	3	1	61	39.0	27.3	143.2	15.0	5.38	4.88	72.3	400.3	73.4
556	3	1	74	23.0	2.1	90.4	22.0	2.50	3.29	51.0	46.8	57.1
557	3	0	42	33.0	3.7	55.7	200.0	1.72	5.16	89.1	146.3	69.9
558	3	0	49	33.0	1.2	36.3	7.0	6.92	3.82	485.9	112.0	58.5
559	3	0	52	39.0	1.3	30.4	21.0	6.33	3.78	158.2	142.5	82.7
560	3	0	58	34.0	15.0	150.0	8.0	6.26	3.98	56.0	49.7	80.6
561	3	0	59	39.0	19.6	285.8	40.0	5.77	4.51	136.1	101.1	70.5
562	3	0	62	32.0	5.9	110.3	50.0	5.57	6.30	55.7	650.9	68.5
563	3	0	64	24.0	2.9	44.4	20.0	1.54	3.02	63.0	35.9	71.3
564	3	0	64	29.0	3.5	99.0	48.0	1.66	3.63	66.7	64.2	82.0
565	3	0	46	33.0	39.0	62.0	20.0	3.56	4.20	52.0	50.0	71.0
566	3	0	59	36.0	100.0	80.0	12.0	9.07	5.30	67.0	34.0	68.0

(d) Since all the clustering approaches used in this lab are based upon distancesor dissimilarity measures, it is strongly recommended to scale the variables previously. The following code allows to scale all the variables in a dataframe called dfHVC :

In [33]:
```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
dfHVC_scaled = scaler.fit_transform(dfHVC)
```

Create a dataframe containing all the numeric variables after being scaled, you will name theresulting output dfHVC_scaled.

In [34]:
```
dfHVC_scaled = pd.DataFrame(dfHVC_scaled)
type(dfHVC_scaled)
```

Out[34]:
```
pandas.core.frame.DataFrame
```

(e)

In [57]:
```
dfHVC_Kmeans4=KMeans(n_clusters = 2, n_init = 50, random_state = 1000).fit(dfHVC_scaled)
dfHVC_Kmeans4.cluster_centers_
```

Out[57]:
```
array([[-0.24487944, -0.01427549, -0.03516566,  0.08789789, -0.04734399,
        -0.20142963, -0.13943136,  0.11561622,  0.08670992, -0.06274669,
        -0.15746062,  0.00580842],
       [ 3.06099296,  0.17844356,  0.43957073, -1.09872364,  0.59179983,
         2.51787043,  1.74289203, -1.44520281, -1.08387394,  0.78433365,
         1.96825773, -0.07260523]])
```

In [60]:
```
pd.crosstab(index=dfHVC.Sex, columns=dfHVC_Kmeans4.labels_, rownames=['Real groups'], colnames=['K-means cluste
```

Out[60]:

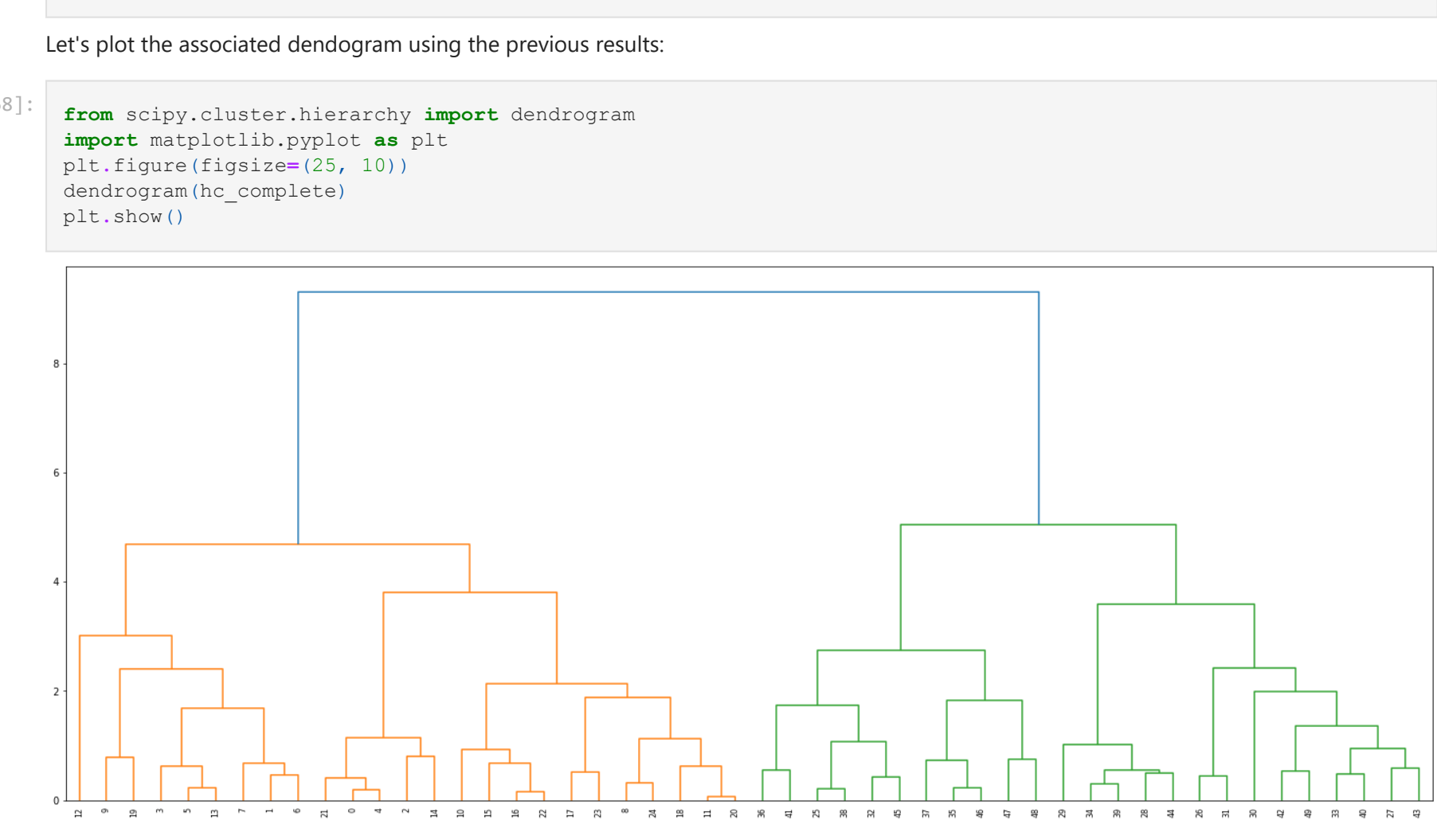
K-means clusters	0	1
Real groups		
0	212	13
1	313	29

2.2

In [67]:
```
from scipy.cluster.hierarchy import linkage
hc_complete = linkage(X, "complete")
```

Let's plot the associated dendogram using the previous results:

In [68]:
```
from scipy.cluster.hierarchy import dendrogram
import matplotlib.pyplot as plt
plt.figure(figsize=(25, 10))
dendrogram(hc_complete)
plt.show()
```



We remark the 2 clusters are clearly identified, which is normal because we performed hierarchical clustering with simulated data. To determine the cluster labels for each observation associated with a given cut of the dendrogram, you can use the cut_tree() function from the scipy.cluster.hierarchy module . For example, to obtain two clusters you can execute the code

In [69]:
```
from scipy.cluster.hierarchy import cut_tree
print(cut_tree(hc_complete, n_clusters=2).T)
```

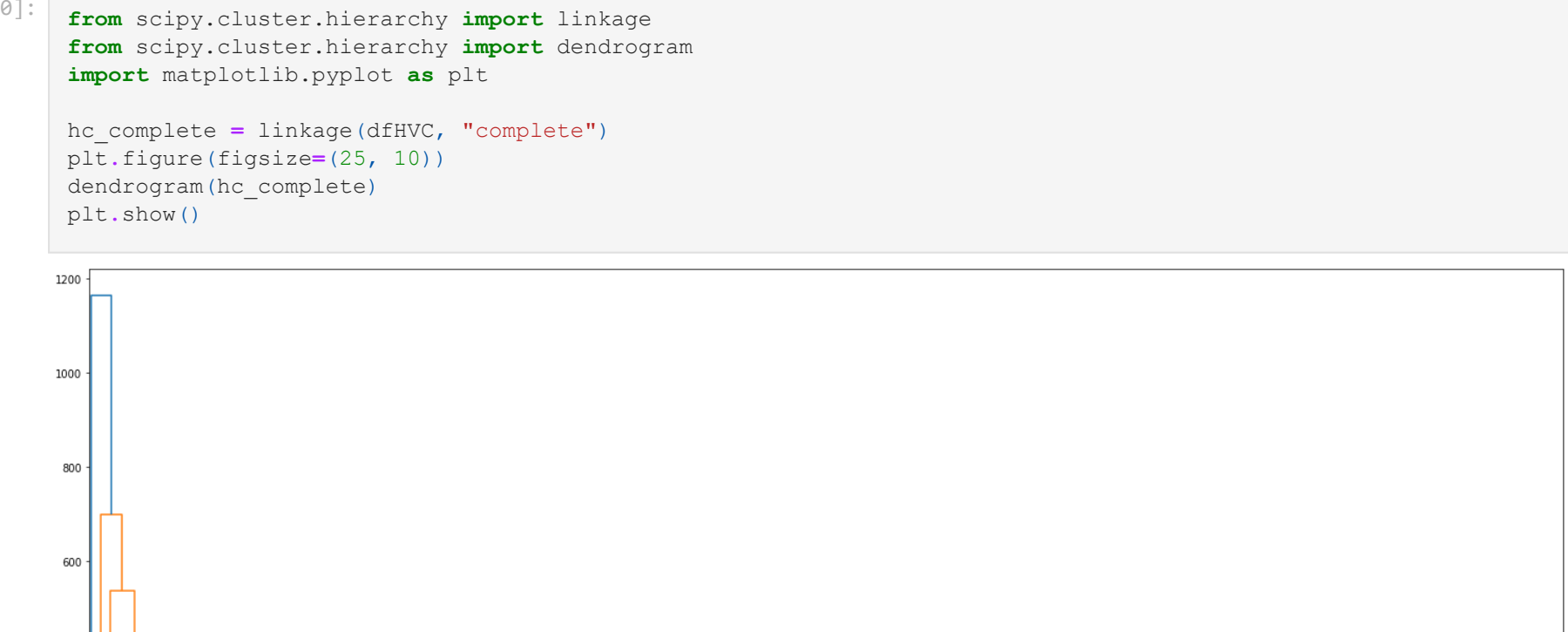
```
[[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1
  1 1 1 1 1 1 1 1 1 1 1 1 1 1]]
```

(a) Perform hierarchical clustering using the HCVdata using complete, average and single linkage. To begin you will cut the dendrogram at 4 clusters. Similarly to the previous section, calculate the matching matrix and comment the results.

Complete

In [70]:
```
from scipy.cluster.hierarchy import linkage
from scipy.cluster.hierarchy import dendrogram
import matplotlib.pyplot as plt

hc_complete = linkage(dfHVC, "complete")
plt.figure(figsize=(25, 10))
dendrogram(hc_complete)
plt.show()
```

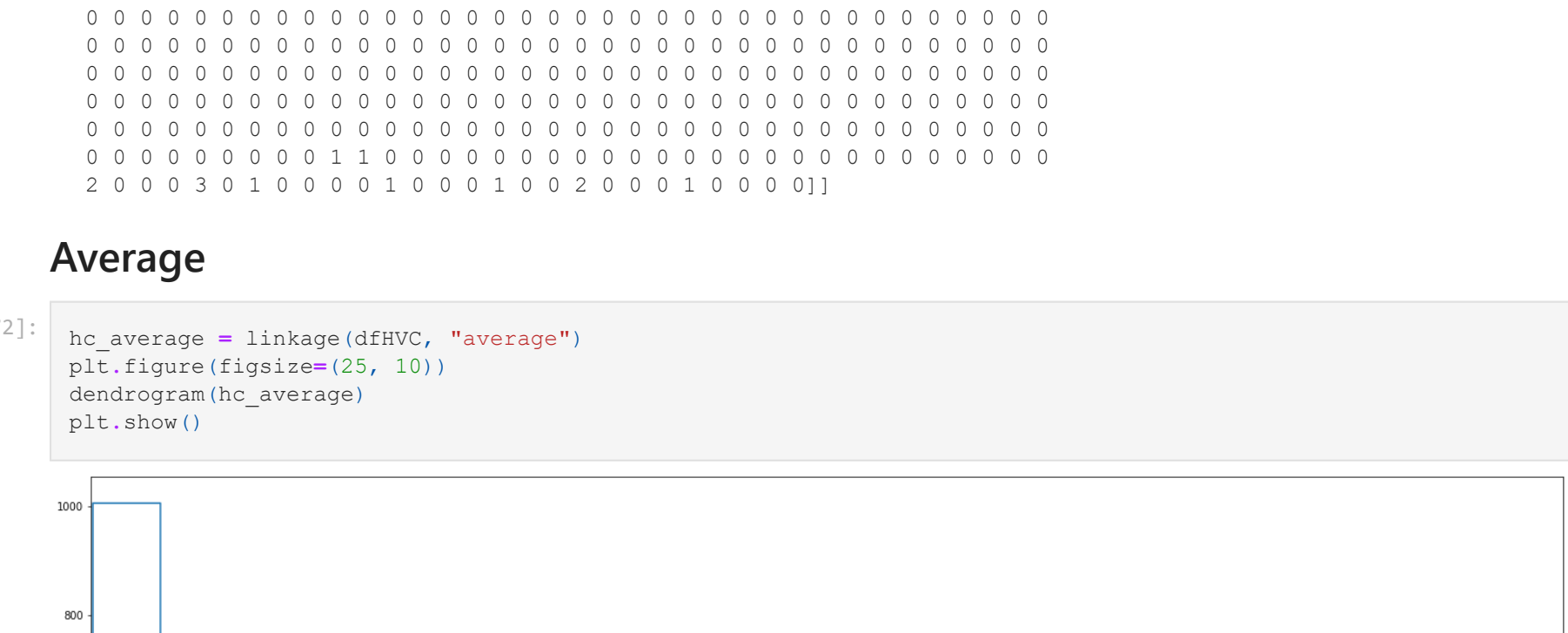


In [71]:
```
print(cut_tree(hc_complete, n_clusters=4).T)
```

```
[[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 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 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 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 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 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 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 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 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 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 0 0 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
  2 0 0 0 3 0 1 0 0 0 0 1 0 0 0 1 0 0 2 0 0 0 1 0 0 0 0]]
```

Average

In [72]:
```
hc_average = linkage(dfHVC, "average")
plt.figure(figsize=(25, 10))
dendrogram(hc_average)
plt.show()
```

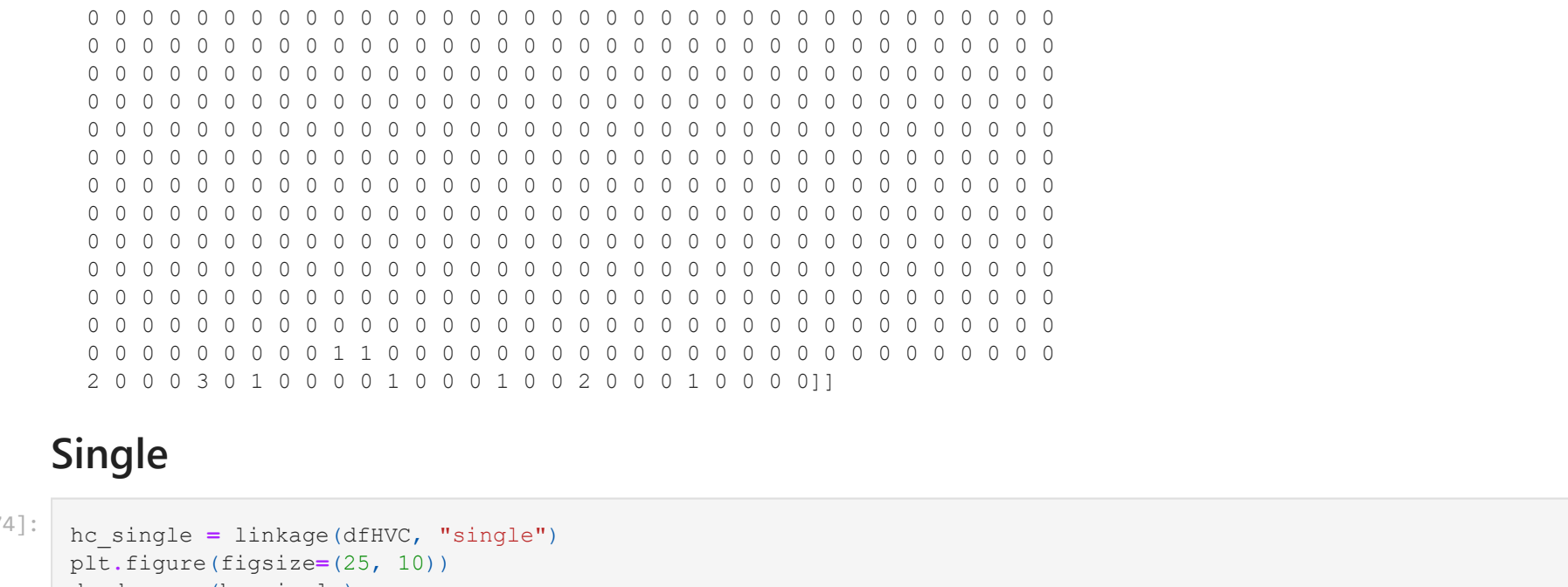


In [73]:
```
print(cut_tree(hc_average, n_clusters=4).T)
```

```
[[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 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 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 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 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 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 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 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 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 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 0 0 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
  2 0 0 0 3 0 1 0 0 0 0 1 0 0 0 1 0 0 2 0 0 0 1 0 0 0 0]]
```

Single

In [74]:
```
hc_single = linkage(dfHVC, "single")
plt.figure(figsize=(25, 10))
dendrogram(hc_single)
plt.show()
```



In [75]:
```
print(cut_tree(hc_single, n_clusters=4).T)
```

```
[[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 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 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 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 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 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 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 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 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 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 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 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 3 0 0 0 0]]
```