<pre>from sklearn.cluste from sklearn.metric from sklearn.prepro # Import visualizat import matplotlib.p import seaborn as s</pre>	es import silhouette_score ocessing import StandardScaler sion packages. Description of the side of t		$t\6$. The nuts and bolts of M	3. Module 3\2. Evaluate K	eans\Files\penguins.csv')			
	bill_length_mm bill_depth_mm flipped 39.1 18.7 39.5 17.4 40.3 18.0 NaN NaN 36.7 19.3 39.3 20.6 38.9 17.8 39.2 19.6	181.0 186.0 195.0 NaN 193.0 190.0	_mass_g sex 3750.0 male 3800.0 female 3250.0 female NaN NaN 3450.0 female 3650.0 male 3625.0 female 4675.0 male					
8 Adelie Torgersen 9 Adelie Torgersen 578 # Review the first penguins.head(n = 1	34.1 18.1 42.0 20.2	193.0 190.0	3475.0 NaN 4250.0 NaN					
 Adelie Torgersen 	39.1 18.7 39.5 17.4 40.3 18.0 NaN NaN 36.7 19.3	181.0 186.0 195.0 NaN	3750.0 male 3800.0 female 3250.0 female NaN NaN 3450.0 female					
 5 Adelie Torgersen 6 Adelie Torgersen 7 Adelie Torgersen 8 Adelie Torgersen 9 Adelie Torgersen 	39.3 20.6 38.9 17.8 39.2 19.6 34.1 18.1 42.0 20.2	193.0	3650.0 male 3625.0 female 4675.0 male 3475.0 NaN 4250.0 NaN					
penguins['species'] [580 array(['Adelie', 'G [582 # Find the count of penguins['species']	Chinstrap', 'Gentoo'], dtype=c							
[582 species Adelie 152 Gentoo 124 Chinstrap 68 Name: count, dtype [584 # Check for missing penguins.isnull().s	g values.							
bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex dtype: int64 # Drop rows with mi # Save DataFrame in	2 2 2 2 11 issing values. n variable `penguins_subset`. penguins.dropna(axis=0).reset_							
penguins_subset.ism [588 species island bill_length_mm bill_depth_mm flipper_length_mm	y values.	index (diop = liu)						
body_mass_g sex dtype: int64 # View first 10 row penguins_subset.hea species island O Adelie Torgersen		er_length_mm body_ 181.0	_mass_g sex 3750.0 male					
 Adelie Torgersen Adelie Torgersen Adelie Torgersen Adelie Torgersen Adelie Torgersen Adelie Torgersen 	39.5 17.4 40.3 18.0 36.7 19.3 39.3 20.6 38.9 17.8	190.0 181.0	3800.0 female 3250.0 female 3450.0 female 3650.0 male 3625.0 female					
 Adelie Torgersen Adelie Torgersen Adelie Torgersen Adelie Torgersen penguins_subset['se 	39.2 19.6 41.1 17.6 38.6 21.2 34.6 21.1 ex'] = penguins_subset['sex'].	182.0 191.0 198.0	4675.0 male 3200.0 female 3800.0 male 4400.0 male					
<pre>penguins_subset = p 596 # Drop the island of penguins_subset = p 598 # Exclude `species`</pre>	penguins_subset.drop(['island' ' variable from X	c, drop_first = Tr	rue, columns=['sex'])					
#Scale the features #Assign the scaled X_scaled = Standard [602 # Fit K-means and e	<pre>c.drop(['species'], axis=1) s. data to variable `X_scaled`. dScaler().fit_transform(X) evaluate inertia for different for i in range(2, 11)]</pre>							
Accepts as arguments a KMeans of Returns each k- """ inertia = [] for num in num_ kms = KMean kms.fit(x_v	ns(n_clusters=num, random_state	the list of ints.						
return inertia [614 # Return a list of inertia = kmeans_in inertia C:\Users\HP\anaconda ment variable OMP_NU	<pre>inertia for k=2 to 10. nertia(num_clusters, X_scaled) a3\Lib\site-packages\sklearn\cdots</pre>		y:1446: UserWarning: KMeans	known to have a memory lea	k on Windows with MKL, when ther	e are less chunks than availabl	e threads. You can avoid it	by setting the e
ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda	M_THREADS=2. 3\Lib\site-packages\sklearn\c. M_THREADS=2. 3\Lib\site-packages\sklearn\c. M_THREADS=2. 3\Lib\site-packages\sklearn\c.	luster_kmeans.py	y:1446: UserWarning: KMeans y:1446: UserWarning: KMeans	known to have a memory leak	k on Windows with MKL, when then	e are less chunks than available e are less chunks than available	e threads. You can avoid it is to be a second in the secon	by setting the e
ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn(.3\Lib\site-packages\sklearn\c. IM_THREADS=2. .3\Lib\site-packages\sklearn\c. IM_THREADS=2. .3\Lib\site-packages\sklearn\c. IM_THREADS=2.	luster_kmeans.py	y:1446: UserWarning: KMeans y:1446: UserWarning: KMeans	known to have a memory leak	k on Windows with MKL, when then k on Windows with MKL, when then k on Windows with MKL, when then	e are less chunks than available e are less chunks than available	e threads. You can avoid it is to be a second in the secon	by setting the e
C:\Users\HP\anaconda ment variable OMP_NU warnings.warn([614 [885.622414365225, 578.8284278107235, 477.22956735281946 284.5464837898288, 218.05156297830223 201.51585567445812 196.58908645819533 180.65751845628574	M_THREADS=2. , 6, , 3, 2, 7,	luster_kmeans.py	y:1446: UserWarning: KMeans	known to have a memory lea	k on Windows with MKL, when ther	e are less chunks than availabl	e threads. You can avoid it l	py setting the e
	c(x=num_clusters, y=inertia, mumber of clusters");	arker = 'o')						
800 700 600 500								
2 3	4 5 6 7 Number of clusters	8 9	10					
<pre>def kmeans_sil(num_ """ Accepts as argu Fits a KMeans m Calculates a si</pre>	to return a list of each k-va	array. the list of ints. ue.						
kms.fit(x_v sil_score.a return sil_scor	ns(n_clusters=num, random_state vals) append(silhouette_score(x_vals							
ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn(M_THREADS=2. 3\Lib\site-packages\sklearn\c. M_THREADS=2. 3\Lib\site-packages\sklearn\c. M_THREADS=2.	luster_kmeans.py	y:1446: UserWarning: KMeans y:1446: UserWarning: KMeans	known to have a memory leak	k on Windows with MKL, when then	e are less chunks than available e are less chunks than available	e threads. You can avoid it is the least threads. You can avoid it is	by setting the e
<pre>ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn(</pre>	.3\Lib\site-packages\sklearn\c. IM_THREADS=2. .3\Lib\site-packages\sklearn\c. IM_THREADS=2. .3\Lib\site-packages\sklearn\c. IM_THREADS=2.	luster_kmeans.py	y:1446: UserWarning: KMeans y:1446: UserWarning: KMeans	known to have a memory leak	k on Windows with MKL, when then k on Windows with MKL, when then k on Windows with MKL, when then	e are less chunks than available e are less chunks than available	e threads. You can avoid it is to be a second in the secon	by setting the e
ment variable OMP_NU warnings.warn(C:\Users\HP\anaconda ment variable OMP_NU warnings.warn([630 [0.4439808835305524 0.4510102409718836 0.4489699212061027 0.519998574860868, 0.5223086008347773	M_THREADS=2. 13\Lib\site-packages\sklearn\c. M_THREADS=2. 43, 64, 7, ,				k on Windows with MKL, when ther			
0.4738635064229315 0.4715443426463867 0.4160561489496056 0.4183063433691055	57, 7, 6,] ot. c(x=num_clusters, y=sil_score, of clusters");	<pre>marker = 'o')</pre>						
0.52 0.50 0.48 0.48								
0.46 0.44 0.42								
kmeans6.fit(X_scale C:\Users\HP\anaconda	_clusters=6, random_state=42) ed) .3\Lib\site-packages\sklearn\c	8 9	10 y:1446: UserWarning: KMeans	known to have a memory lea	k on Windows with MKL, when ther	e are less chunks than availabl	e threads. You can avoid it	by setting the e
KMeans(n_clusters=	eans	;_))						
penguins_subset.hea [636 species bill_length_	umn `cluster`. Luster'] = kmeans6.labels_		ex_MALE cluster True 5					
2 Adelie 4 3 Adelie 3 4 Adelie 3	39.5 17.4 186. 40.3 18.0 195. 36.7 19.3 193. 39.3 20.6 190.	3250.0 3450.0 3650.0	False 2 False 2 False 2 True 5					
penguins_subset.gro [638 cluster species 0 Chinstrap 1 Gentoo 2 Adelie Chinstrap 3 Adelie Chinstrap 4 Gentoo 5 Adelie	58 73 2 2]).size()						
dtype: int64	oupby (by=['cluster', 'species' Clusters differentiated by species'		<pre>par(title='Clusters different figsize=(6, 5), ylabel='Size', xlabel='(Cluster, Species)</pre>					
60 50 40								
30 20 10 0 (dg. (oo	(e) (f) (f) (h) (h) (h) (h) (h) (h) (h) (h) (h) (h	(6)						
(0, Chinst (0, Chinst (1, Gent	(Cluster, Species) (Cluster` can be differentiated outply (by=['cluster', 'species', Chinstrap)	l by `species` ANI		alse)				
Cluster species Adelie Adelie Gentoo Gentoo Chinstrap Chinstrap Chinstrap Adelie dtype: int64	sex_MALE False 73 True 71 True 61 False 58 True 34 False 32							
plt.legend(bbox_to_ [644 <matplotlib.legend< td=""><td></td><td></td><td></td><td>fi yl</td><td><pre>le='Clusters differentiated by s size=(6, 5), bel='Size', bel='(Cluster, Sex)')</pre></td><td>species and sex',</td><td></td><td></td></matplotlib.legend<>				fi yl	<pre>le='Clusters differentiated by s size=(6, 5), bel='Size', bel='(Cluster, Sex)')</pre>	species and sex',		
70 60 50 40			Adelie Chinstrap Gentoo					
v)								
30 20 10 0 (eslas)		True)						

In [572... # Import standard operational packages.
import numpy as np
import pandas as pd