

# DataNexus ANALYZE • INTERPRET •

## INTRO TO PYTHON 4

Be sure to get an account at

https://research.google.com/colaboratory/

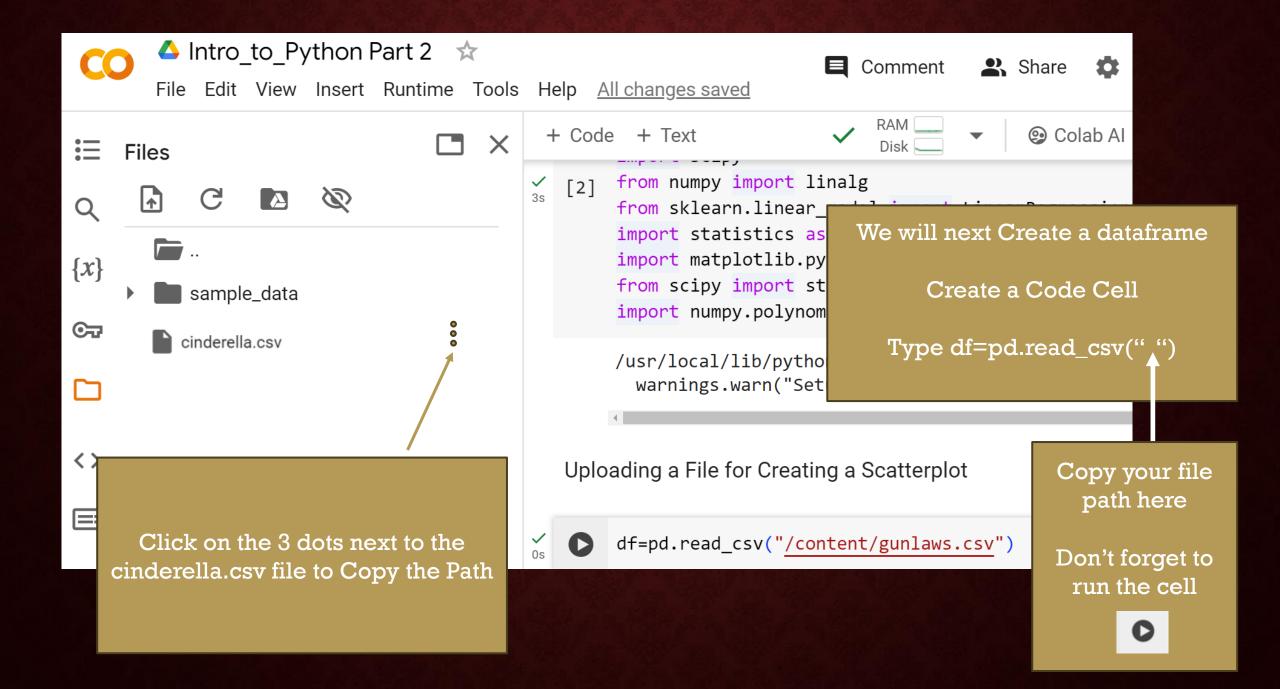


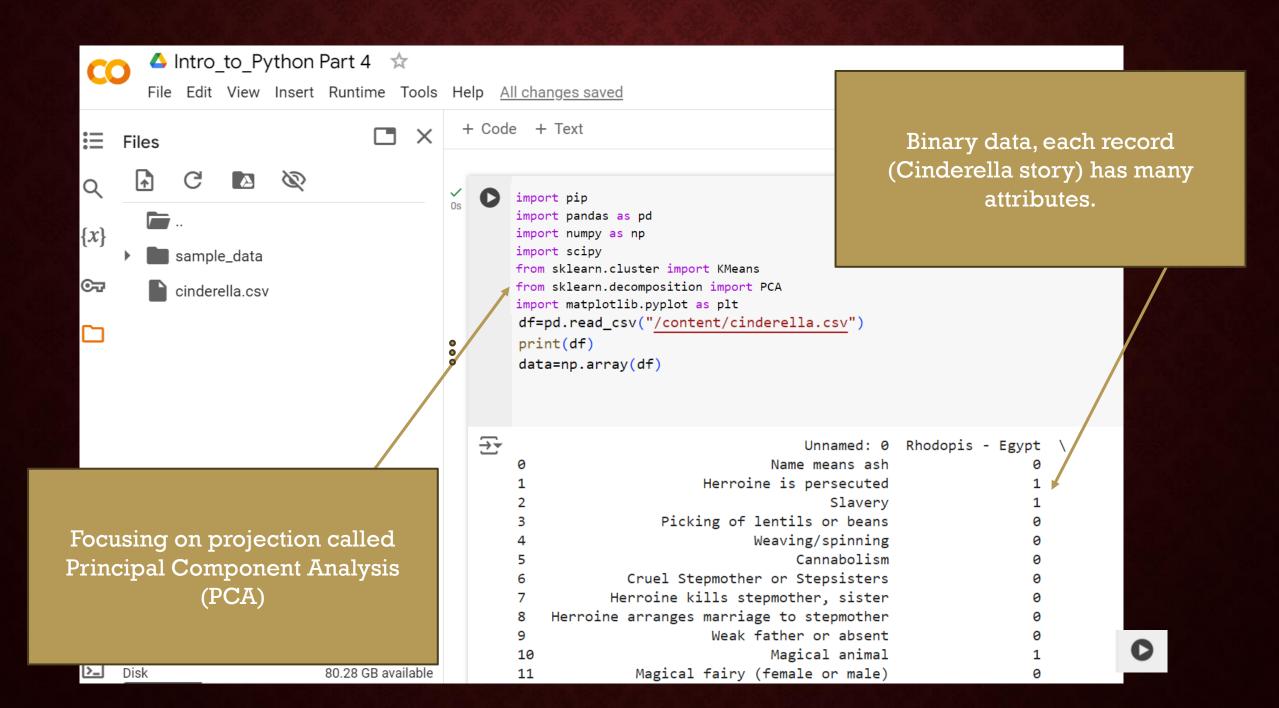
## DOWNLOAD THE DATA FOR THIS SESSION

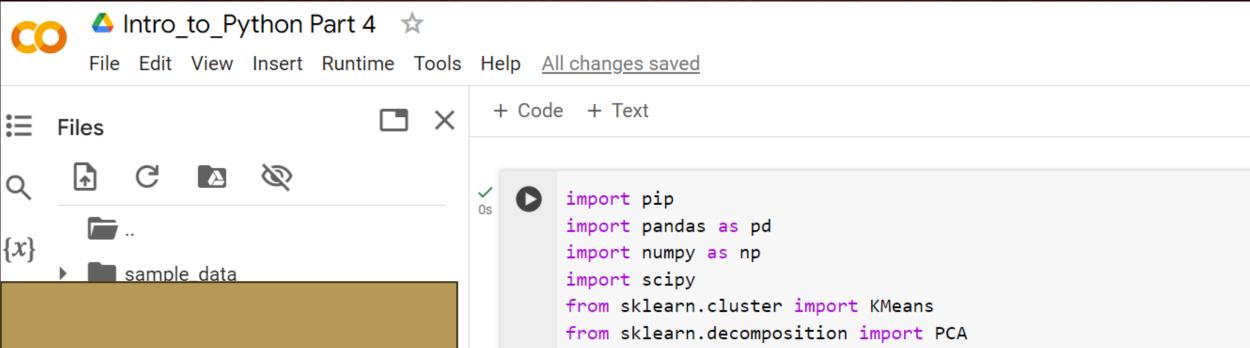
Before we begin download

cinderella\_tales.csv from our website

# DataNexus ANALYZE • INTERPRET







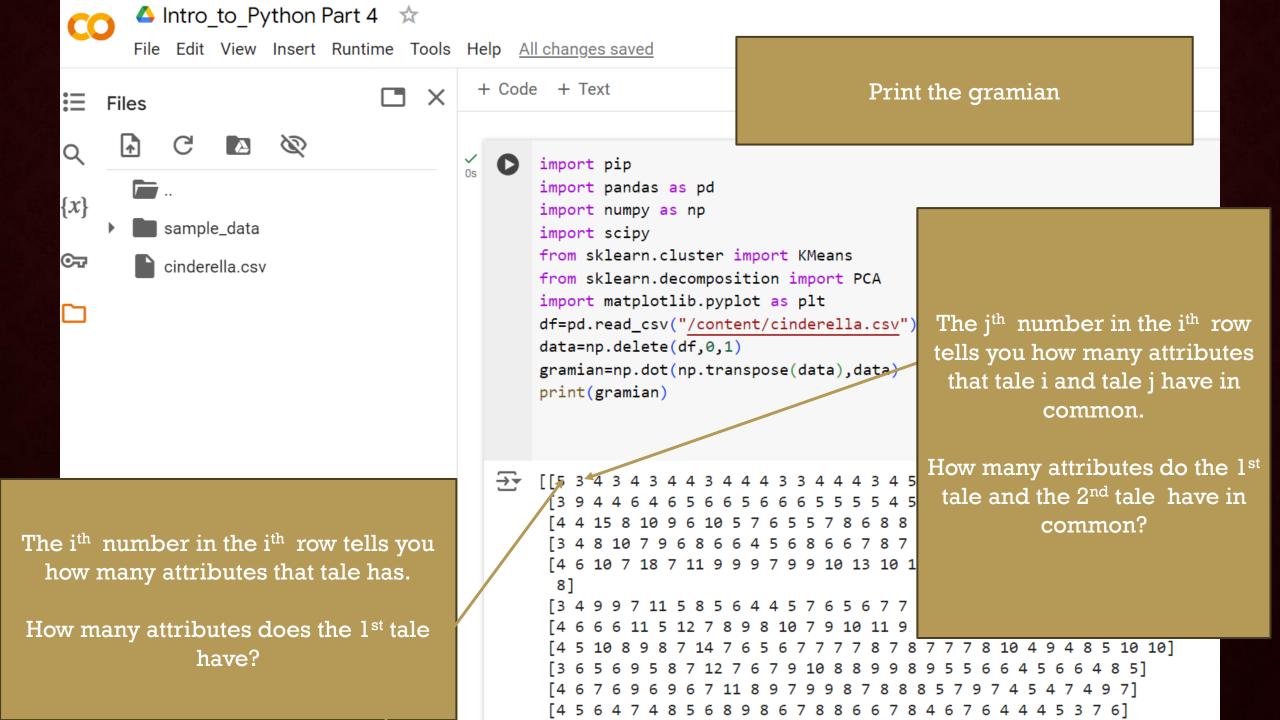
You might just want to see the relationship between the tales (your records) in this case take a look at the Gramian.

Note the tales are in the columns here.

from sklearn.cluster import KMeans
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt
df=pd.read\_csv("/content/cinderella.csv")
data=np.delete(df,0,1)

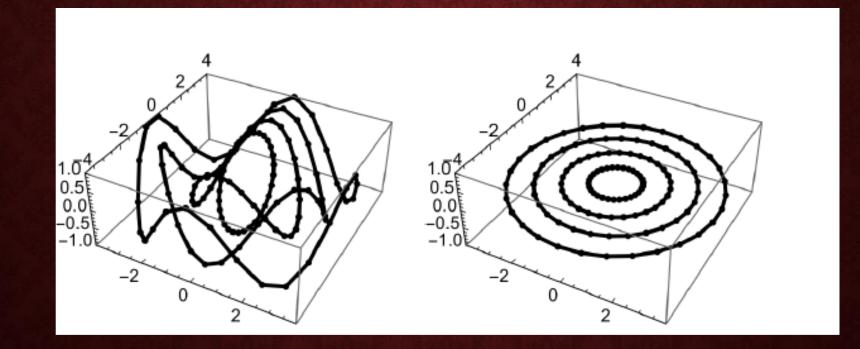
gramian=np.dot(np.transpose(data),data)

If your records are in the rows: np.dot(data,np.transpose(data))

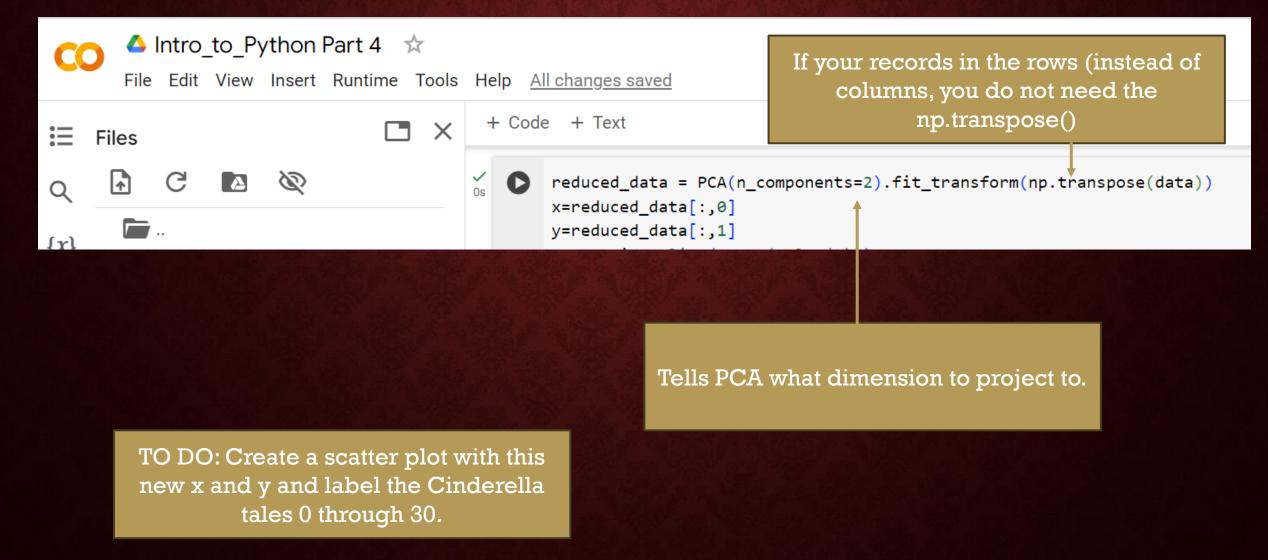


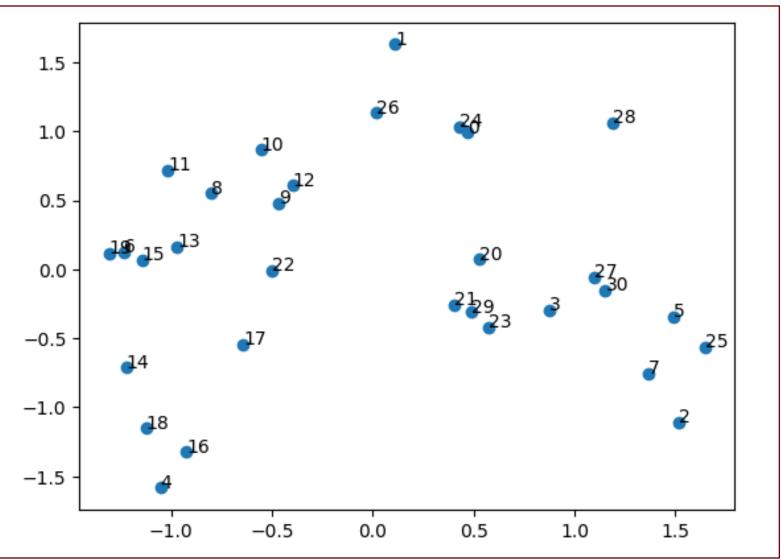
### WE NEXT FOCUS ON PROJECTION WHAT IS A PROJECTION?

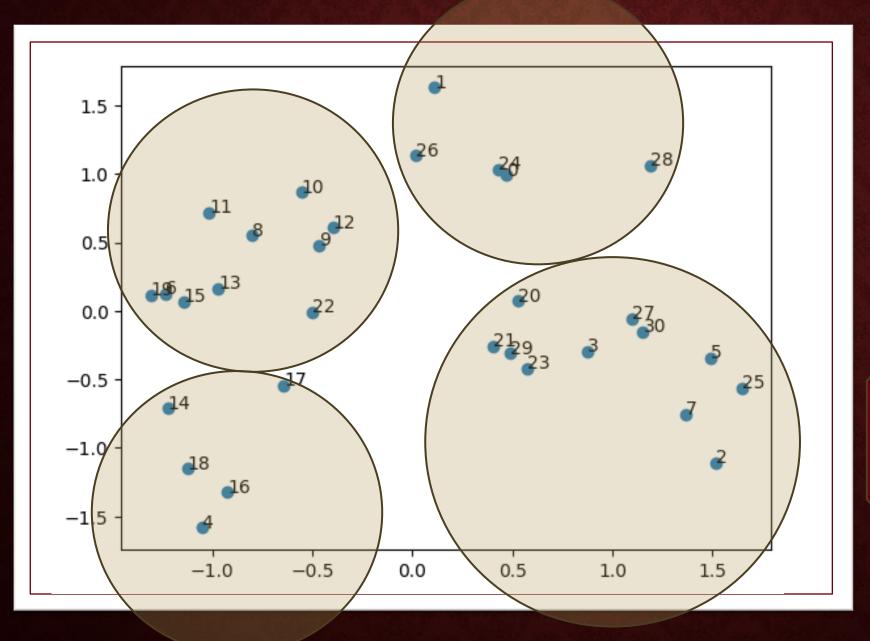
#### WHAT IS A PROJECTION?



#### **PRINCIPAL COMPONENT ANALYSIS**







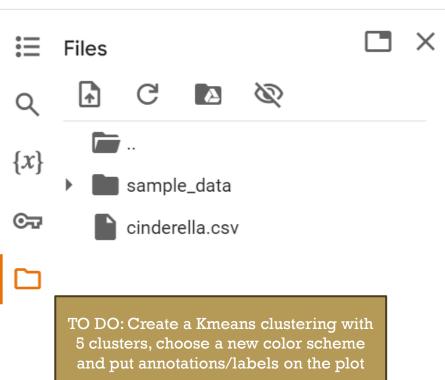
You can use PCA with non-binary data but standardize it first.

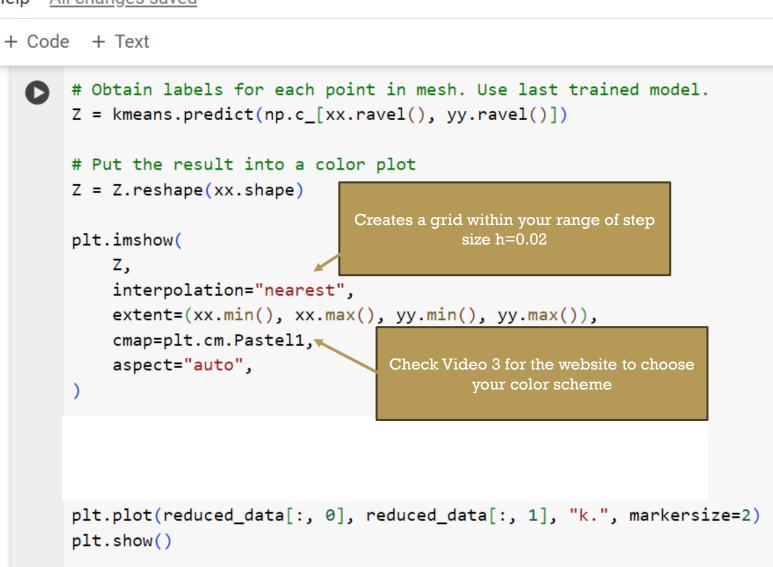
Contact Data Nexus if you have questions about this

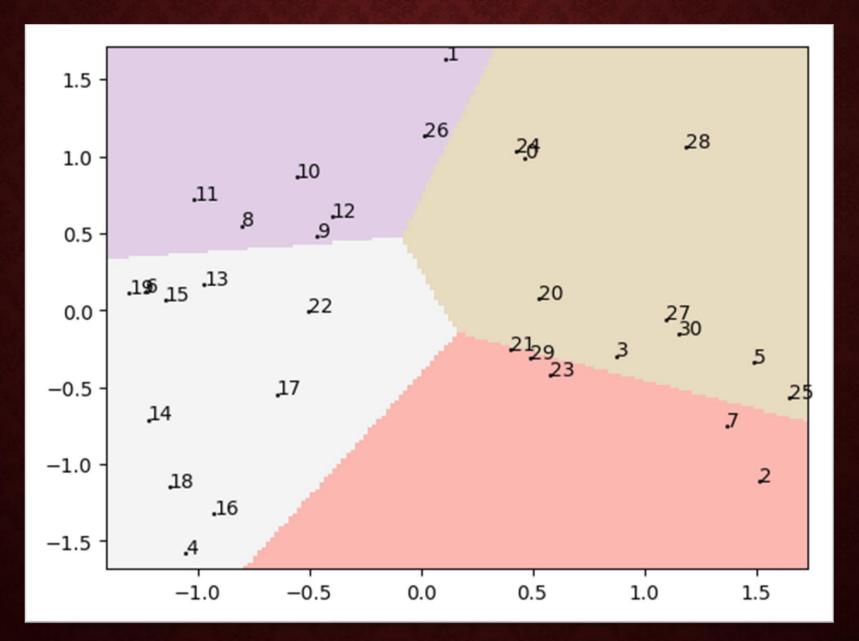
		Λ	Intro	to P	thon	Part 1	A_								
	0		🛆 Intro_to_Python Part 4 🛭 🛠 File Edit View Insert Runtime <u>Tools Help All changes saved</u>									[			
		File	Edit	ait view insert Run				Help All chai							
≣	F	iles							neans++ or random troids of the regions			ber of regions lustering.	Number of iterations of kmeans with different centroids		
Q		<b>↑</b>	G	A	Ø										
		· · ·							<pre>kmeans = KMeans(init="k-means++", n_clusters=5, n_init=4)</pre>						
$\{x\}$			sampl	e dete				kmea	ans.fit(reduced_	data)					
$\sim$	,			ample_data				# St	# Step size of the mesh. Decrease to increase the quality						
07			cinder	ella.csv	/			h =	h = 0.02  # point in the mesh [x_min, x_max]x[y_min, y_max].						
								_ # P]	lot the decision	boundar	v. For that	. we will ass	ign a color to each		
_			Creates a x and y range just 1 less than						<pre># Plot the decision boundary. For that, we will assign a color to each   x_min, x_max = reduced_data[:, 0].min() - 1, reduced_data[:, 0].max() + 1</pre>						
			the actual mins and maxs, you can choose other values.						<pre>y_min, y_max = reduced_data[:, 1].min() - 1, reduced_data[:, 1].max() + 1</pre>						
				CI		iler values.		хх,	yy = np.meshgri	d(np.ara	nge(x_min, >	k_max, h), np	.arange(y_min, y_max, h))		
												Creates a gri	id within your range of step		
													size h=0.02		
I	Kme	eans clustering uses an average value to separate yo						your regions	TO DO: Use this code to c .01 step size and 4		~				
									_						

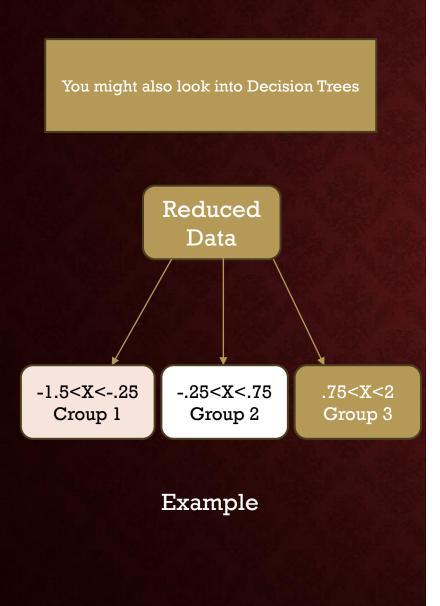
#### 🛆 Intro\_to\_Python Part 4 🛛 🛣

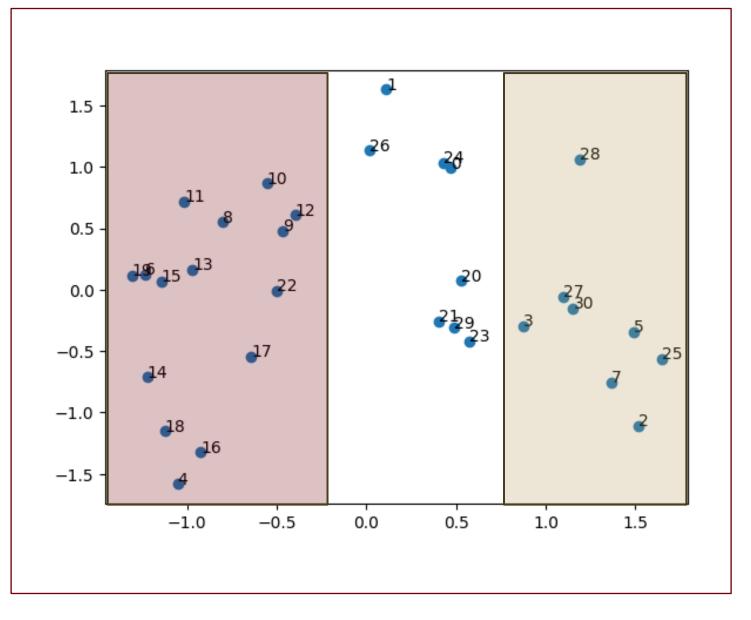
File Edit View Insert Runtime Tools Help All changes saved



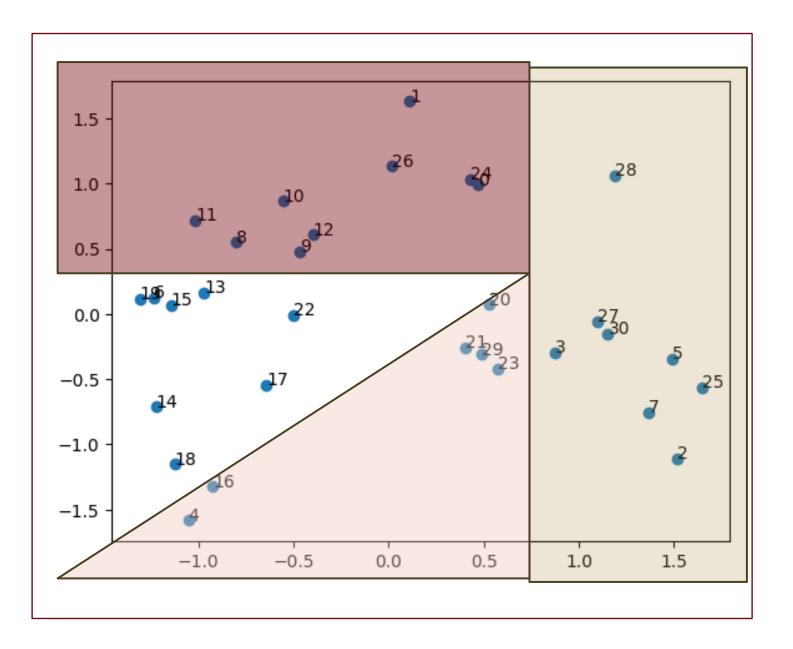








You might also look into Decision Trees Reduced Data .75<X<2 -1.5<X<.75 Group 3 .25<Y<1.5 -2<Y<.25 Croup 4 Y is above Y is below Line l and Line 1 below Y = .25Group 1 Group 2 Example



VISIT DATA NEXUS IN **INNOVATION HALL 108C** FOR OTHER SUGGESTIONS

\_ 1.5 26 28 20 1.0 10 11 0.5 **1**5 **1**3 22 0.0 -230 2129 23 3 17 -0.5 -14 -1.018 -1.5 --1.0-0.50.0 0.5 1.0

25

2

1.5

IF YOU WANT TO LEARN MORE ABOUT ANY OF THESE TOPICS CONSIDER

