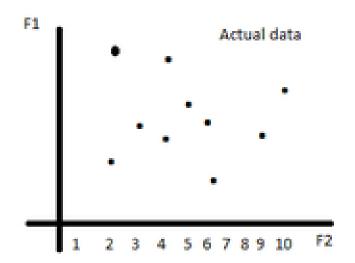
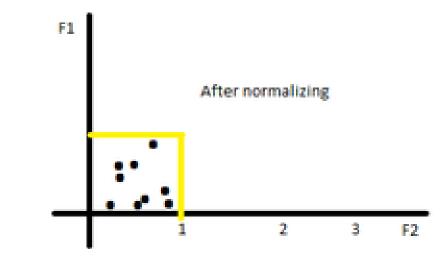
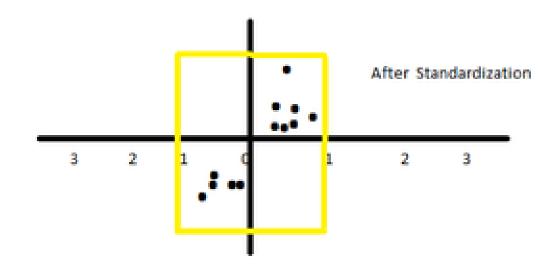


Standardization and normalization are best comrades of statistics

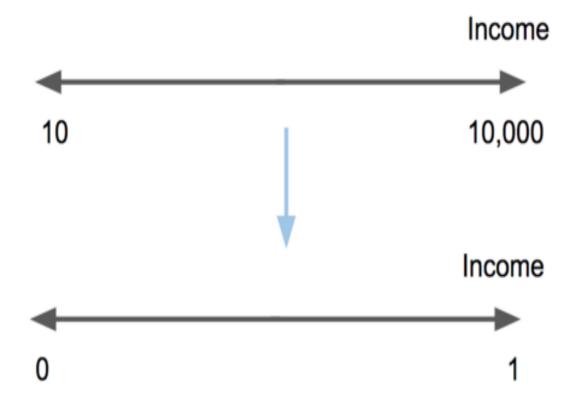








Normalize

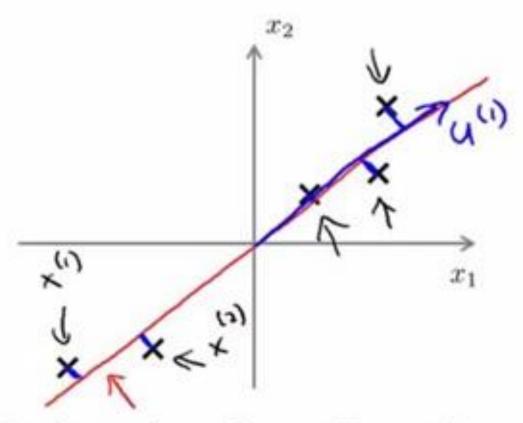


Standardize

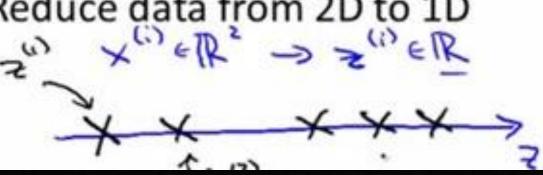
$$z = \frac{x - \mu}{\sigma}$$

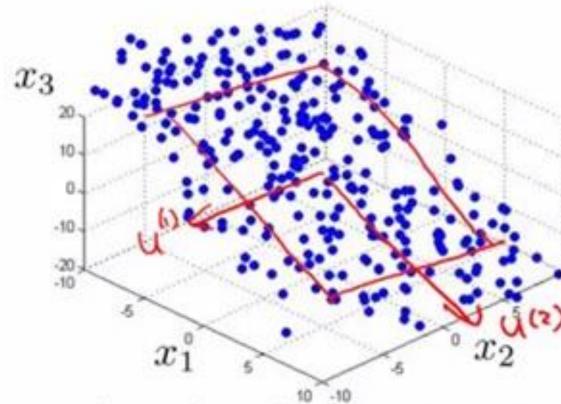
$$\mu=$$
 Mean $\sigma=$ Standard Deviation

Principal Component Analysis (PCA) algorithm

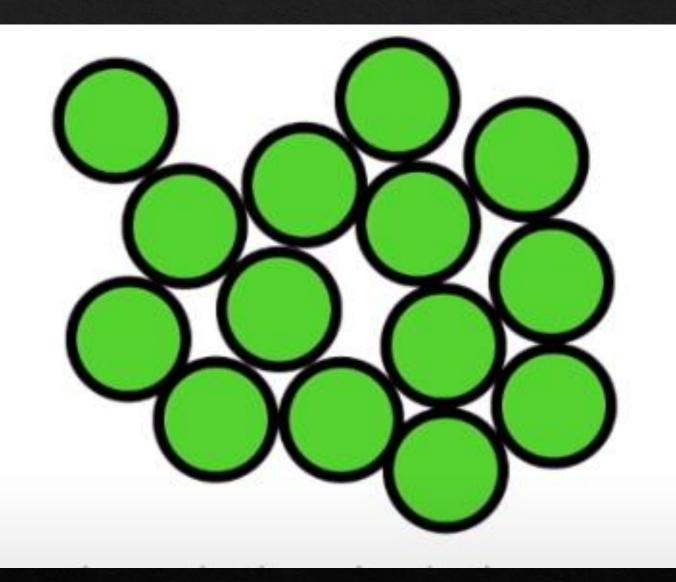


Reduce data from 2D to 1D



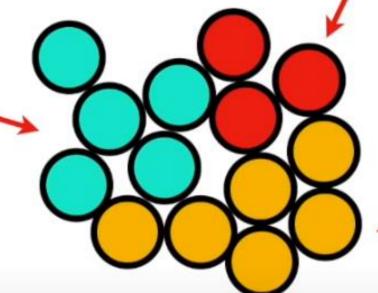


Reduce data from 3D to 2D

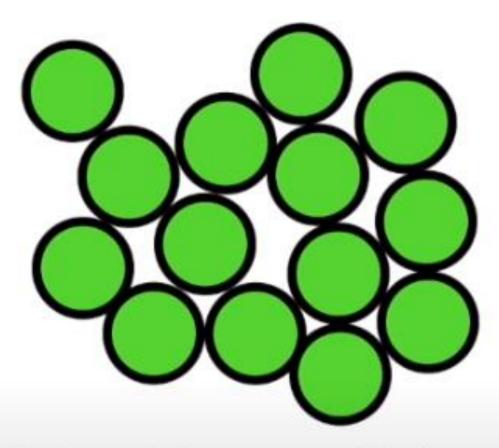


These might be another type of cell...

These might be one type of cell...

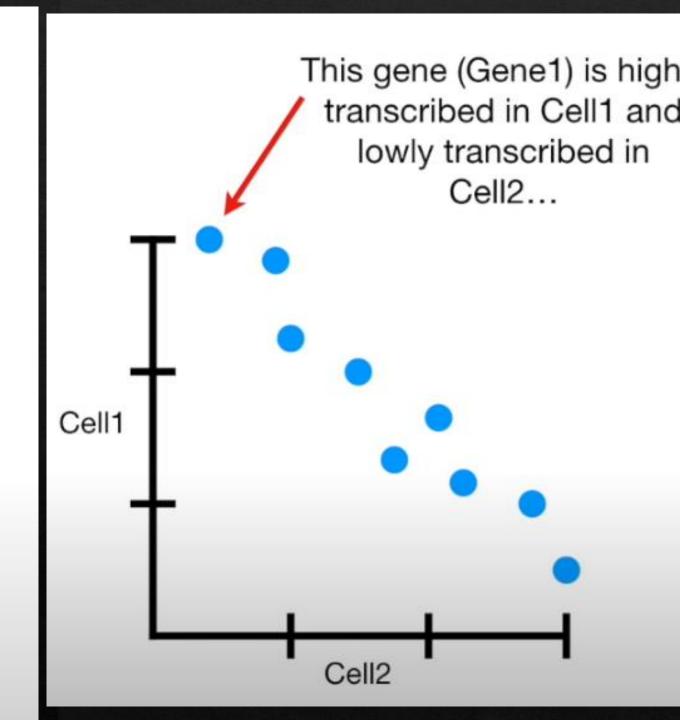


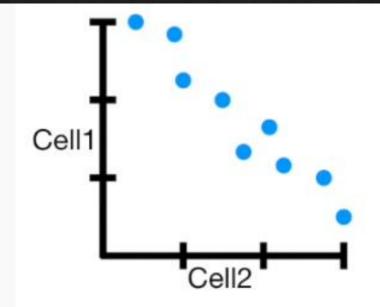
These might be a third type of cell...

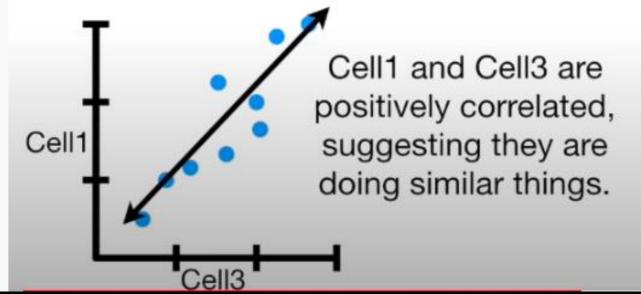


Unfortunately, we can't observe the differences from the outside...

	Cell1	Cell2
Gene1	3	0.25
Gene2	2.9	0.8
Gene3	2.2	1
Gene4	2	1.4
Gene5	1.3	1.6
Gene6	1.5	2
Gene7	1.1	2.2
00	-	0.7

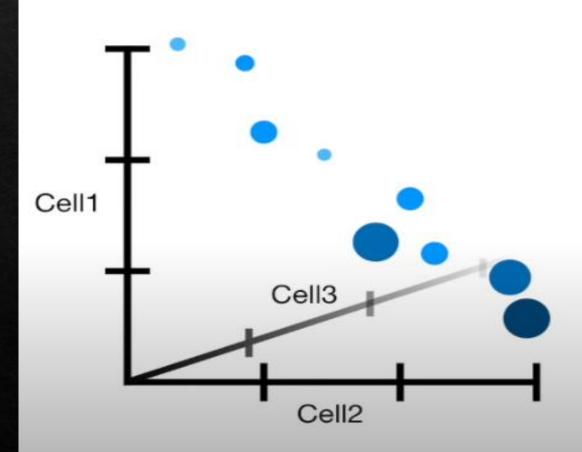




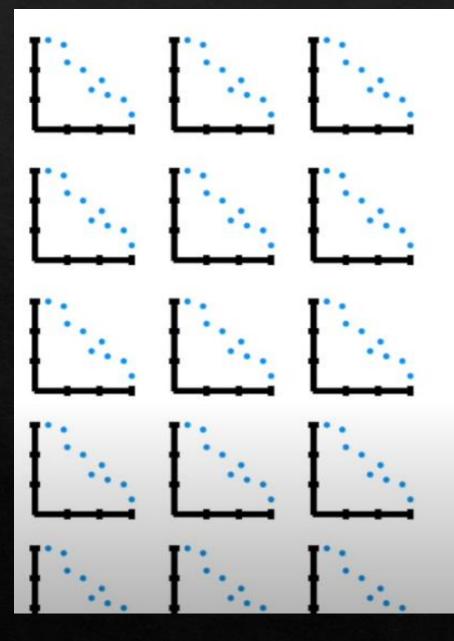


	Cell1	Cell2	Cell3
Gene1	3	0.25	2.8
Gene2	2.9	0.8	2.2
Gene3	2.2	1	1.5
Gene4	2	1.4	2
Gene5	1.3	1.6	1.6
Gene6	1.5	2	2.1
Gene7	1.1	2.2	1.2
Gene8	1	2.7	0.9
Gene9	0.4	3	0.6

Alternatively, we could try to plot all three cells at once on a 3-dimensional graph.



	Cell1	Cell2	Cell3
Gene1	3	0.25	2.8
Gene2	2.9	0.8	2.2
Gene3	2.2	1	1.5
Gene4	2	1.4	2
Gene5	1.3	1.6	1.6
Gene6	1.5	2	2.1
Gene7	1.1	2.2	1.2
Gene8	1	2.7	0.9
Gene9	0.4	3	0.6

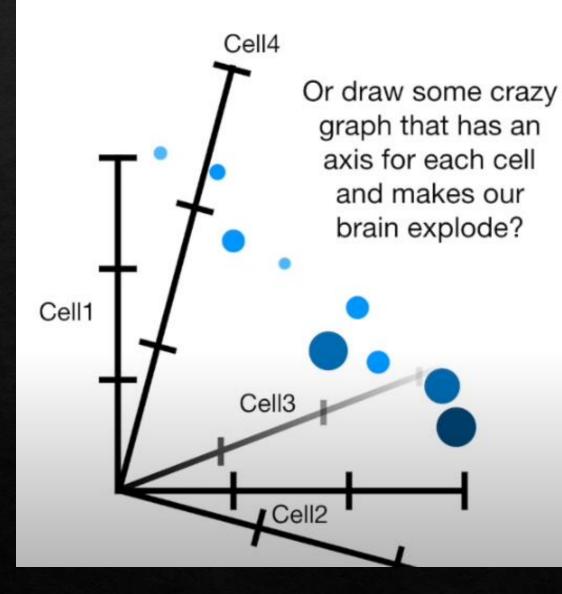


Draw tons and tons of 2 cell plots and try to make sense of

them all?

lt	would	be
	Trivial	11

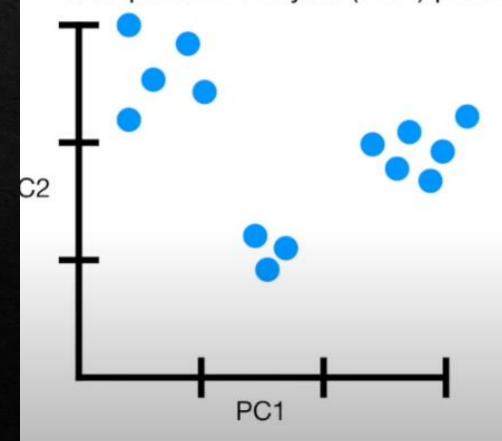
ļ.,	Cell1	Cell2	Cell3	Cell4	
Gene1	3	0.25	2.8	0.1	
Gene2	2.9	0.8	2.2	1.8	
Gene3	2.2	1	1.5	3.2	
Gene4	2	1.4	2	0.3	
Gene5	1.3	1.6	1.6	0	
Gene6	1.5	2	2.1	3	
Gene7	1.1	2.2	1.2	2.8	
Gene8	1	2.7	0.9	0.3	
Gene9	0.4	3	0.6	0.1	****



	Cell1	Cell2	Cell3	Cell4	
Gene1	3	0.25	2.8	0.1	
Gene2	2.9	0.8	2.2	1.8	
Gene3	2.2	1	1.5	3.2	
Gene4	2	1.4	2	0.3	
Gene5	1.3	1.6	1.6	0	
Gene6	1.5	2	2.1	3	
Gene7	1.1	2.2	1.2	2.8	•••
Gene8	1	2.7	0.9	0.3	
Gene9	0.4	3	0.6	0.1	

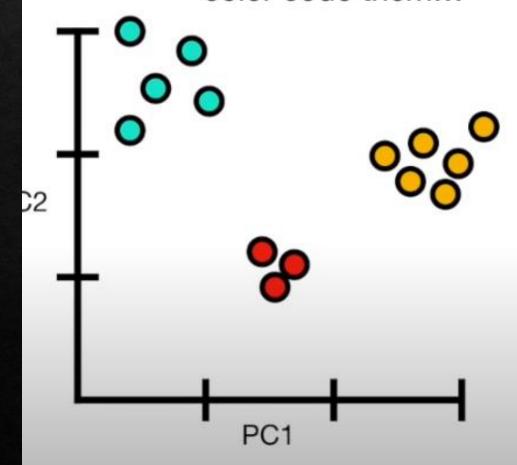
No, both of those options are just plain silly.

Instead, we draw a Principal Component Analysis (PCA) plot...



	Cell1	Cell2	Cell3	Cell4	
Gene1	3	0.25	2.8	0.1	
Gene2	2.9	0.8	2.2	1.8	
Gene3	2.2	1	1.5	3.2	
Gene4	2	1.4	2	0.3	
Gene5	1.3	1.6	1.6	0	
Gene6	1.5	2	2.1	3	
Gene7	1.1	2.2	1.2	2.8	
Gene8	1	2.7	0.9	0.3	
Gene9	0.4	3	0.6	0.1	

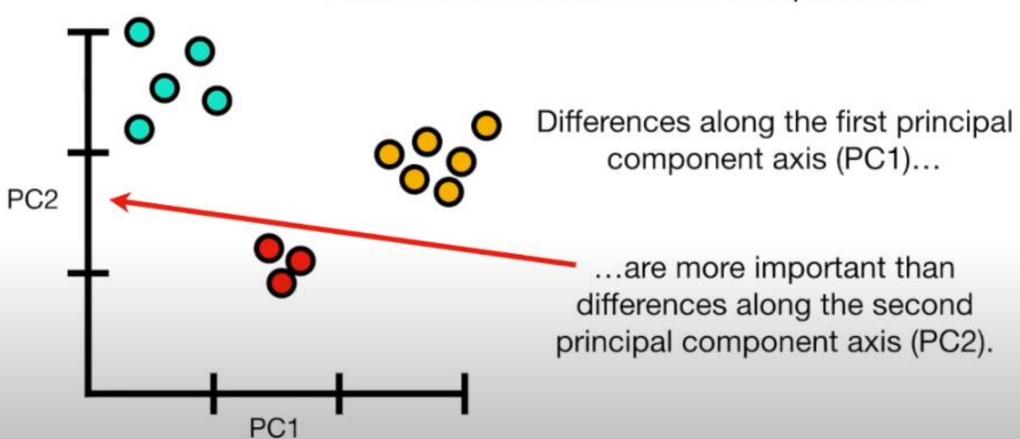
To make the clusters easier to see, we can color code them...



	Cell1	Cell2	Cell3	Cell4	
Gene1	3	0.25	2.8	0.1	
Gene2	2.9	0.8	2.2	1.8	•••
Gene3	2.2	1	1.5	3.2	
Gene4	2	1.4	2	0.3	
Gene5	1.3	1.6	1.6	0	
Gene6	1.5	2	2.1	3	•••
Gene7	1.1	2.2	1.2	2.8	
Gene8	1	2.7	0.9	0.3	
Gene9	0.4	3	0.6	0.1	

Here's one last main idea about how to interpret PCA plots:

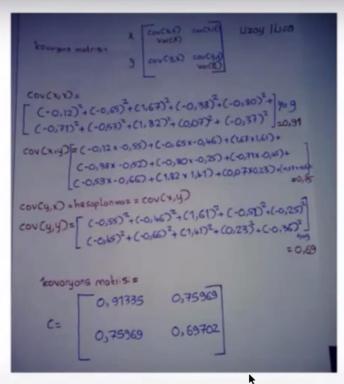
The axes are ranked in order of importance.



PCA Temel Bileşenler Analizi | Veri Madenciliği Eğitim Seti Ders 30 SORU Ortalamadan çıkardık

Örnekler	x	Y
1	0.72	0.13
2	0.18	0.23
3	2.50	2.30
4	0.45	0.16
5	0.04	0.44
6	0.13	0.24
7	0.30	0.03
8	2.65	2.10
9	0.91	0.91
10	0.46	0.32
Ortalama	0.83	0.69

X	Y
0.72 - 0.83 = -0.12	0.13 - 0.69 = - 0.55
0.18 - 0.83 = -0.65	0.23 - 0.69 = - 0.46
2.50 - 0.83 = 1.67	2.30 - 0.69 = 1.61
0.45 - 0.83 = -0.38	0.16 - 0.69 = - 0.52
0.04 - 0.83 = -0.80	0.44 - 0.69 = - 0.25
0.13 - 0.83 = -0.71	0.24 - 0.69 = - 0.45
0.30 - 0.83 = -0.53	0.03 - 0.69 = - 0.66
2.65 - 0.83 = 1.82	2.10 - 0.69 = 1.41
0.91 - 0.83 = 0.07	0.91 - 0.69 = 0.23
0.46 - 0.83 = -0.37	0.32 - 0.69 = -0.36



3.)Bu adımda elimizdeki bu 2×2 matrisin Özdeğerlerini (Eigenvalues) ve Özvektörlerini (Eigenvectors) buluyoruz.

2. Bu adımda aşağıdaki formülü kullanarak bu verinin kovaryans matrisini buluyoruz.

Örnekler	X	Y
1	0.72	0.13
2	0.18	0.23
3	2.50	2.30
4	0.45	0.16
5	0.04	0.44
6	0.13	0.24
7	0.30	0.03
8	2.65	2.10
9	0.91	0.91
10	0.46	0.32
Ortalama	0.83	0.69

X	Y
0.72 - 0.83 = -0.12	0.13 - 0.69 = - 0.55
0.18 - 0.83 = -0.65	0.23 - 0.69 = - 0.46
2.50 - 0.83 = 1.67	2.30 - 0.69 = 1.61
0.45 - 0.83 = -0.38	0.16 - 0.69 = - 0.52
0.04 - 0.83 = -0.80	0.44 - 0.69 = - 0.25
0.13 - 0.83 = -0.71	0.24 - 0.69 = - 0.45
0.30 - 0.83 = -0.53	0.03 - 0.69 = - 0.66
2.65 - 0.83 = 1.82	2.10 - 0.69 = 1.41
0.91 - 0.83 = 0.07	0.91 - 0.69 = 0.23
0.46 - 0.83 = -0.37	0.32 - 0.69 = -0.36

$$cov(x,y) = \frac{\sum_{i=1}^{n} (X_i - \bar{X})(Y_i - \bar{Y})}{n-1}$$

$$cov(Y,Y) = \frac{((-0.55)^2 + (-0.46)^2 + (1.61)^2 + (-0.52)^2 + (-0.25)^2 + (-0.45)^2 + (-0.66)^2 + (1.41)^2 + (0.23)^2 + (-0.36)^2)}{10 - 1}$$

$$cov(Y,Y) = 0.697029$$

Covariance matrix = $C = \begin{bmatrix} 0.91335 & 0.75969 \\ 0.75969 & 0.69702 \end{bmatrix}$

 $\left[(-0.12)^{2} + (-0.65)^{2} + (1.67)^{2} + (-0.38)^{2} + (-0.80)^{2} + \right] \% 9$ $\left[(-0.71)^{2} + (-0.53)^{2} + (1.82)^{2} + (0.07)^{2} + (-0.37)^{2} \right] = 0.91$ COV (x14)=(-0,12x-0,55)+(-0,65x-0,46)+(1,67x1,61)+ (-0,38x-0,52)+(-0,80x-0,25)+(-0,71x-0,45)+ C-0,53x-0,66)+(1,82 x 1,41)+(0,07x0,23)+(0,37x0x) covCy,x) = hesoplonmoz = covCx,y) $cov(y,y) = [(-0,55)^{2} + (-0,46)^{2} + (1,61)^{2} + (-0,51)^{2} + (-0,25)^{2}]$ $(-0,45)^{2} + (-0,66)^{2} + (1,41)^{2} + (0,23)^{2} + (-0,36)^{2}$ = 0,69 kovoryons matrisi= 0,75969 0,91335 0,69702 0,75969

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