STATISTICS AND BIG DATA '25-'26

Hierarchical Clustering

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Hierarchical clustering concepts

1 **clusters with heatmap**

2 **hierarchical clust**

pseudocode in R

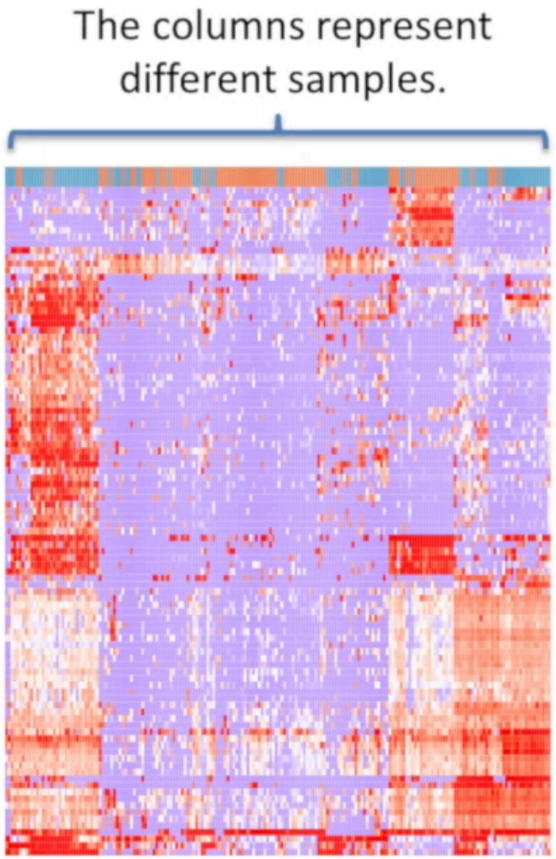
3

live coding session!

Section 1

Principles

cluster with **heatmaps**

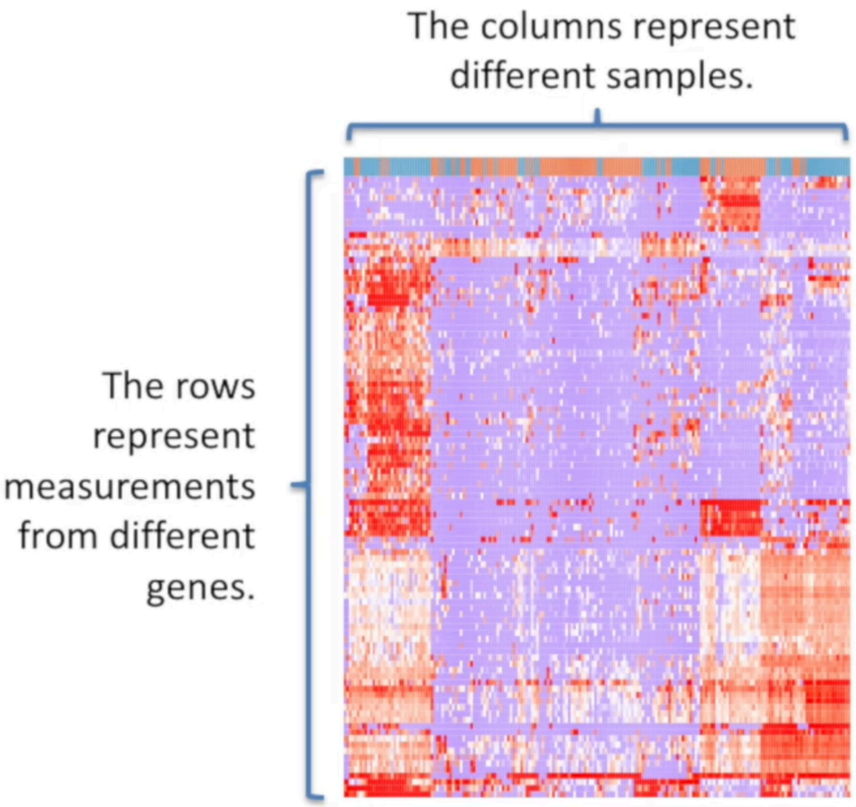


heatmaps

Have you ever seen an heatmap?

"A heatmap is a graphical representation of data that uses color-coded cells to represent different values. Heatmaps are typically used to visualize the distribution of data across two or more variables, with the color of each cell representing the value of a particular variable. Heatmaps can also be used to show correlations"

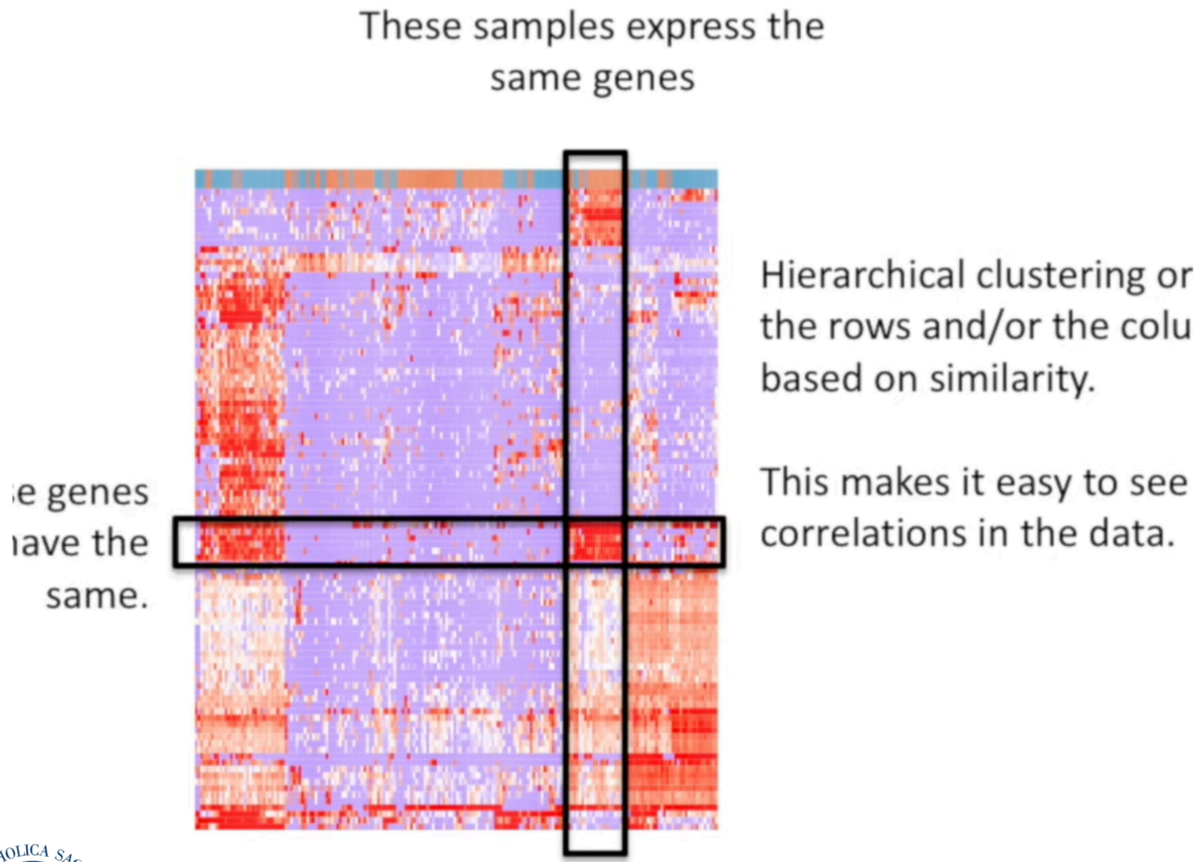
cluster with **heatmaps**



how to read this?

columns are different samples (data points). columnas are measuramente for different genes (the categorical variable)

cluster with **heatmaps**



These samples express the
same genes

Hierarchical clustering or
the rows and/or the colu
based on similarity.

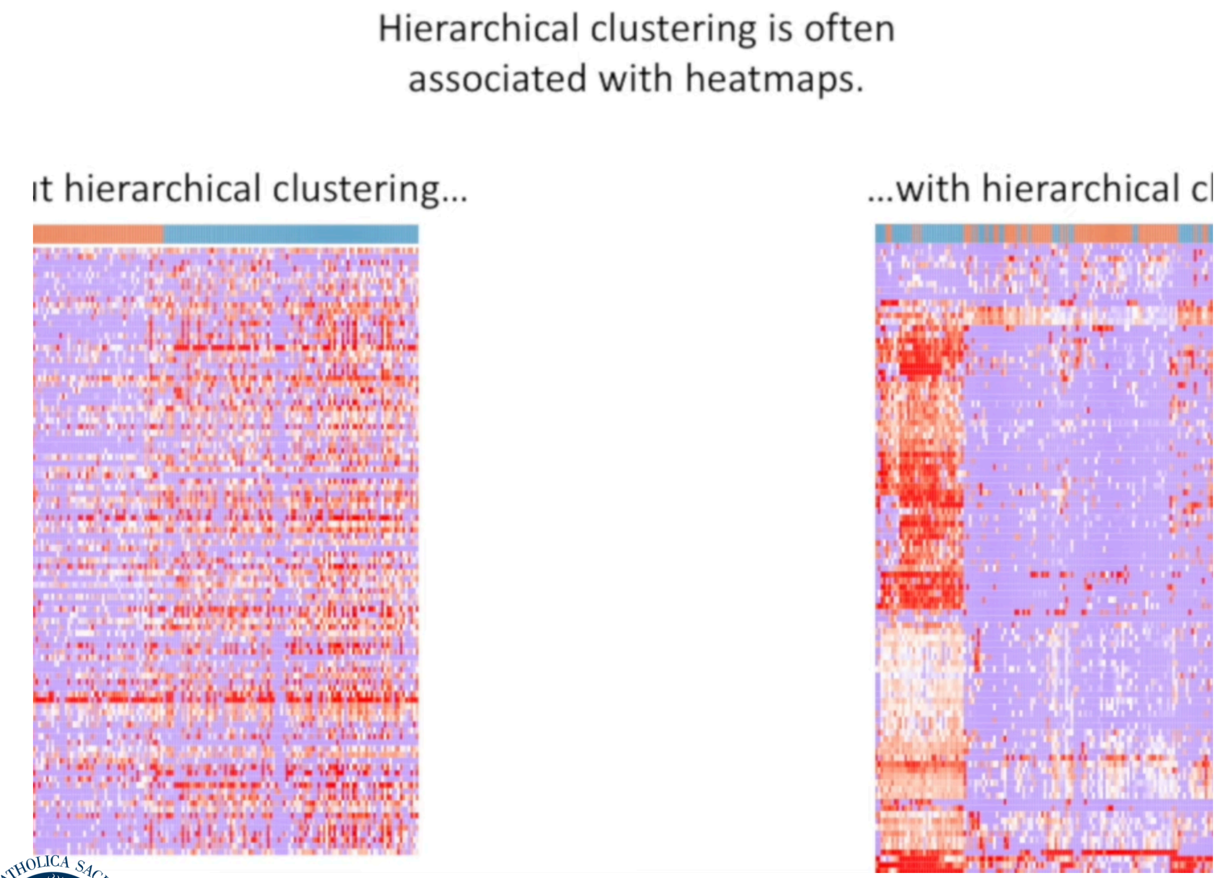
This makes it easy to see
correlations in the data.

e genes
ave the
same.

the cluster?

cluster are aggregation of data point.
These aggregations may be random or
based on some chars.

cluster with **heatmaps**



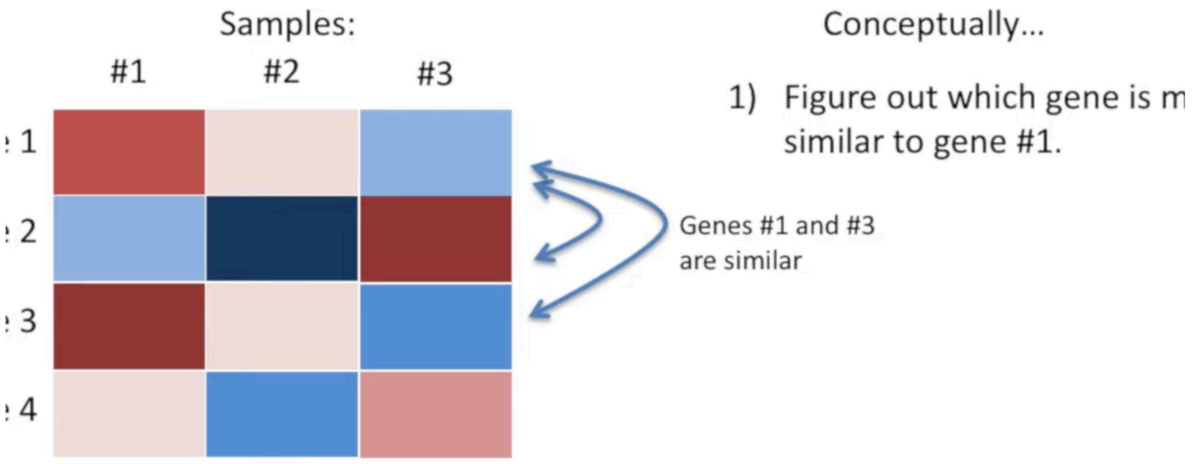
Hierarchical clustering is often associated with heatmaps.

t hierarchical clustering...

...with hierarchical cl

let's draw hier clust

hierarchical clustering



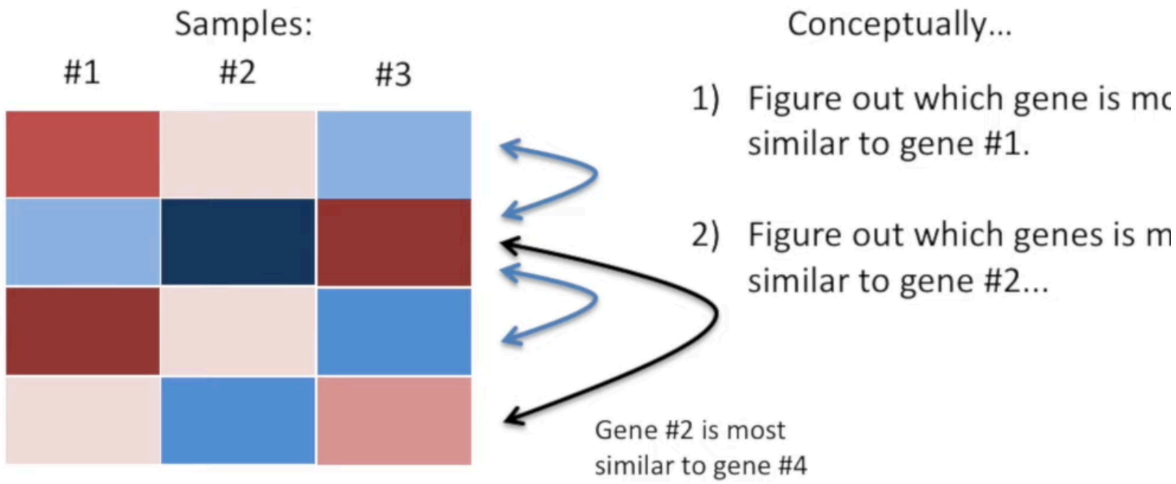
Conceptually...

1) Figure out which gene is m
similar to gene #1.

give me data

these are 3 samples per 4 genes specifies.

hierarchical clustering



Conceptually…

1) Figure out which gene is mo
similar to gene #1.

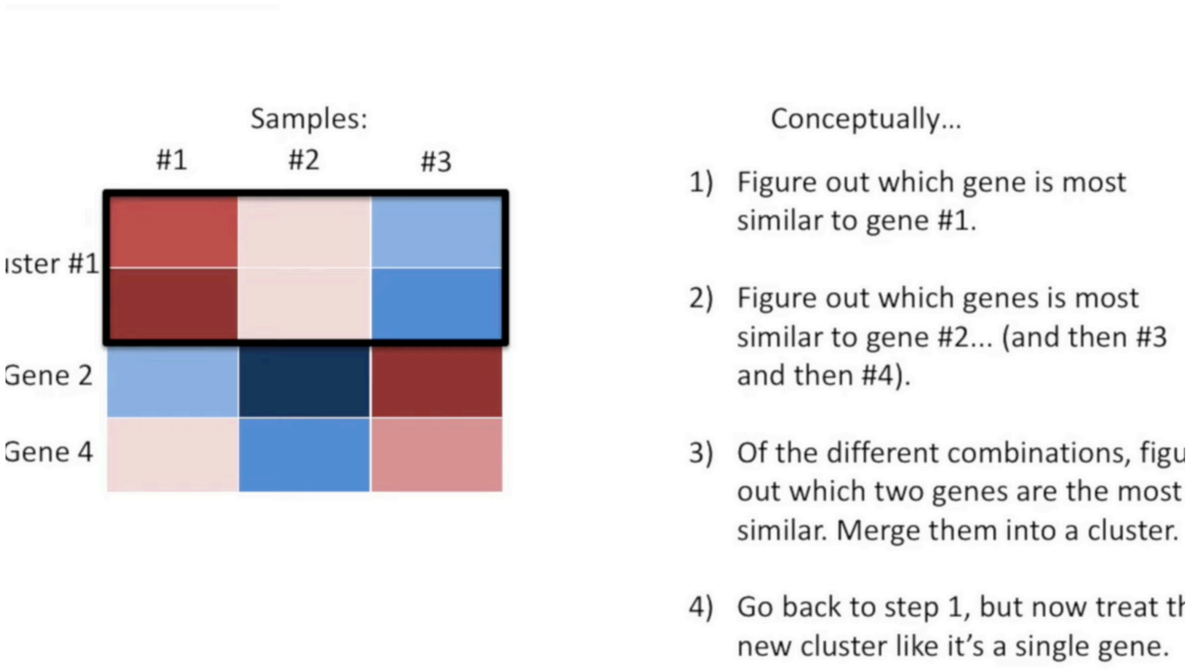
2) Figure out which genes is m
similar to gene #2…

Gene #2 is most
similar to gene #4

HWY group it?

you do that pairwise and you select the pair ob observation that are closer to each other.

hierarchical clustering

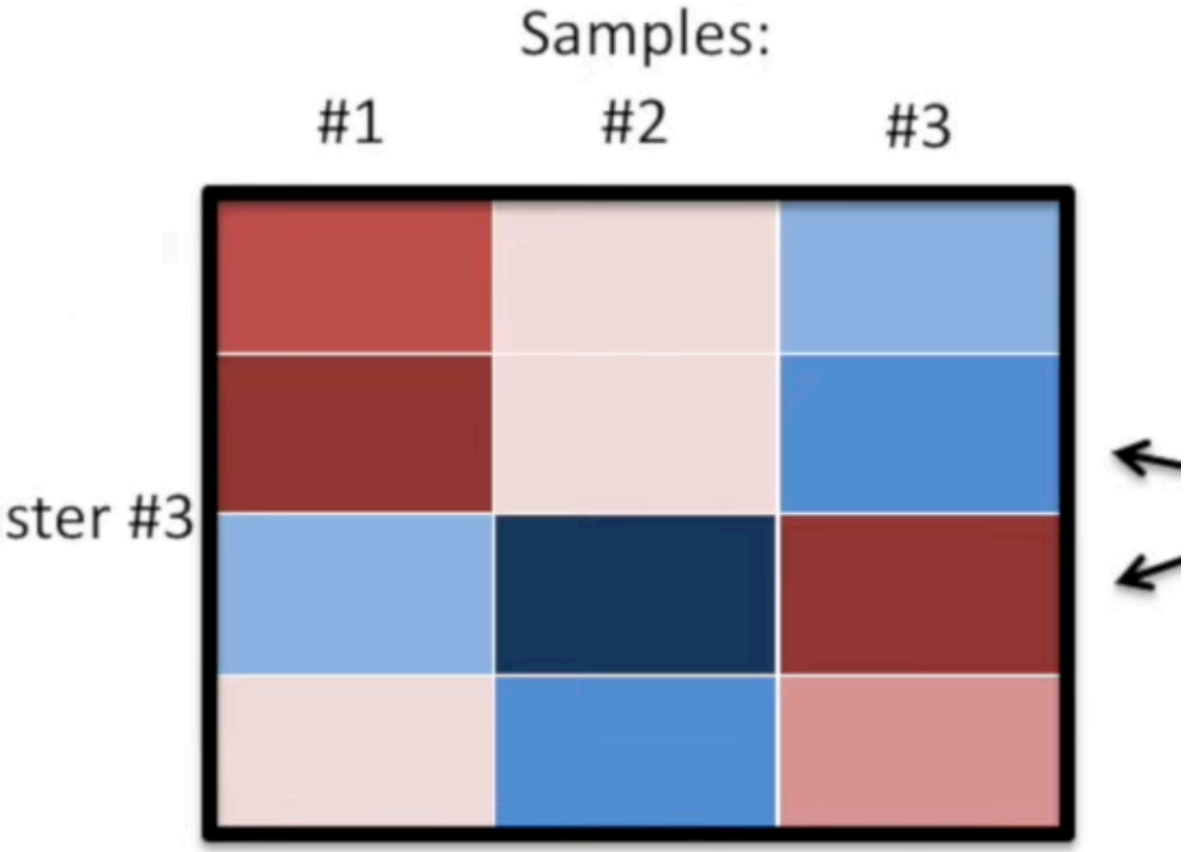


Conceptually…

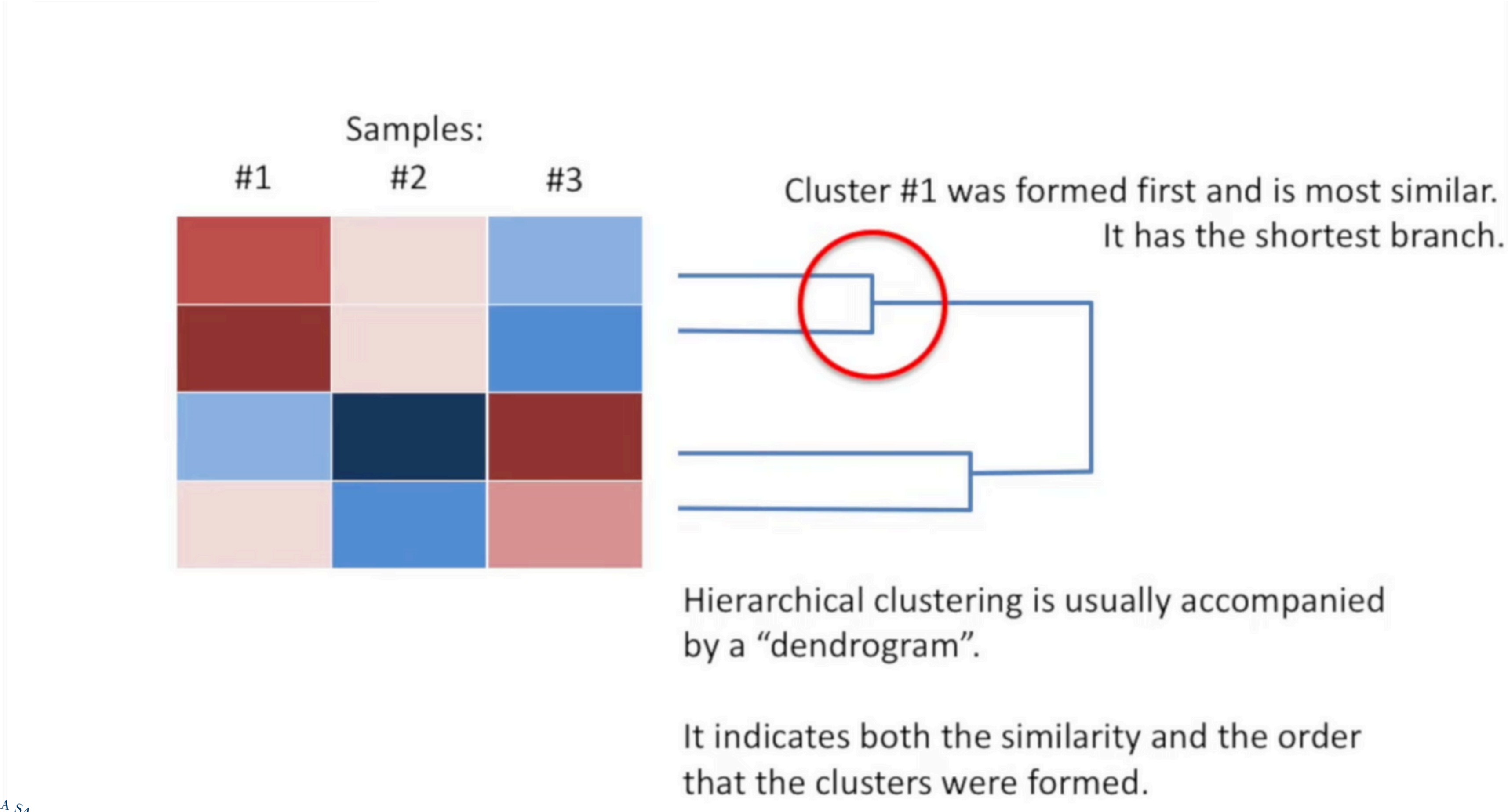
1) Figure out which gene is most similar to gene #1.
2) Figure out which genes is most similar to gene #2… (and then #3 and then #4).
3) Of the different combinations, figu out which two genes are the most similar. Merge them into a cluster.
4) Go back to step 1, but now treat tl new cluster like it's a single gene.

gene #1 and #3 are the closest

hierarchical clustering



hierarchical clustering

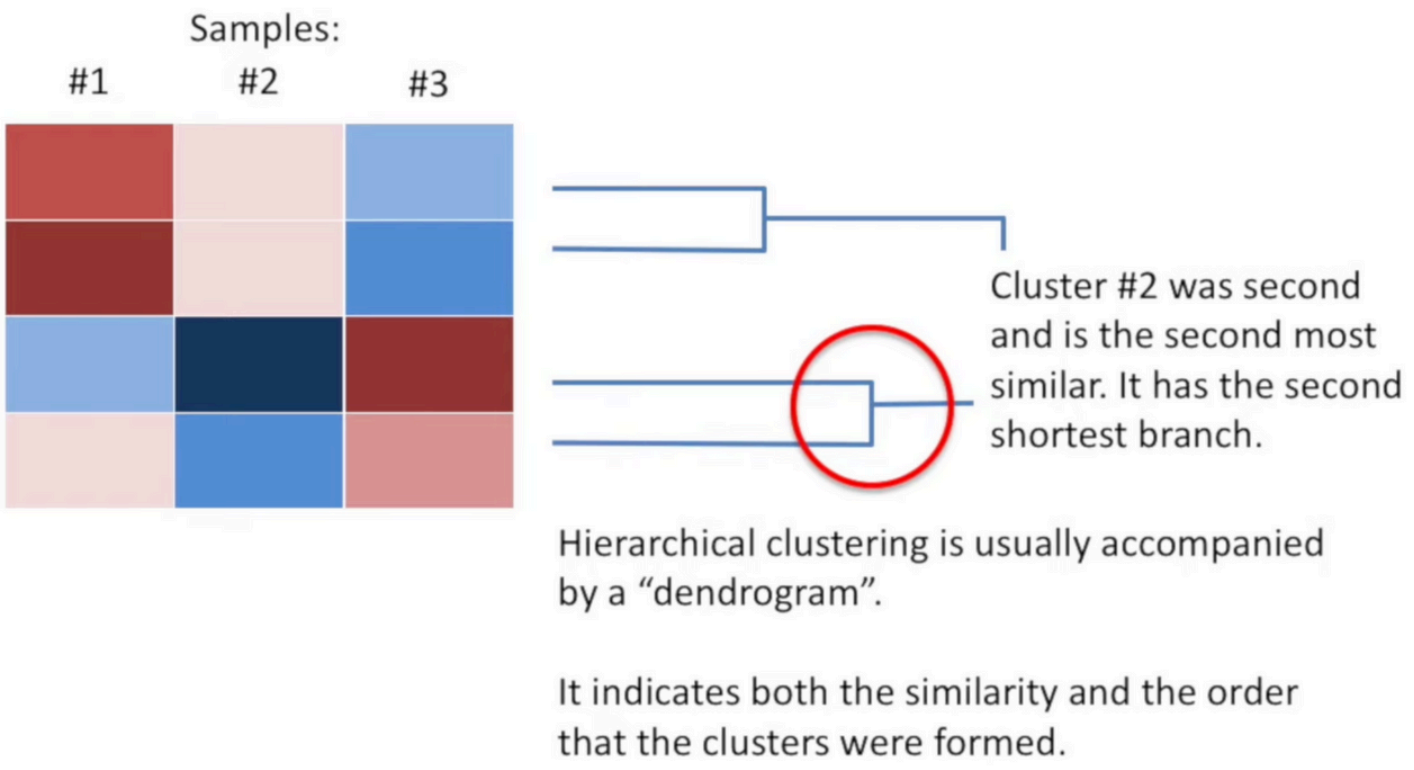


Cluster #1 was formed first and is most similar. It has the shortest branch.

Hierarchical clustering is usually accompanied by a “dendrogram”.

It indicates both the similarity and the order that the clusters were formed.

hierarchical clustering

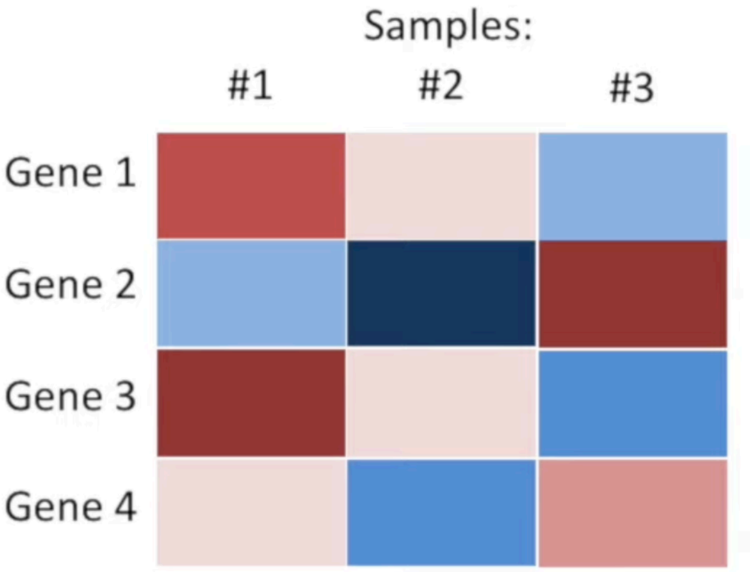


Cluster #2 was second and is the second most similar. It has the second shortest branch.

Hierarchical clustering is usually accompanied by a "dendrogram".

It indicates both the similarity and the order that the clusters were formed.

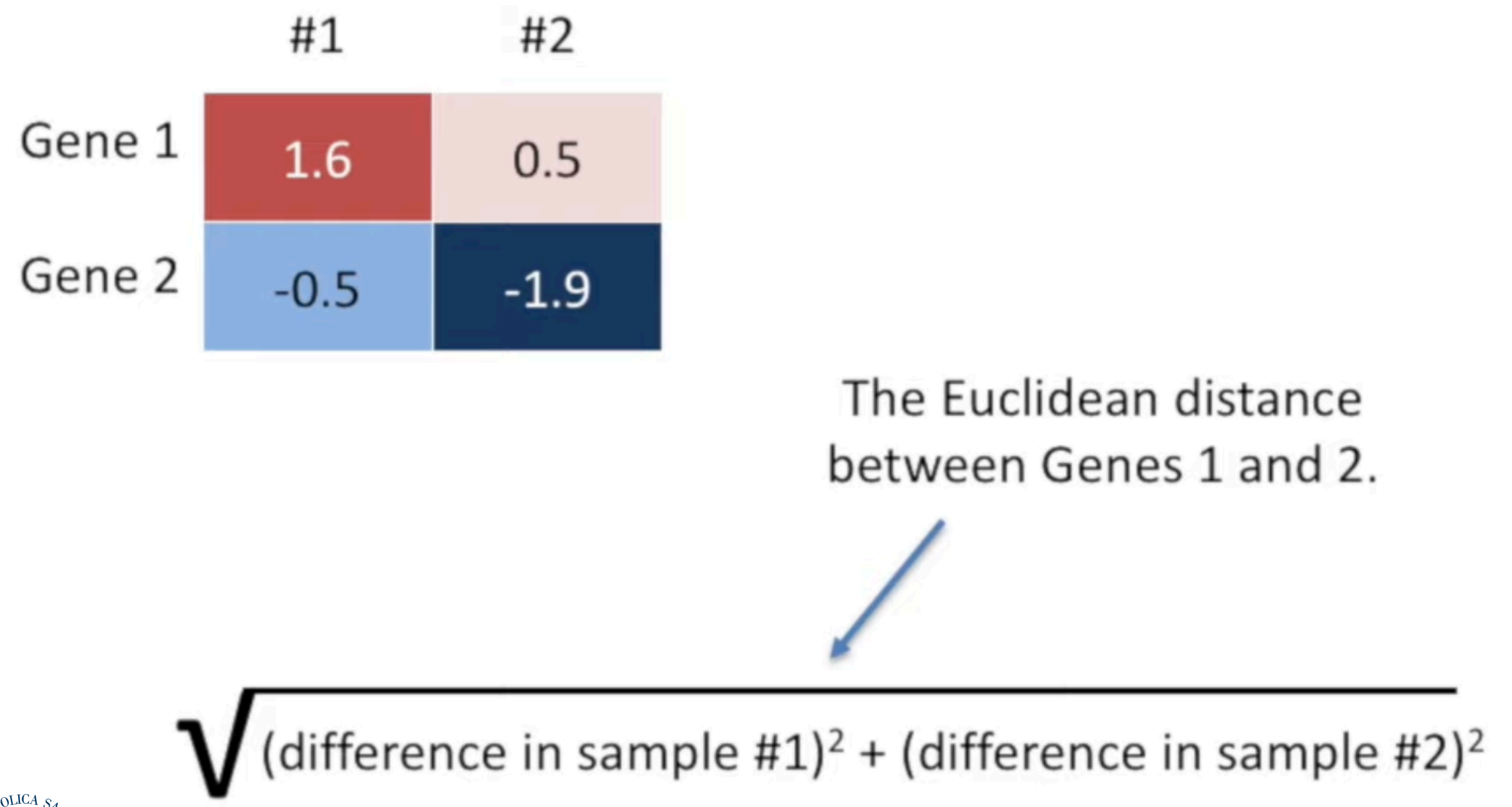
hierarchical clustering



1) Figure out which gene is **most similar** to gene #1.

The method for determining similarity is arbitrarily chosen. However, the Euclidian distance between genes is used a lot.

hierarchical clustering

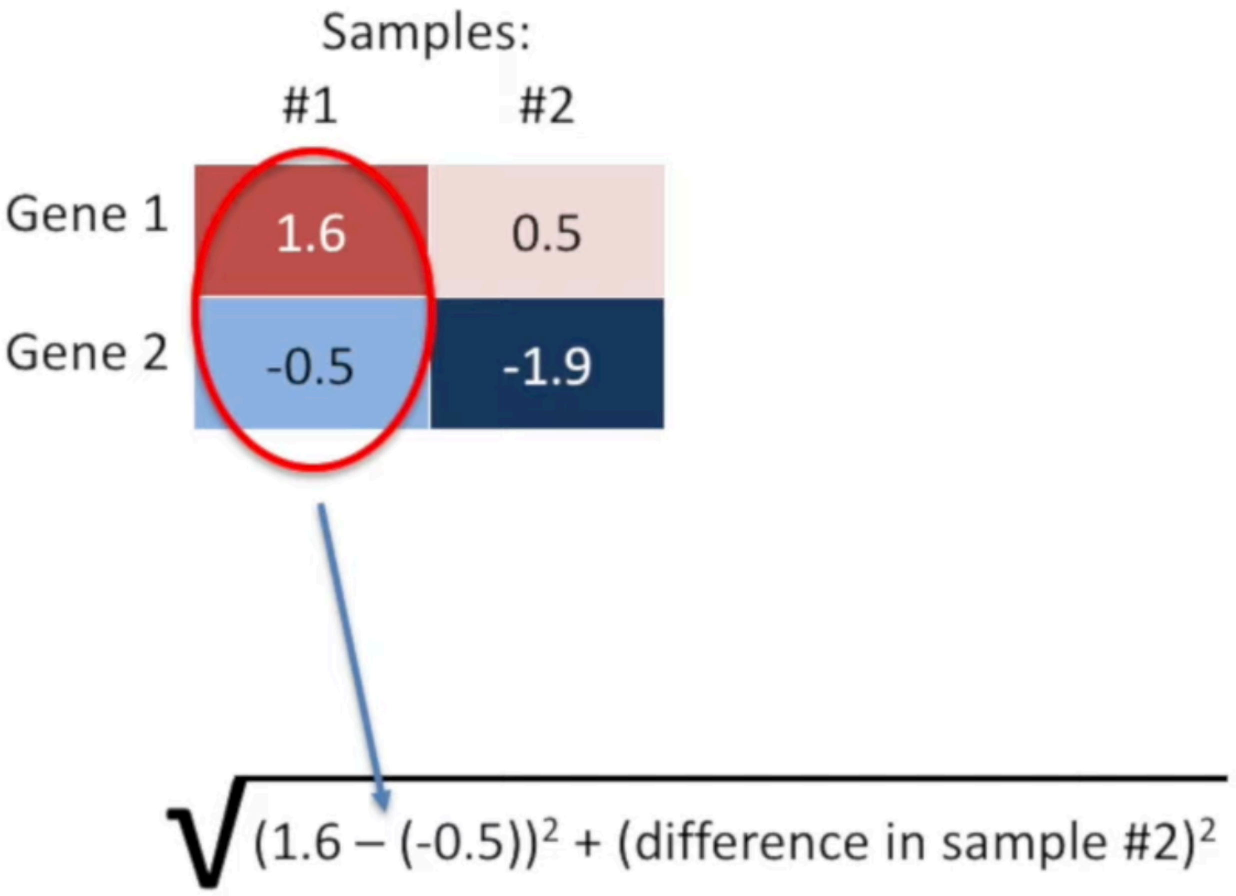


	#1	#2
Gene 1	1.6	0.5
Gene 2	-0.5	-1.9

The Euclidean distance between Genes 1 and 2.

$$\sqrt{(\text{difference in sample \#1})^2 + (\text{difference in sample \#2})^2}$$

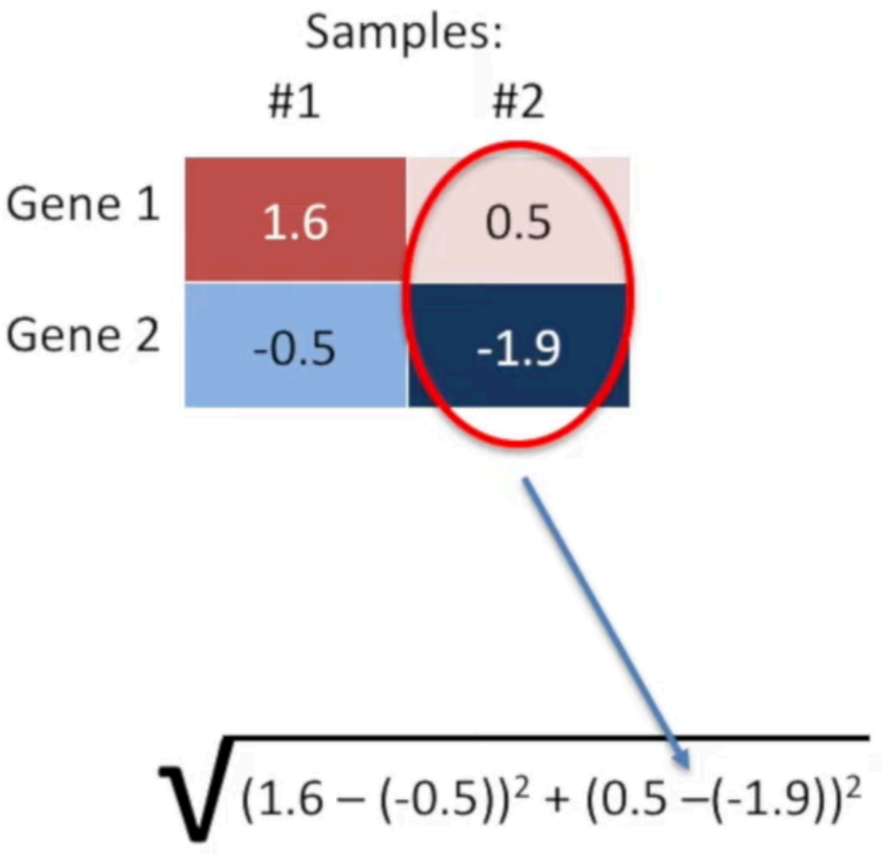
hierarchical clustering



	Samples: #1	#2
Gene 1	1.6	0.5
Gene 2	-0.5	-1.9

$$\sqrt{(1.6-(-0.5))^2+(\text{difference in sample \#2})^2}$$

hierarchical clustering



Samples:

	#1	#2
Gene 1	1.6	0.5
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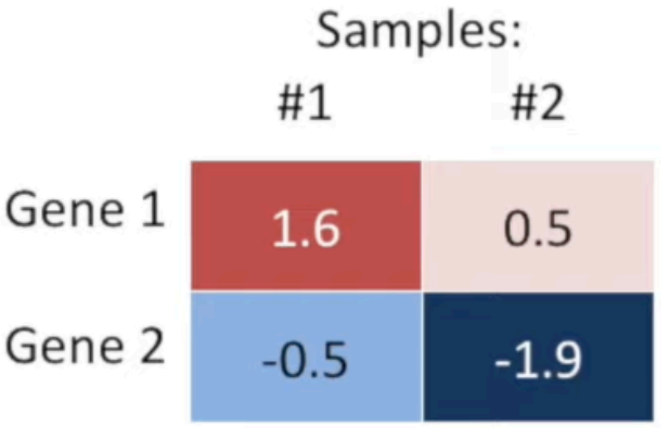
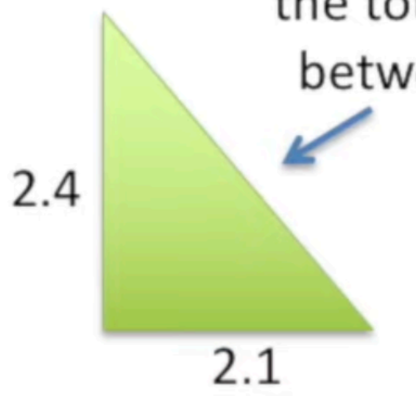
$$\sqrt{(1.6-(-0.5))^2+(0.5-(-1.9))^2}$$

hierarchical clustering



Samples:

	#1	#2
Gene 1	1.6	0.5
Gene 2	-0.5	-1.9



The hypotenuse is the total "distance" between genes #1 and #2.

$$\sqrt{(2.1)^2 + (2.4^2)}$$

Section 2

Pseudocode in R

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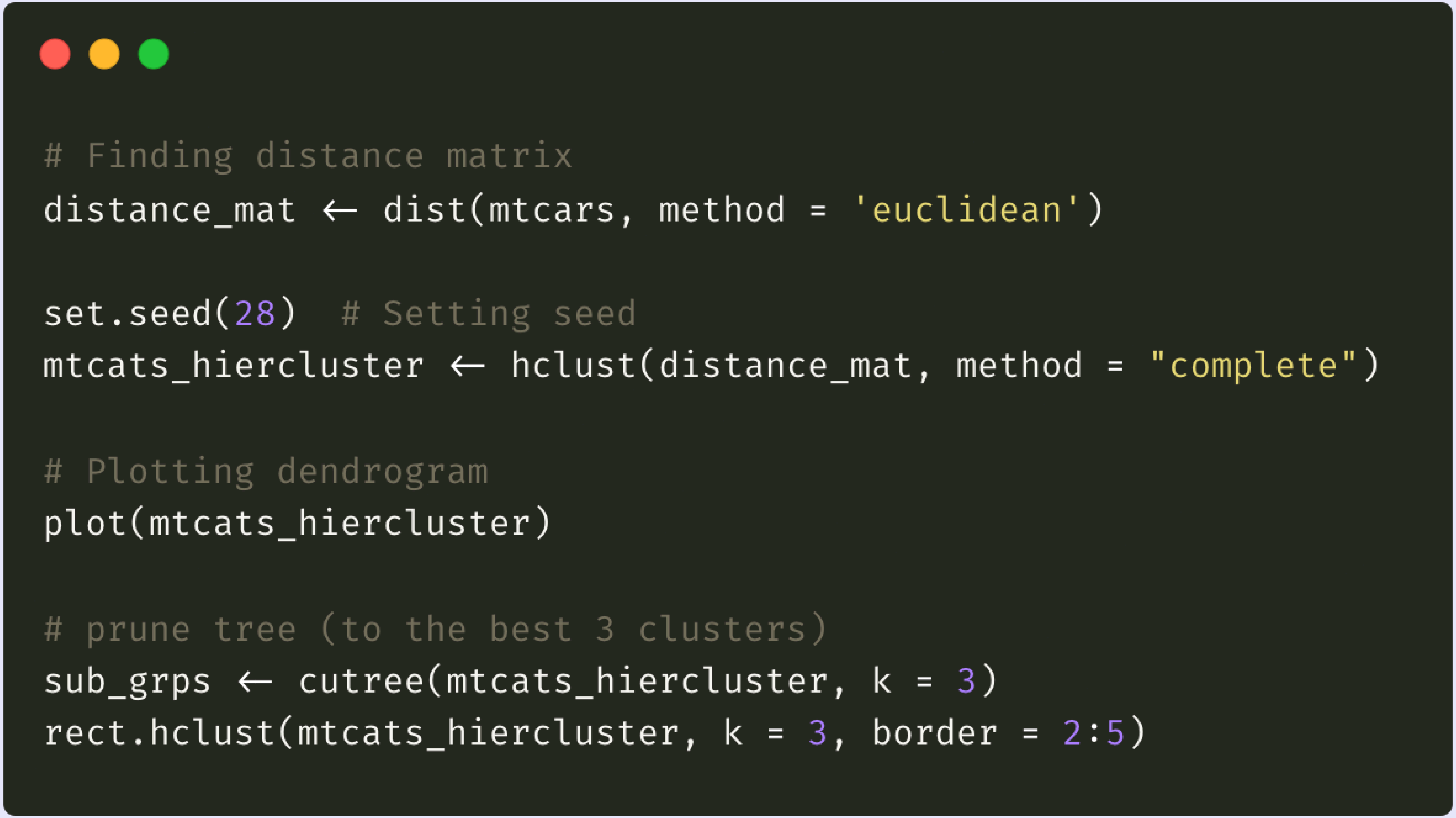

```
# Finding distance matrix
distance_mat ← dist(mtcars, method = 'euclidean')

set.seed(28)  # Setting seed
mtcats_hiercluster ← hclust(distance_mat, method = "complete")

# Plotting dendrogram
plot(mtcats_hiercluster)

# prune tree (to the best 3 clusters)
sub_grps ← cutree(mtcats_hiercluster, k = 3)
rect.hclust(mtcats_hiercluster, k = 3, border = 2:5)
```

Section 4

Live coding session!

JUMP TO RSTUDIO!

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