

StatQuest!

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Linear Discriminant Analysis

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- It kind of is – but not really
- Let's see what it does and then work it out!

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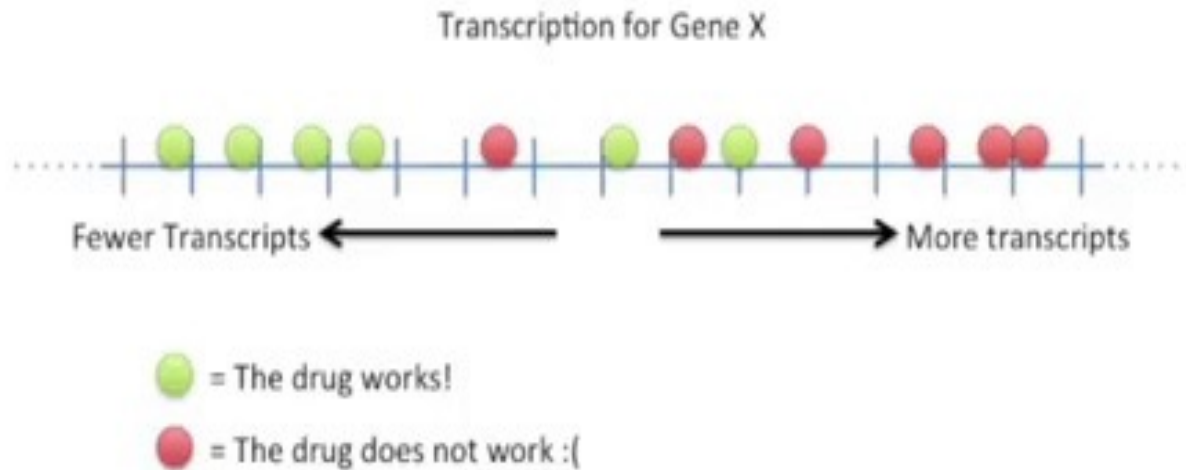
The Problem...

- We've got a cancer drug
 - It works great for some people...
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- How do we decide who to give the drug to?

The Problem...

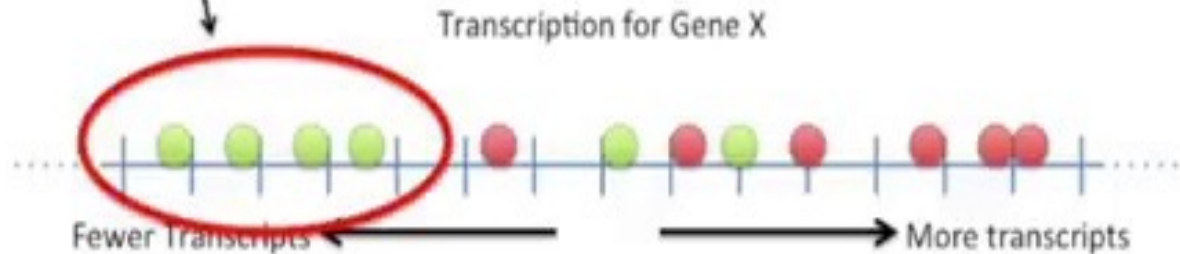
- We've got a cancer drug
 - It works great for some people...
 - ... but it makes other people feel worse. :(
- How do we decide who to give the drug to?
 - Maybe gene expression can help us decide.

Using one gene to decide...



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For the most part, the drug works
in people with low transcription of
gene X.



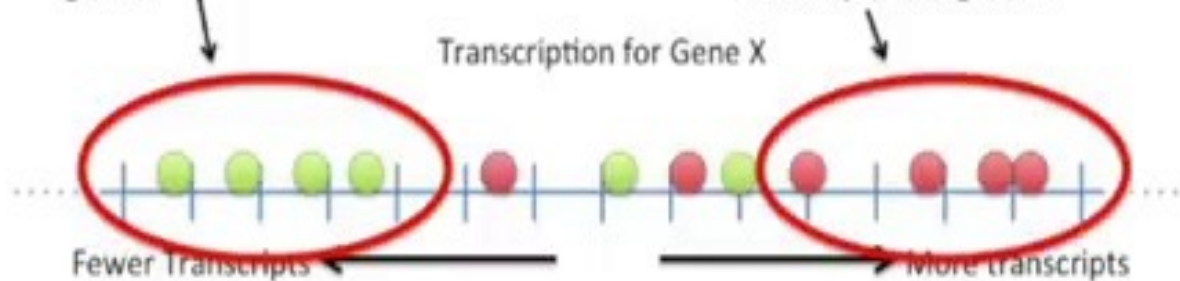
● = The drug works!

● = The drug does not work :(

Using one gene to decide...

For the most part, the drug works in people with low transcription of gene X.

And, for the most part, the drug does not work in people with high transcription of gene X.

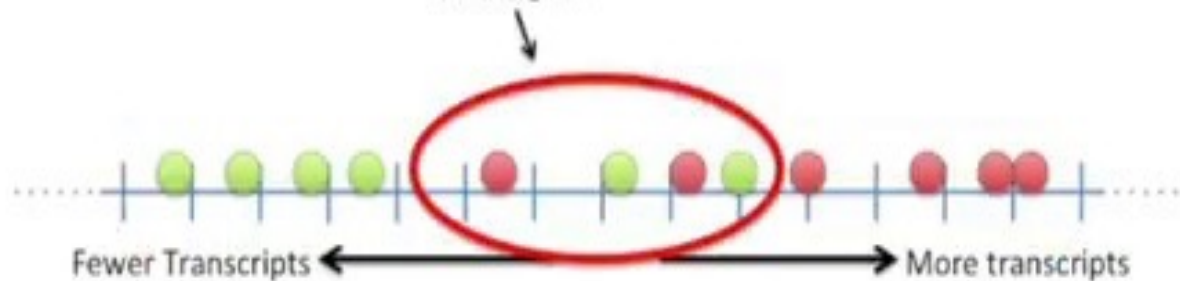


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Using one gene to decide...

However, there is overlap and no obvious "cutoff" for who to give the drug to.

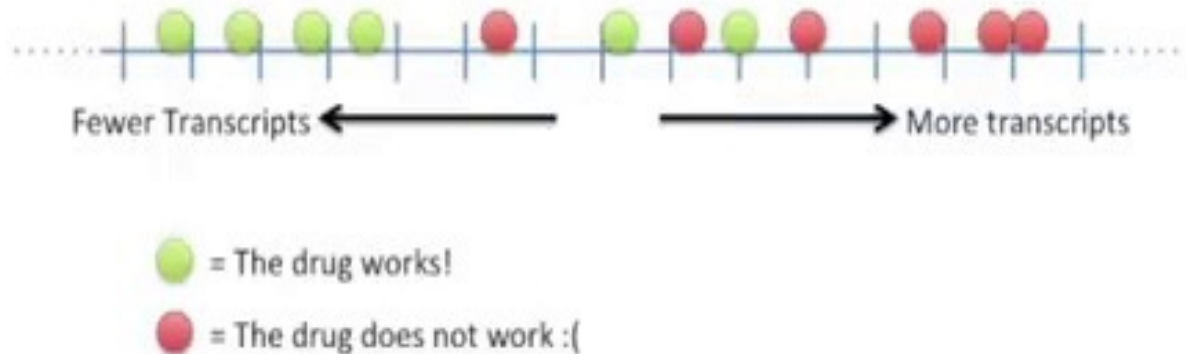


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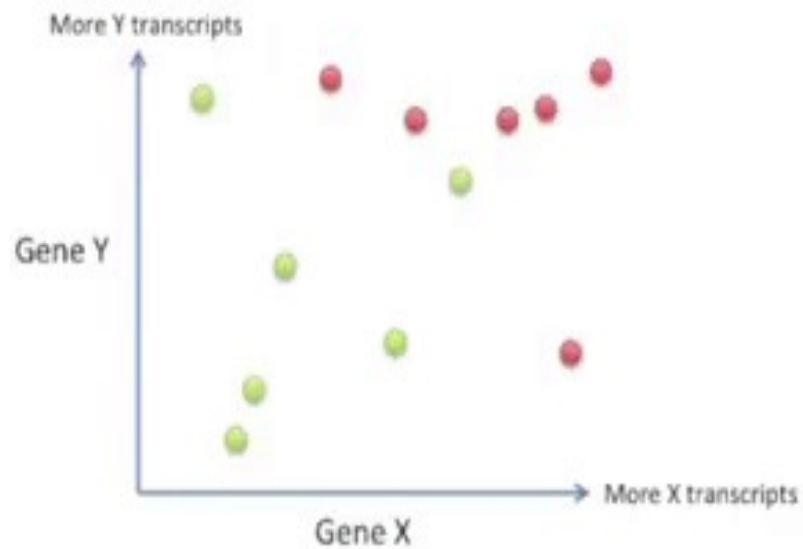
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Using one gene to decide...

In summary, Gene X does an OK job at telling us who should take the drug (and who shouldn't).



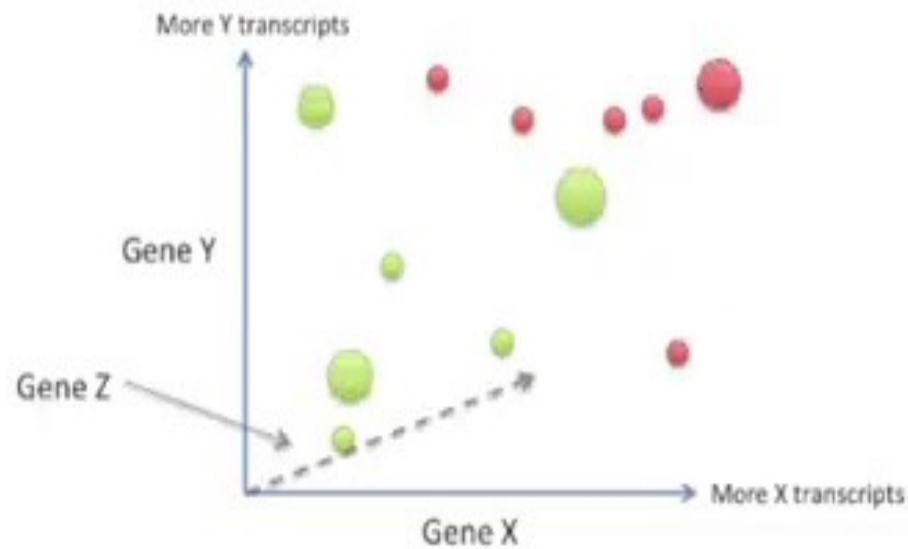
Using two genes to decide...



● = The drug works!

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Using three genes to decide...



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What if we need four (or more) genes to
separate the two categories?

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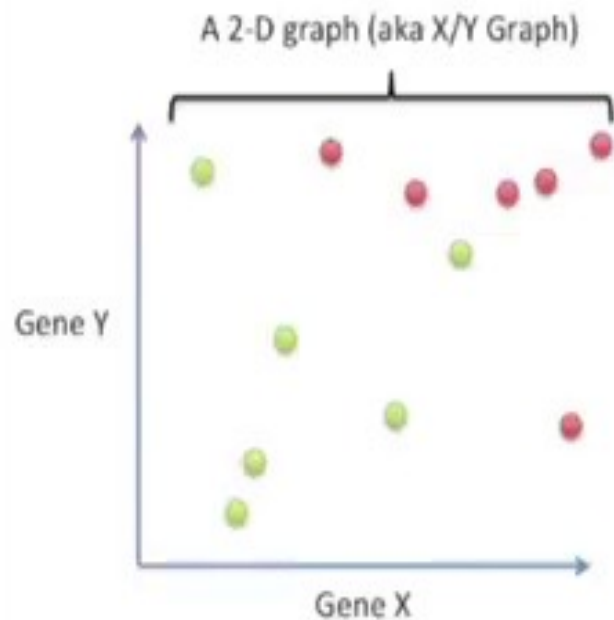
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A super simple example

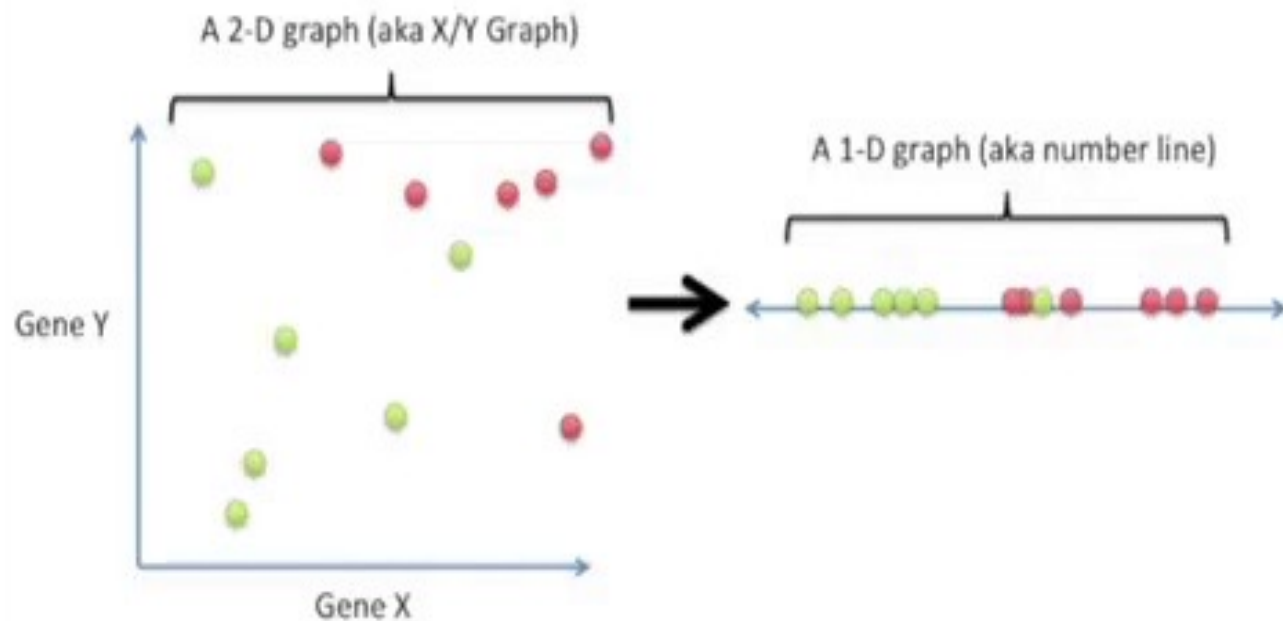
A super simple example

Reducing a 2-D graph to a 1-D graph

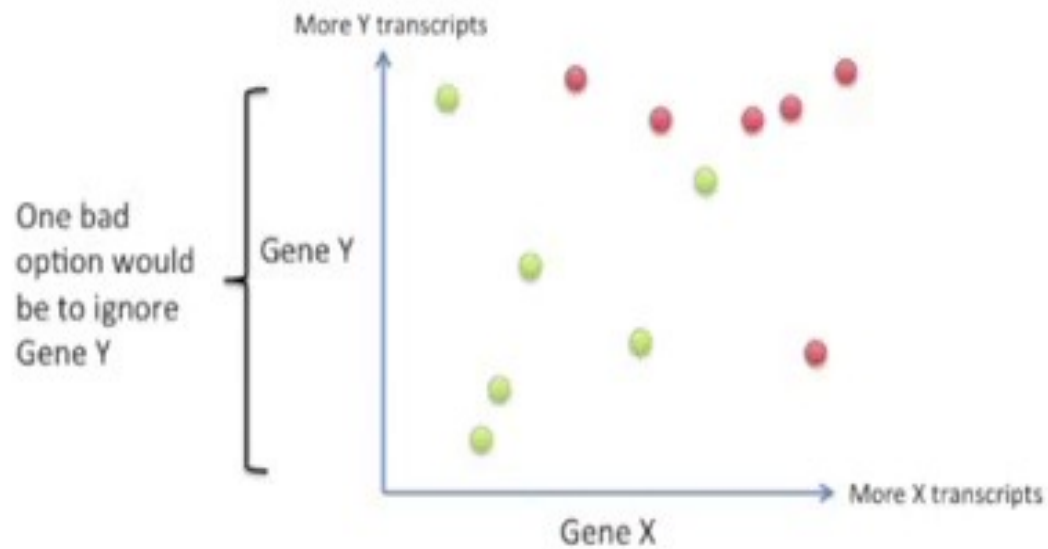


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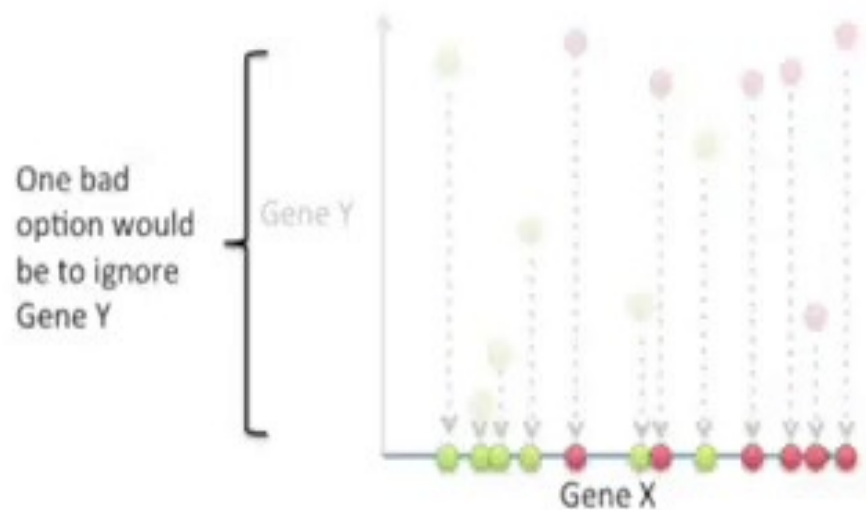
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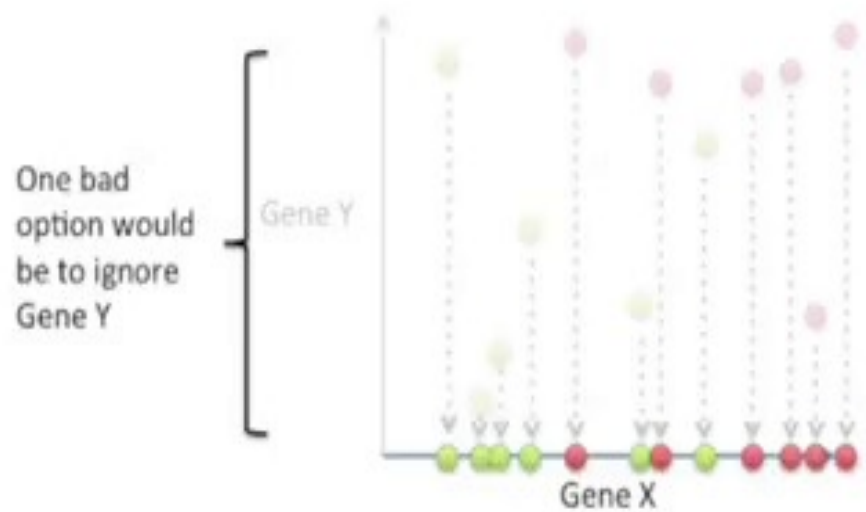
Reducing a 2-D graph to a 1-D graph



This way is bad because it ignores the useful information that Gene Y provides...

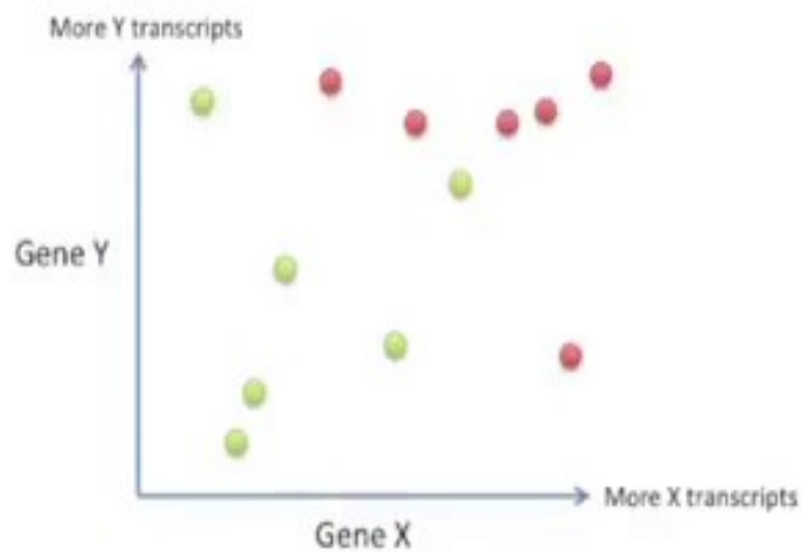
Projecting the genes onto the Y-axis (i.e. ignoring Gene X) isn't any better

Reducing a 2-D graph to a 1-D graph

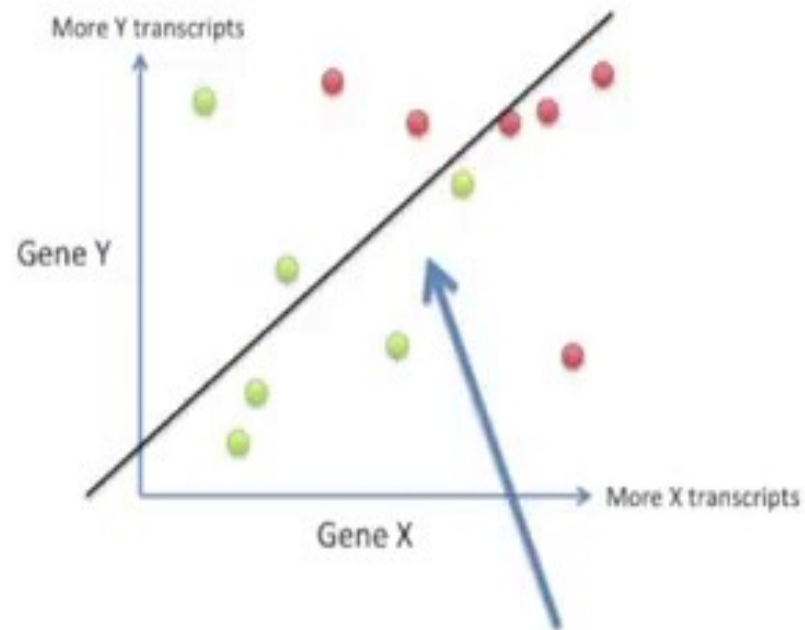


LDA provides a better way!!!

Reducing a 2-D graph to a 1-D graph with LDA

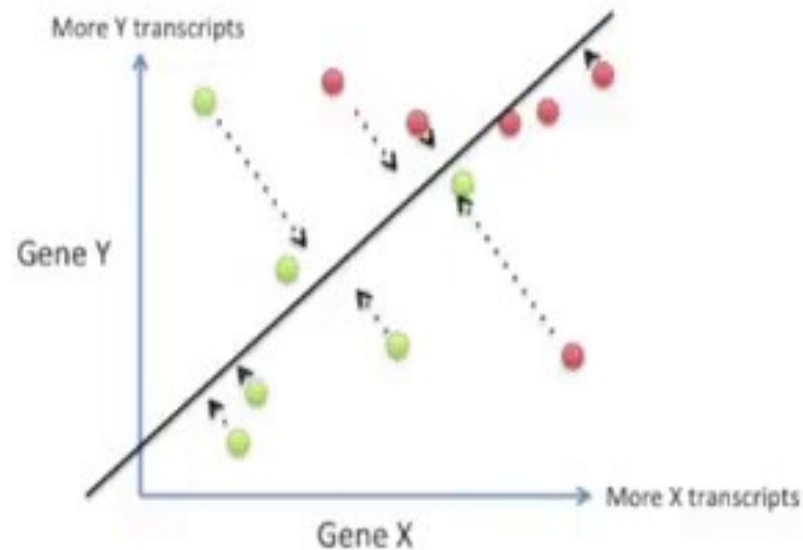


Reducing a 2-D graph to a 1-D graph with LDA



LDA uses both genes to create a new axis...

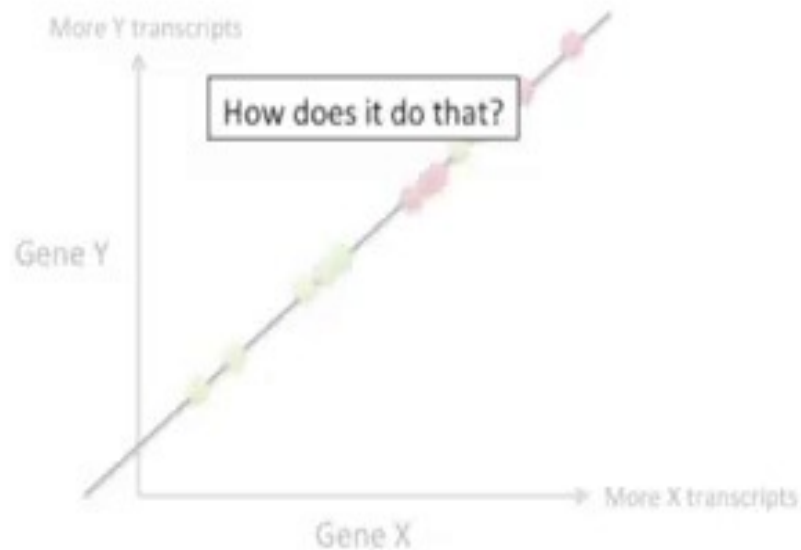
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LDA uses both genes to create a new axis...

...and projects the data onto this new axis in a way to maximize the separation of the two categories.

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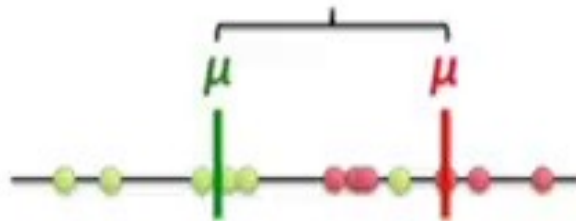
How LDA creates a new axis...



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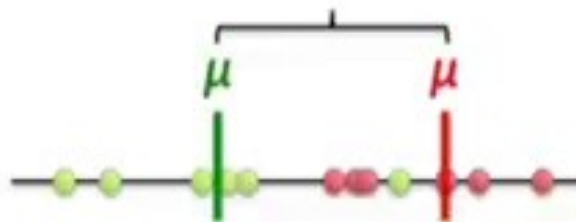
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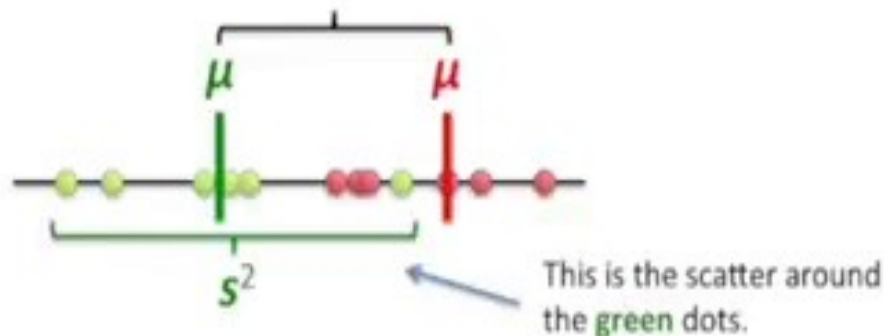


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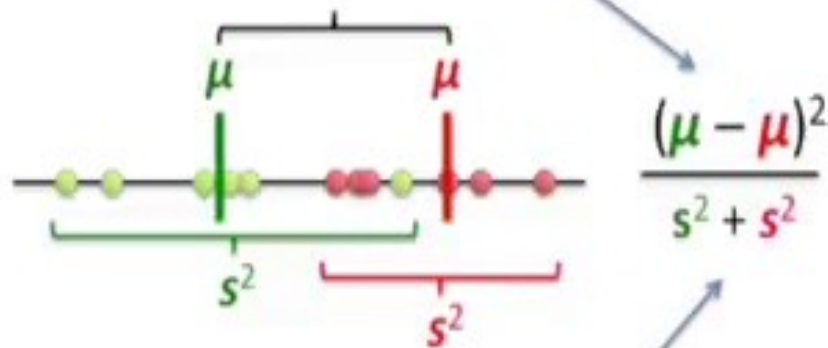


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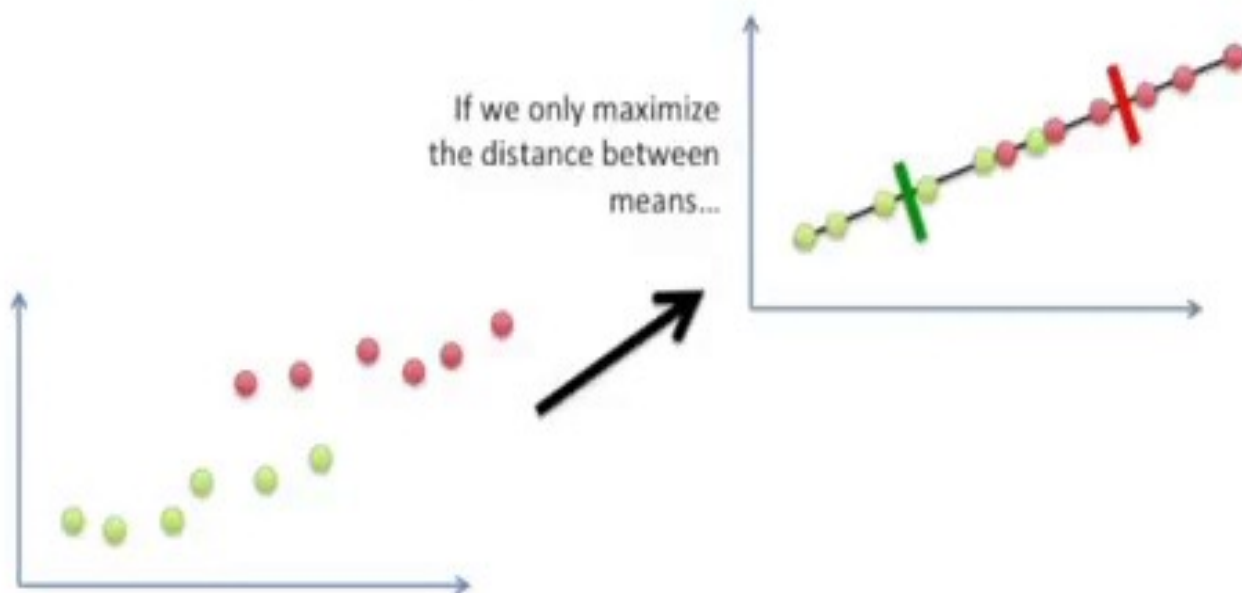
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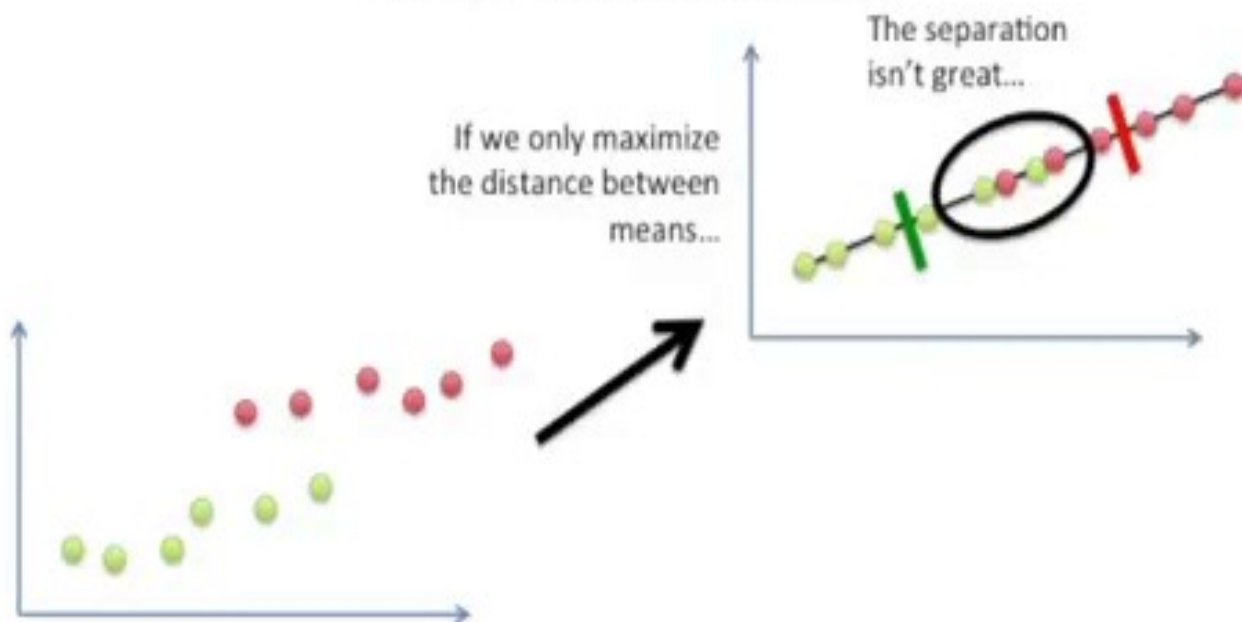
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An example showing why both distance and scatter are important.

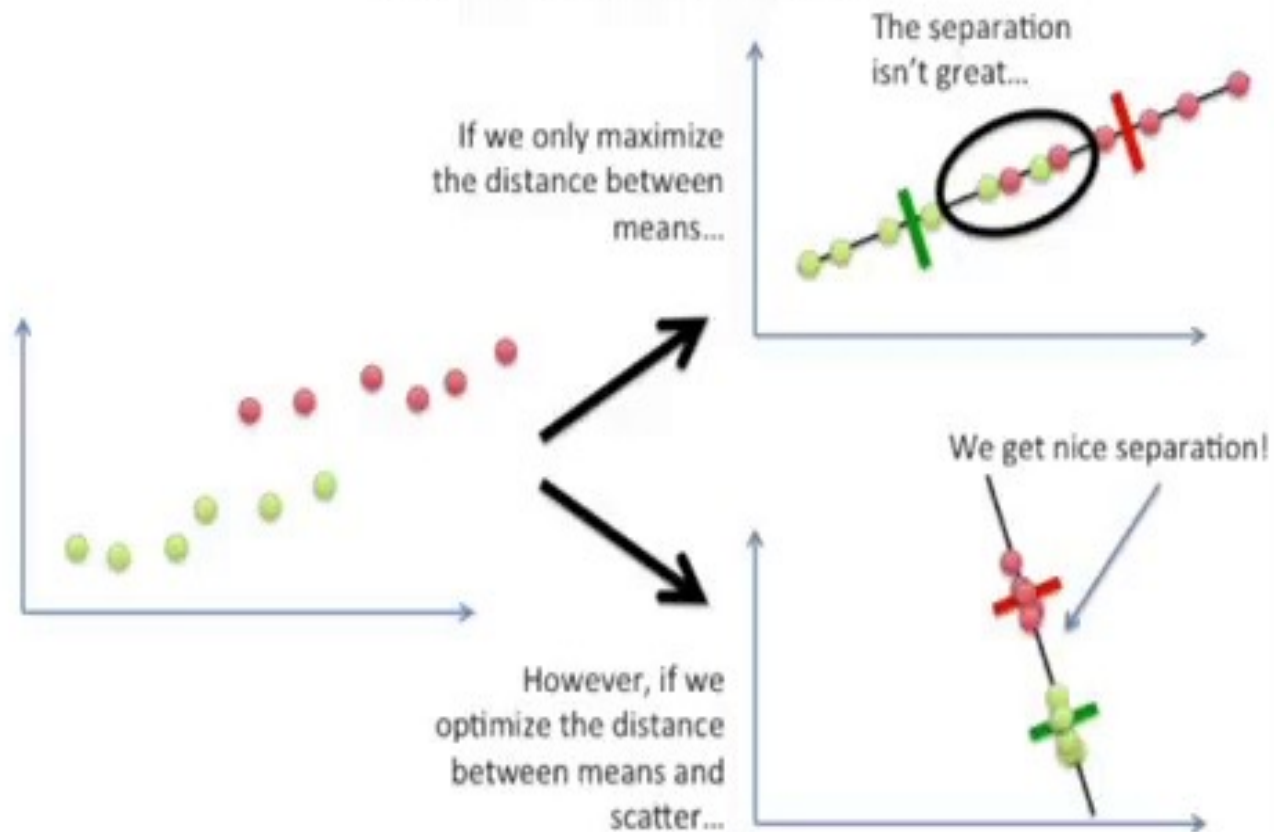
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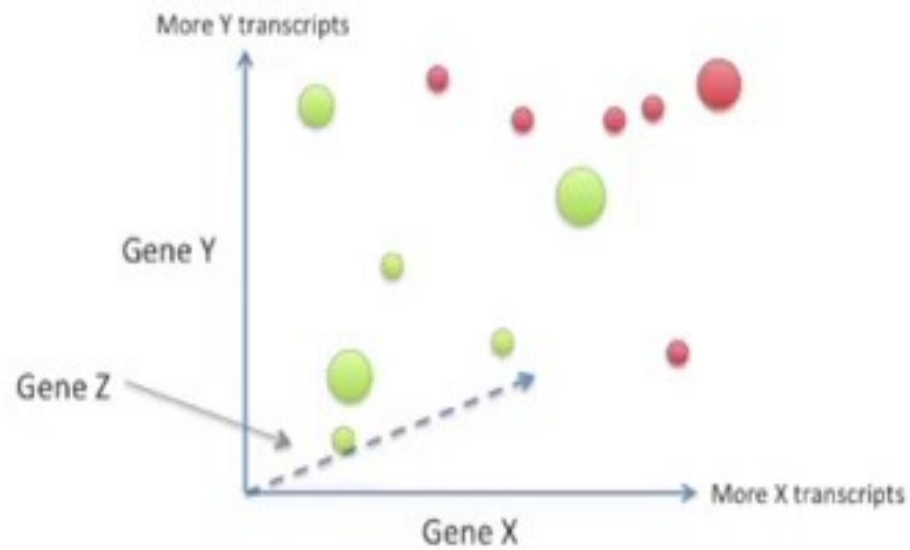


What if we have more than 2 genes
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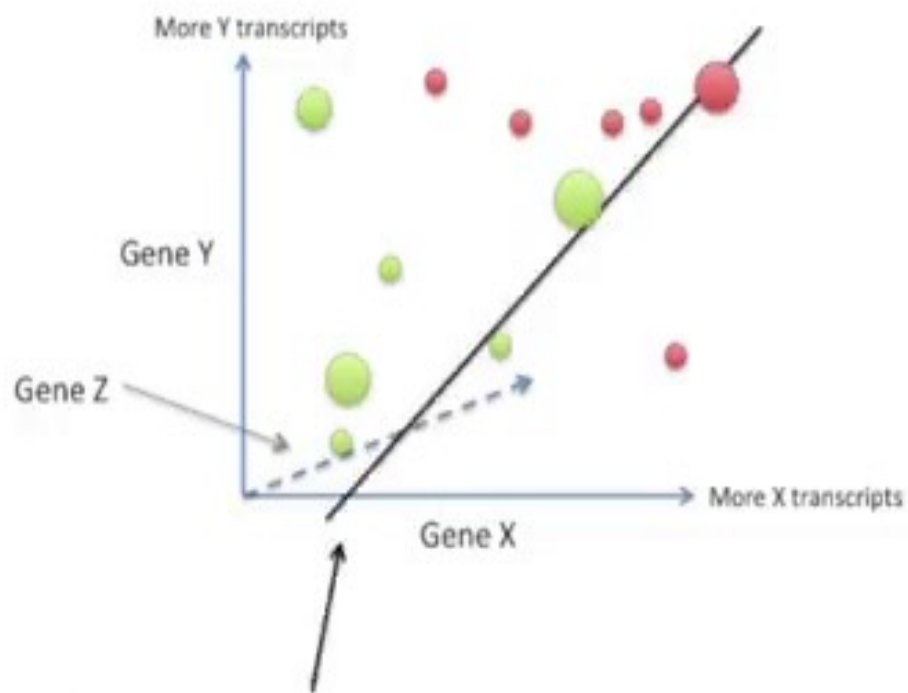
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- The process is the same:
 - Create an axis that maximizes the distance between the means for the two categories while minimizing the scatter.

LDA with 3 genes.



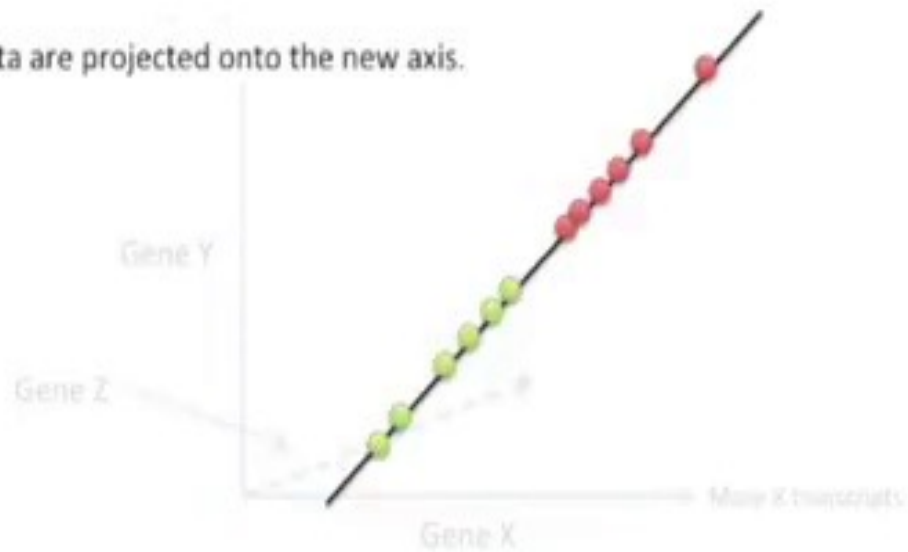
LDA with 3 genes.



Here's the new axis that LDA created.

LDA with 3 genes.

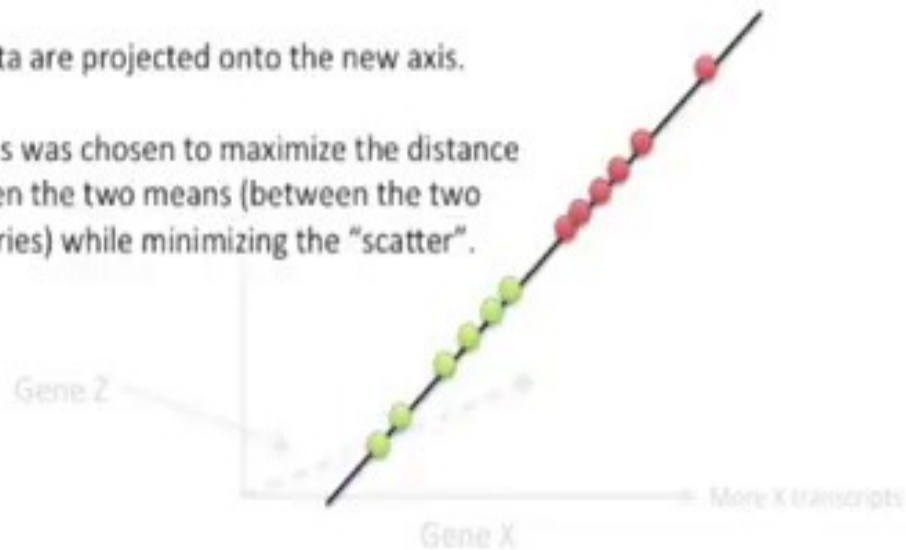
The data are projected onto the new axis.



LDA with 3 genes.

The data are projected onto the new axis.

The axis was chosen to maximize the distance between the two means (between the two categories) while minimizing the "scatter".

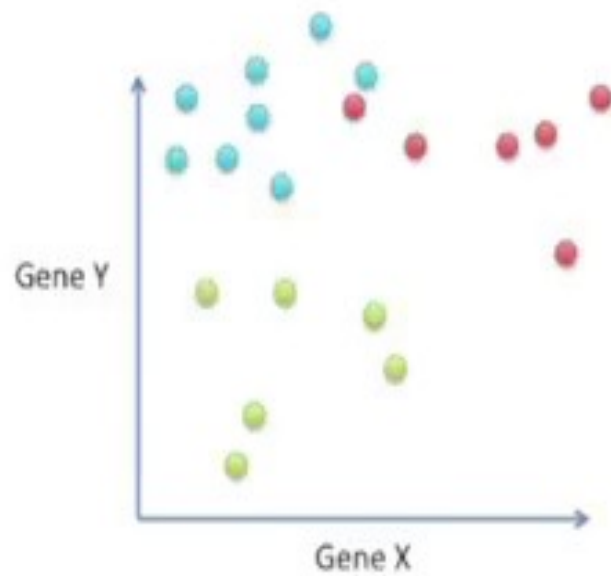


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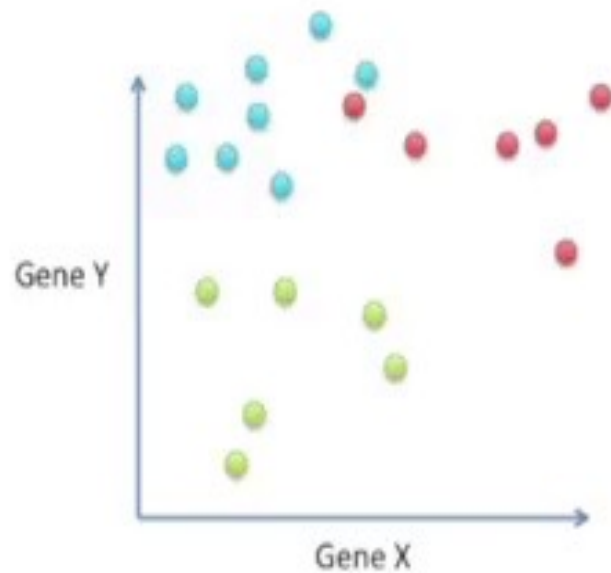
- Two things change, but barely...

LDA for 3 categories

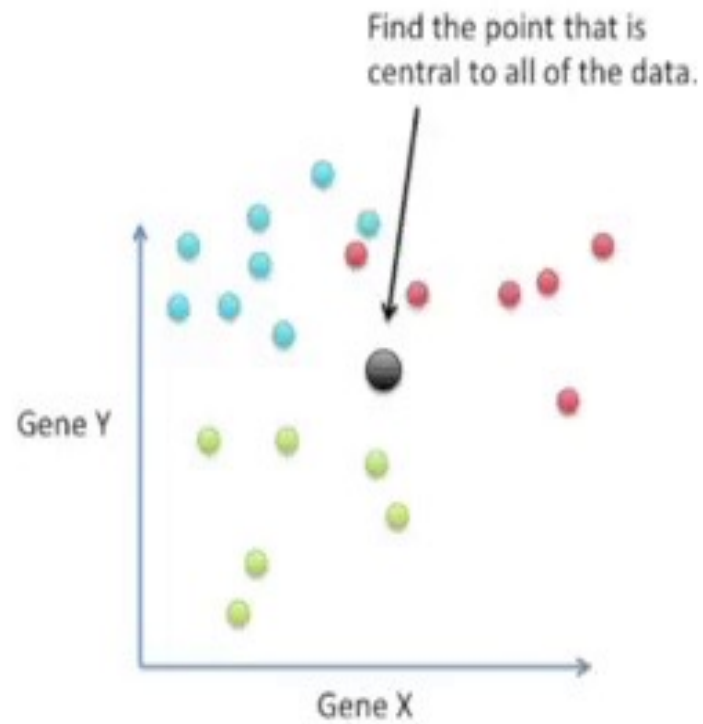


LDA for 3 categories

The **first difference** is how you measure the distances among the means.

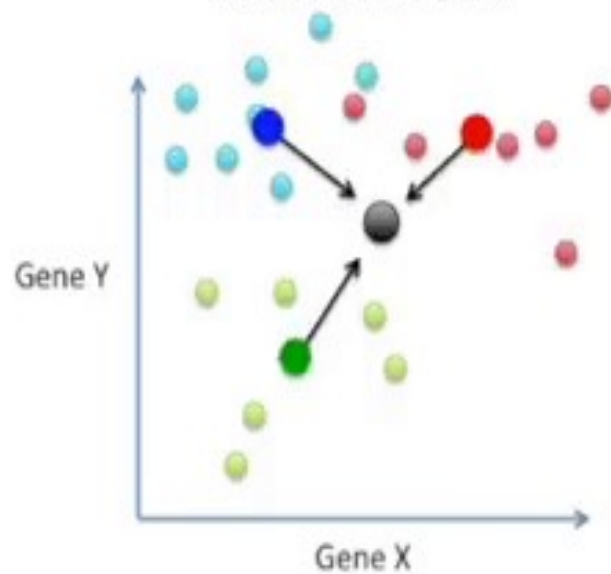


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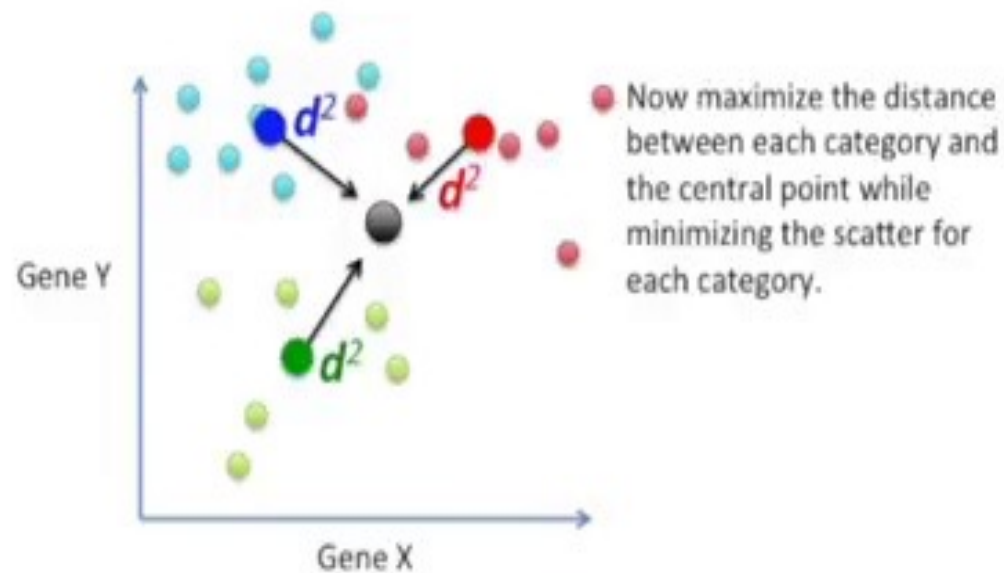


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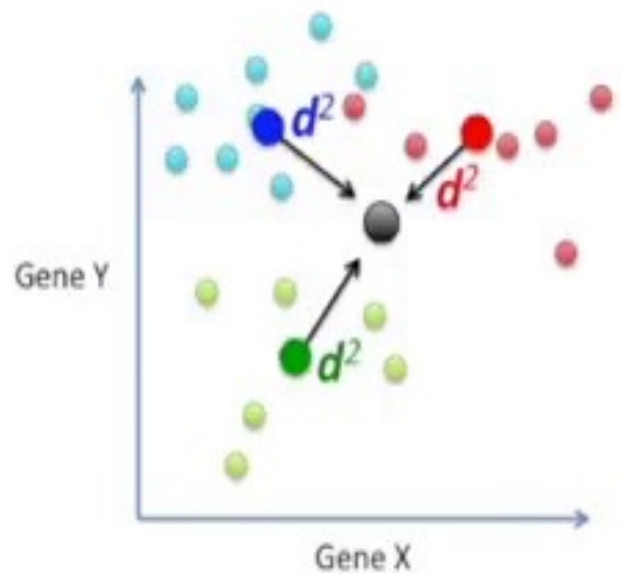
Then measure the distances between a point that is central in each category and the main central point.



LDA for 3 categories



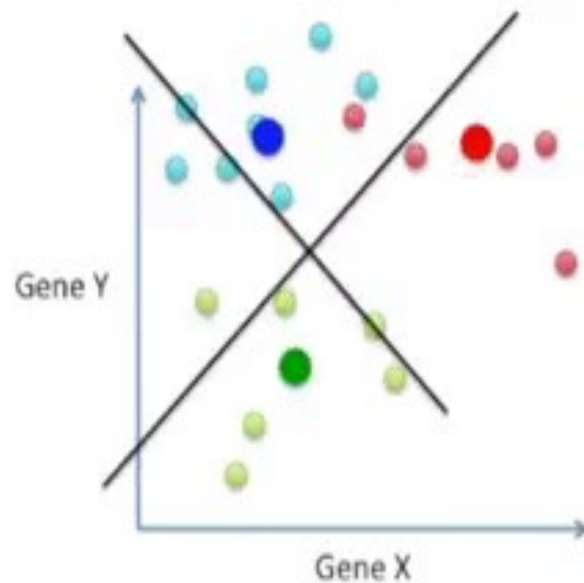
LDA for 3 categories



$$\frac{d^2 + d^2 + d^2}{s^2 + s^2 + s^2}$$

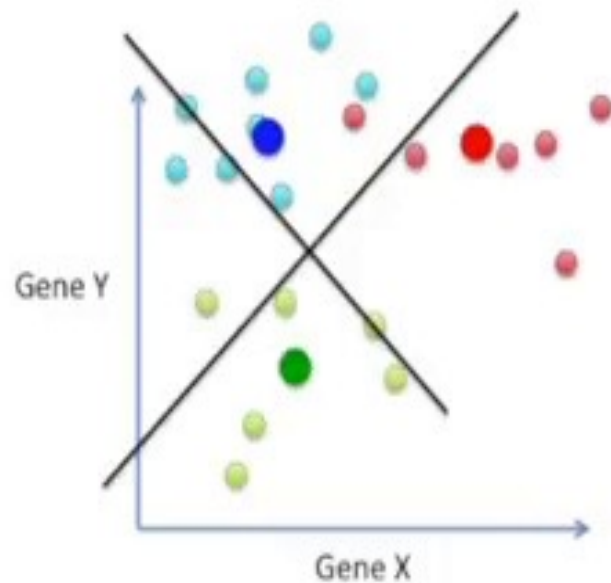
LDA for 3 categories

The second difference is LDA creates 2 axes to separate the data.
This is because the 3 central points for each category define a plane.
(Remember from high school: 2 points define a line, 3 points define a plane...)



LDA for 3 categories

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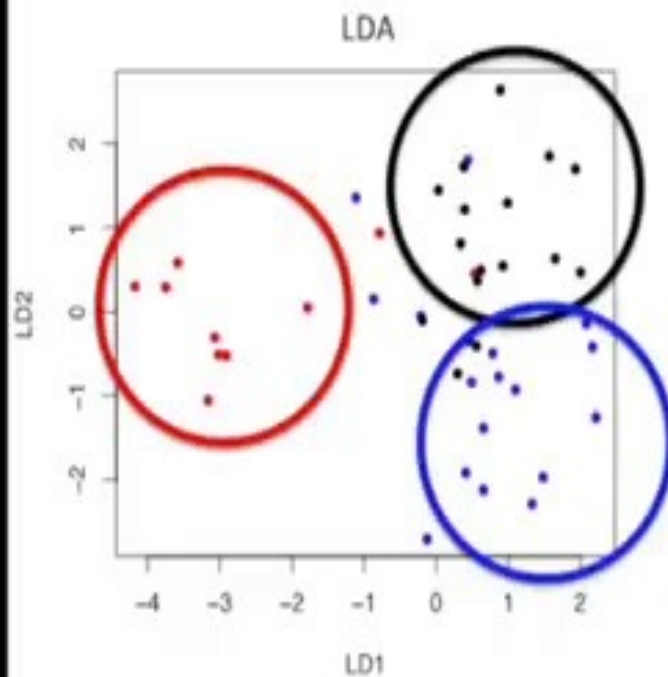
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That would mean we'd need 10,000 dimensions to draw the data.

Suddenly, being able to create 2 axes that maximize the separation of three categories is super cool!!!!

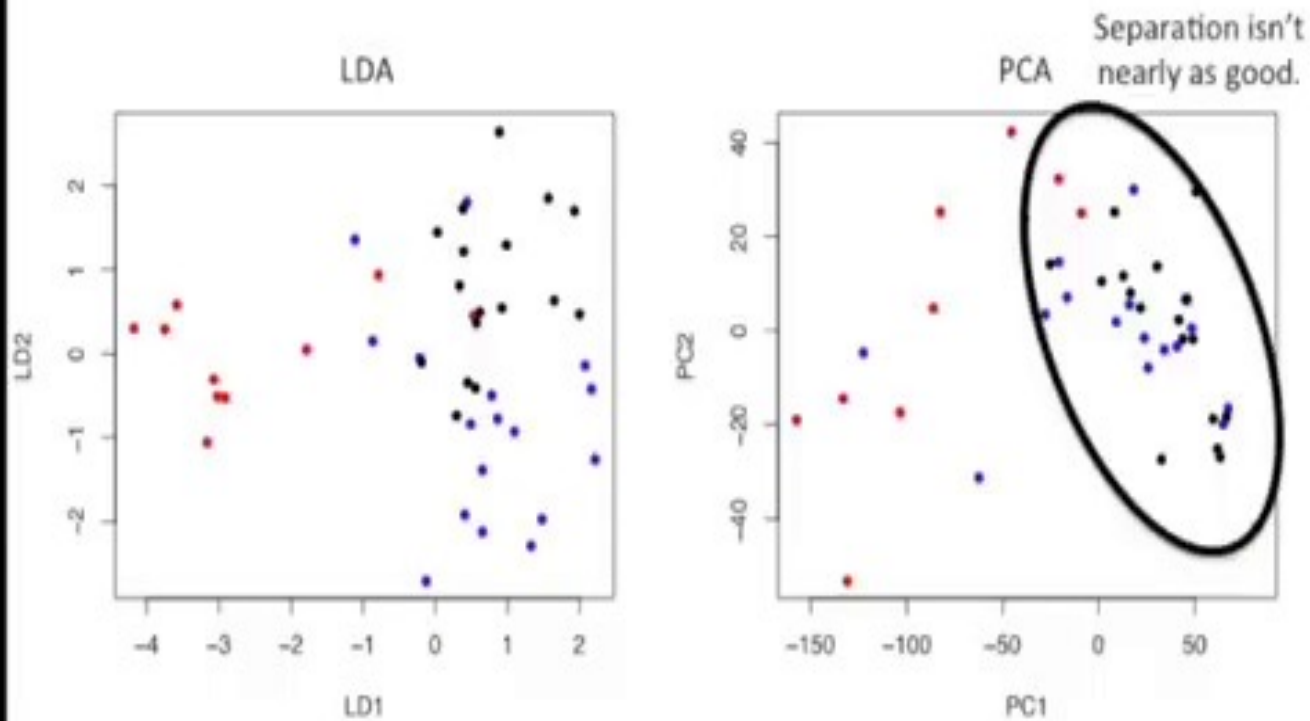
LDA with 3 categories and 10,000 genes.



Although the separation isn't perfect, it is still easy to see three separate categories.

Comparing LDA to PCA with 10,000 genes.

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THE END!!!