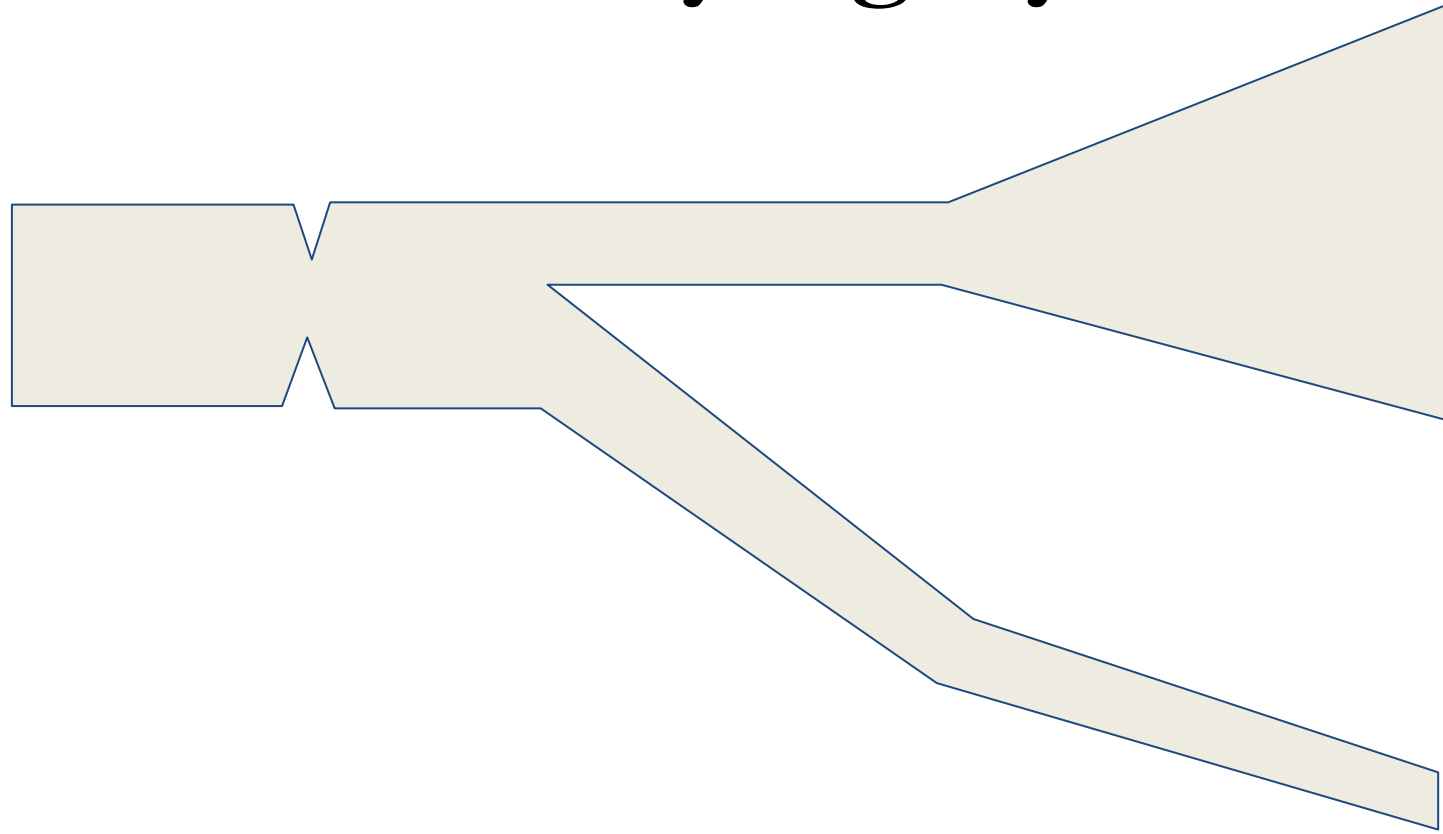


# Analysing SNP data

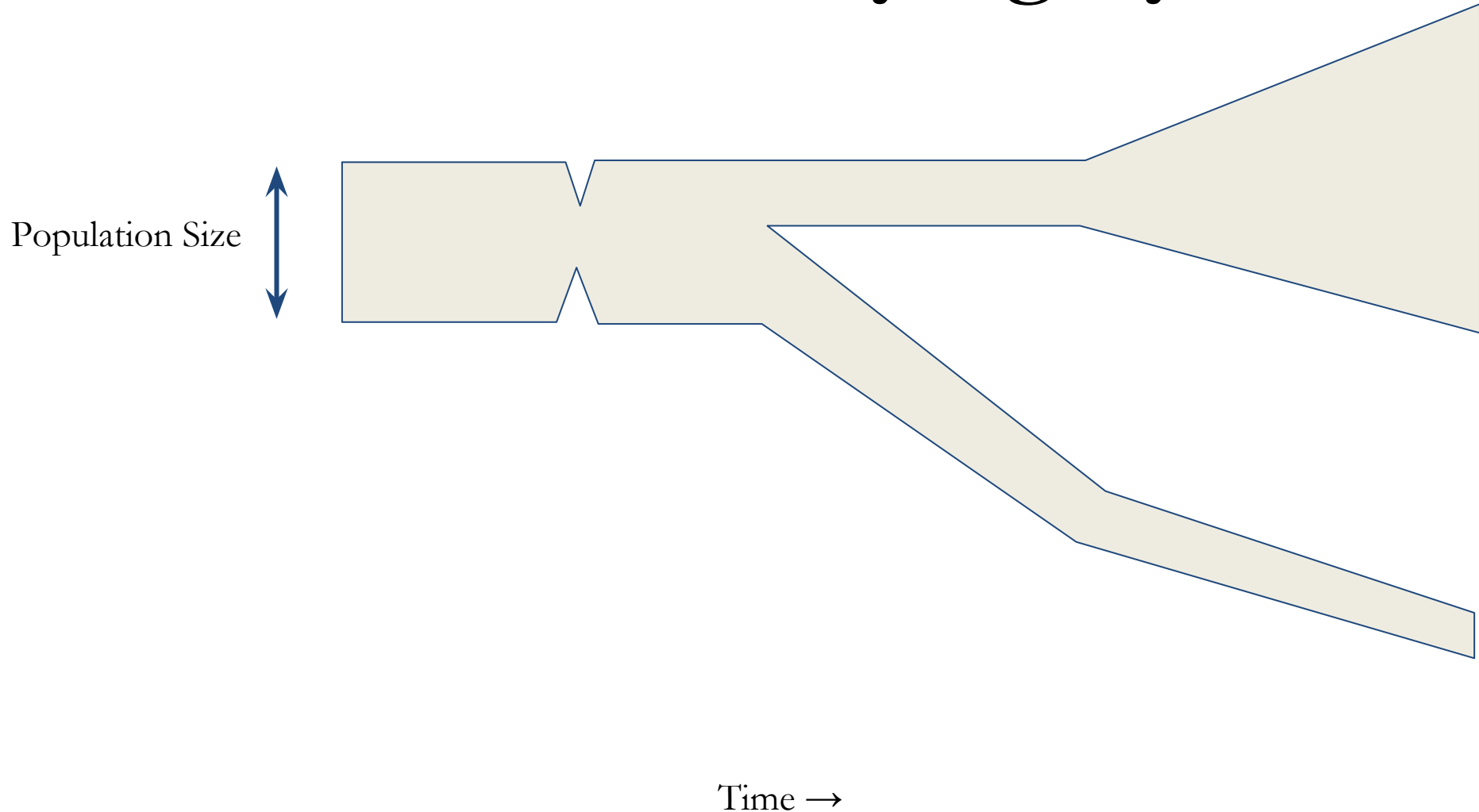
PCA and GWAS

# Population Genetic Diversity: An evolutionary legacy

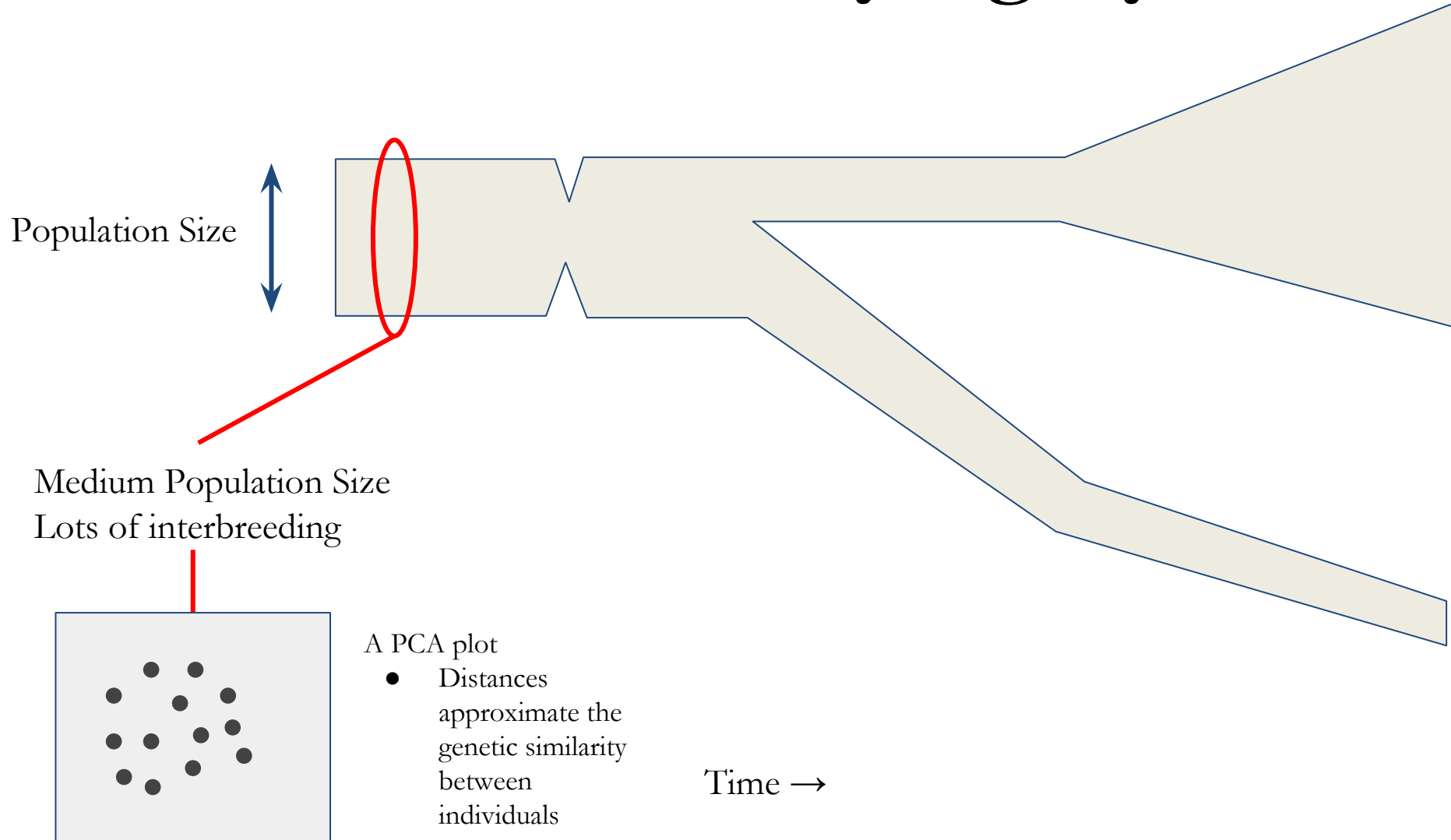


Time →

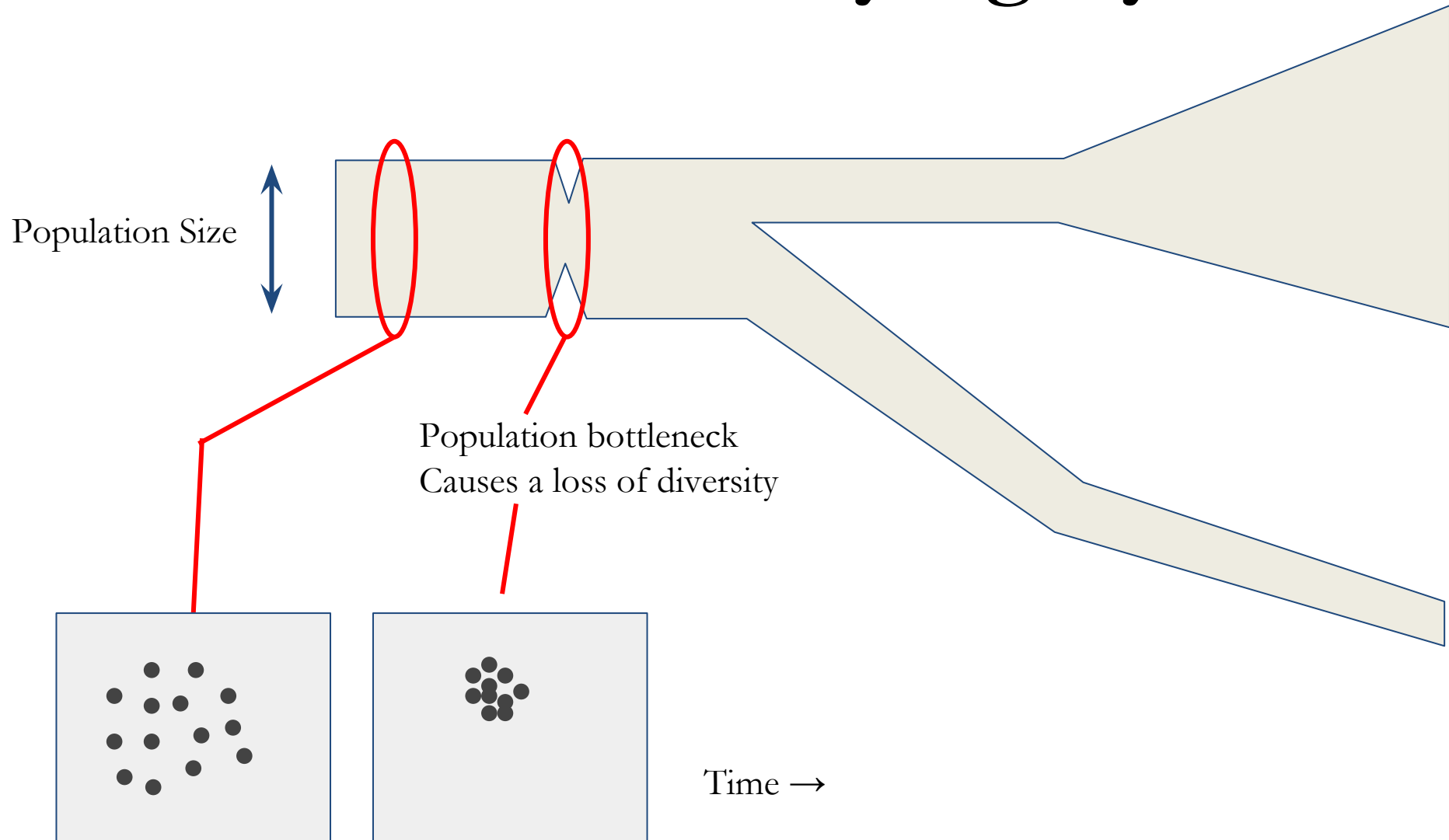
# Population Genetic Diversity: An evolutionary legacy



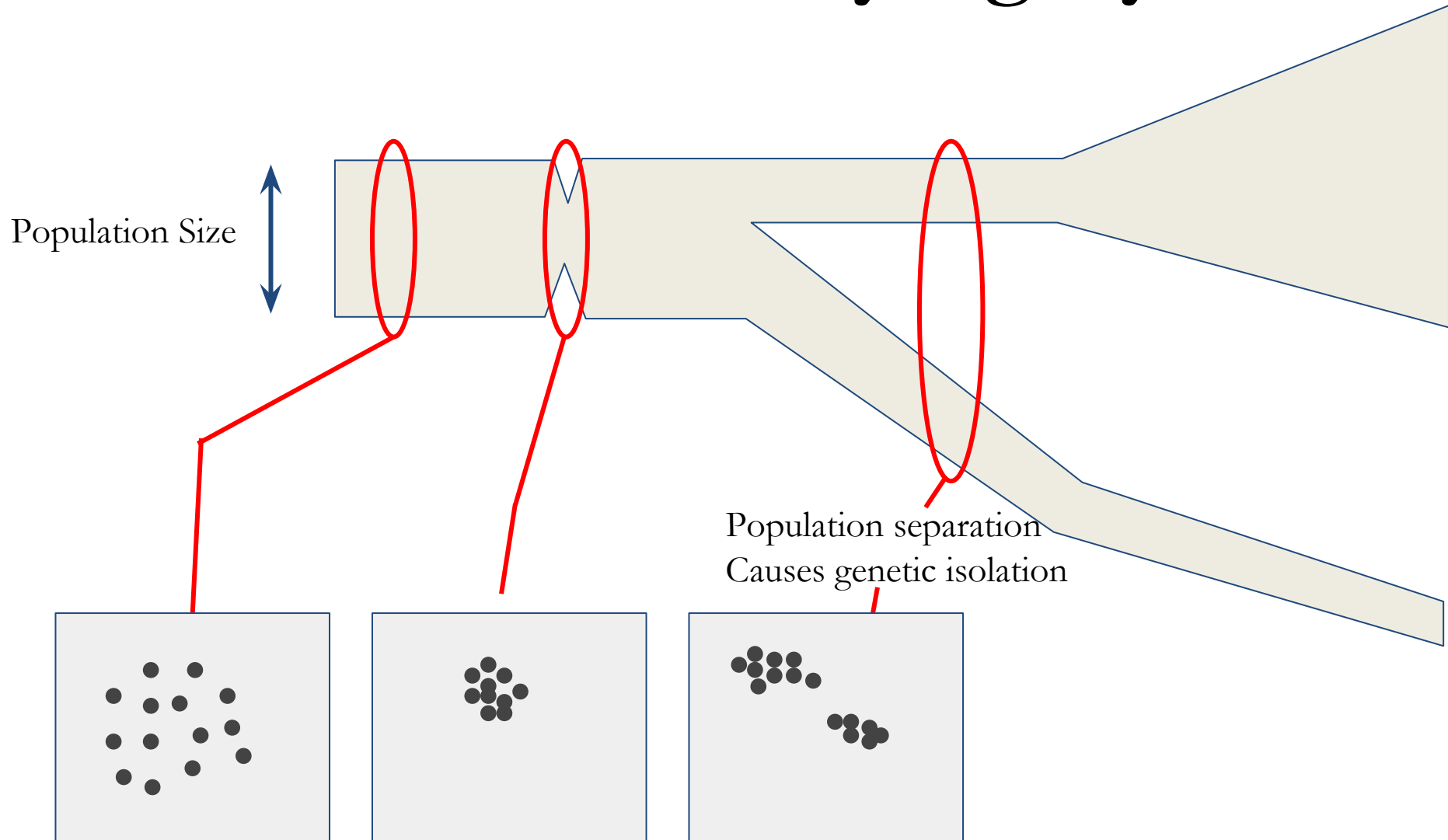
# Population Genetic Diversity: An evolutionary legacy



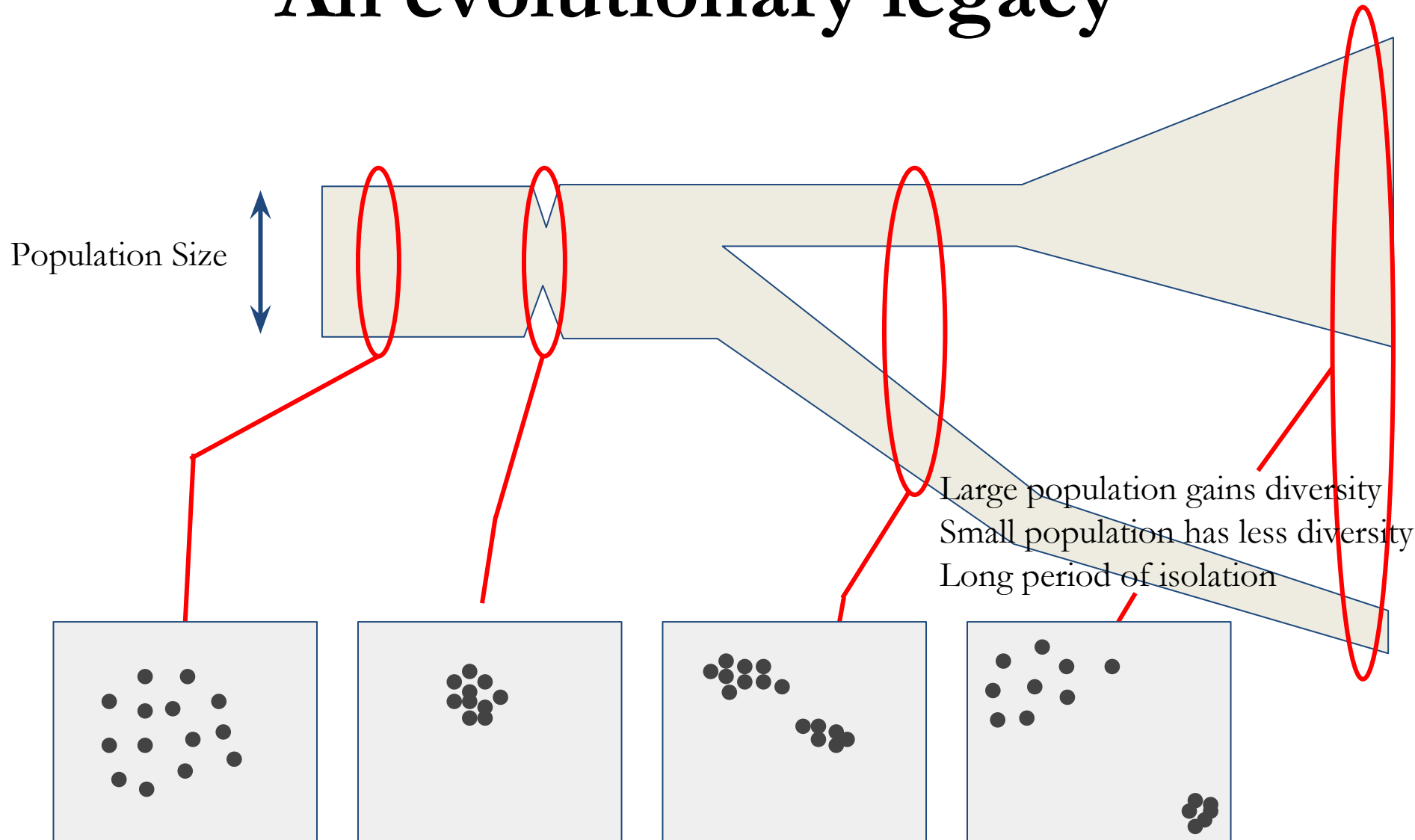
# Population Genetic Diversity: An evolutionary legacy



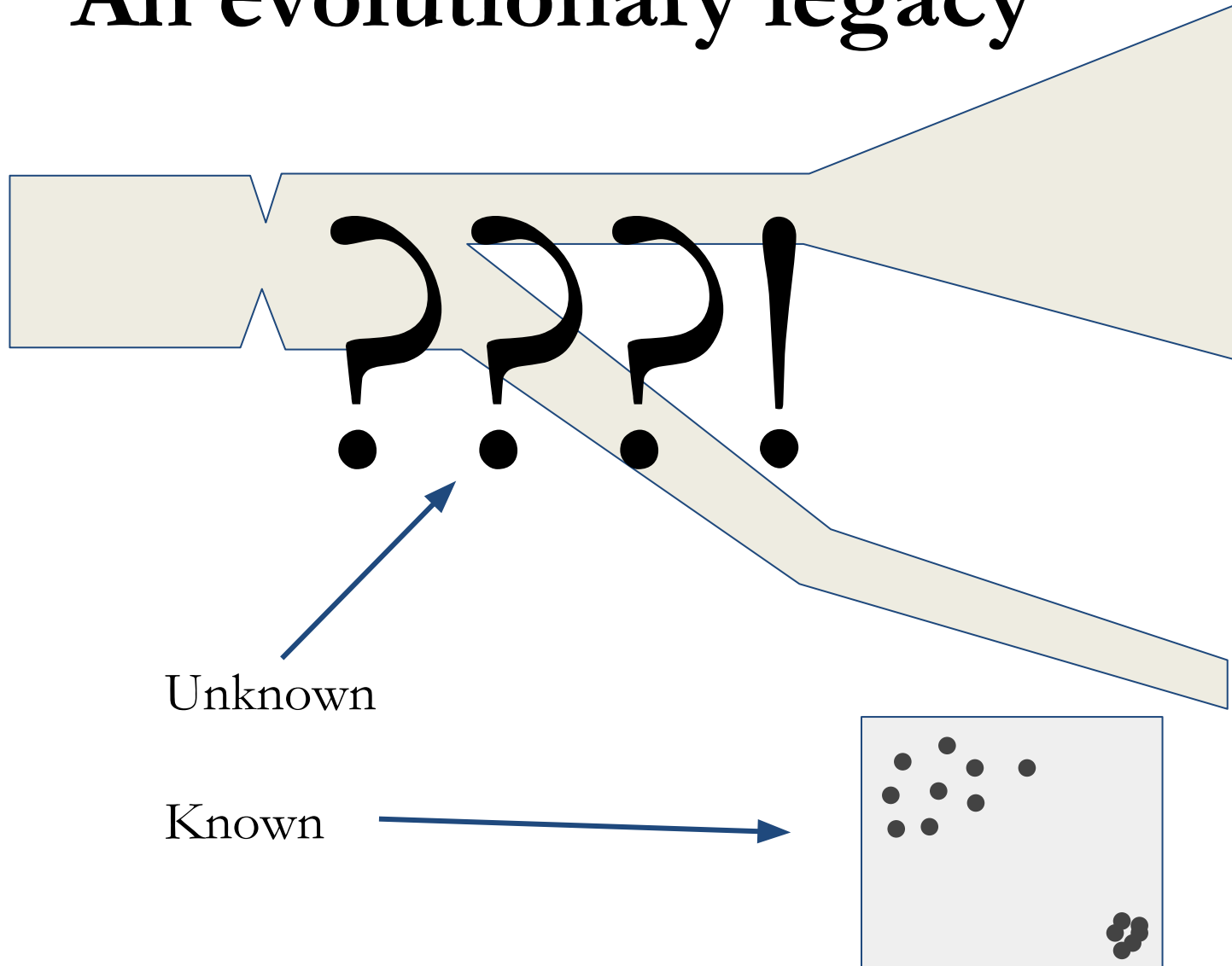
# Population Genetic Diversity: An evolutionary legacy



# Population Genetic Diversity: An evolutionary legacy



# Population Genetic Diversity: An evolutionary legacy



Unknown

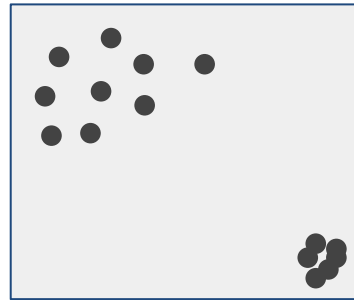
Known



# Population Genetic Diversity:

## A valuable resource

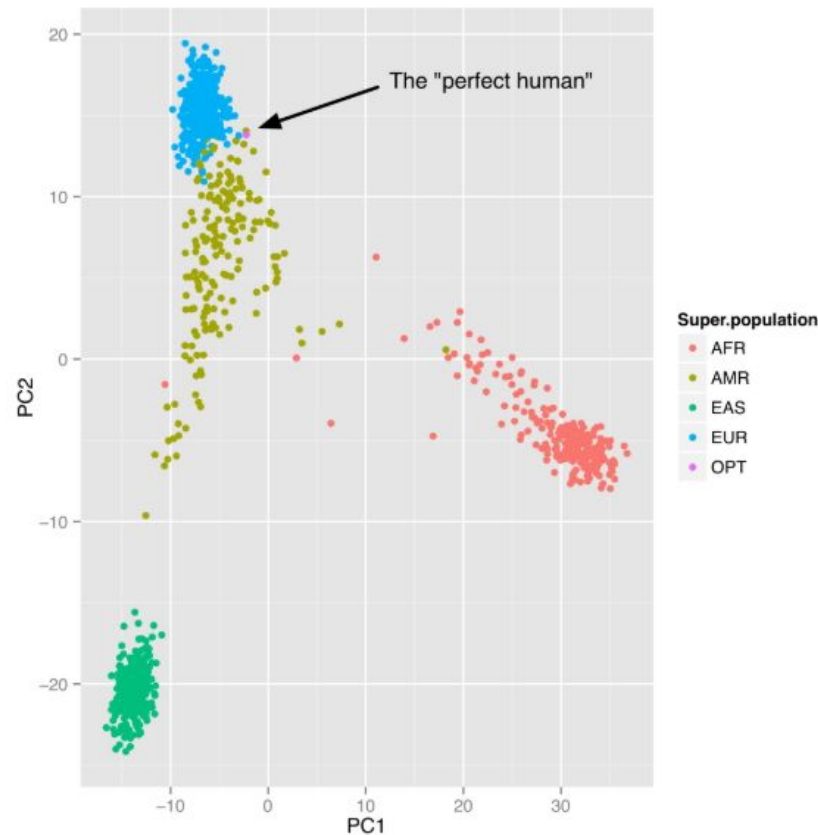
Each individual's genetic material is the product of millions of years of evolution to to tolerate different ...



- Temperatures
- Moisture levels
- Viruses
- Soil conditions
- Day lengths
- Cold periods or frost
- Wind conditions
- Bacteria
- Nematodes, insects
- Fungal pathogens
- Seasonal extremes
- Droughts
- Nutrient deficiencies
- Nutrient excesses
- Salt levels
- Herbivores
- Symbioses
- ... etc etc etc

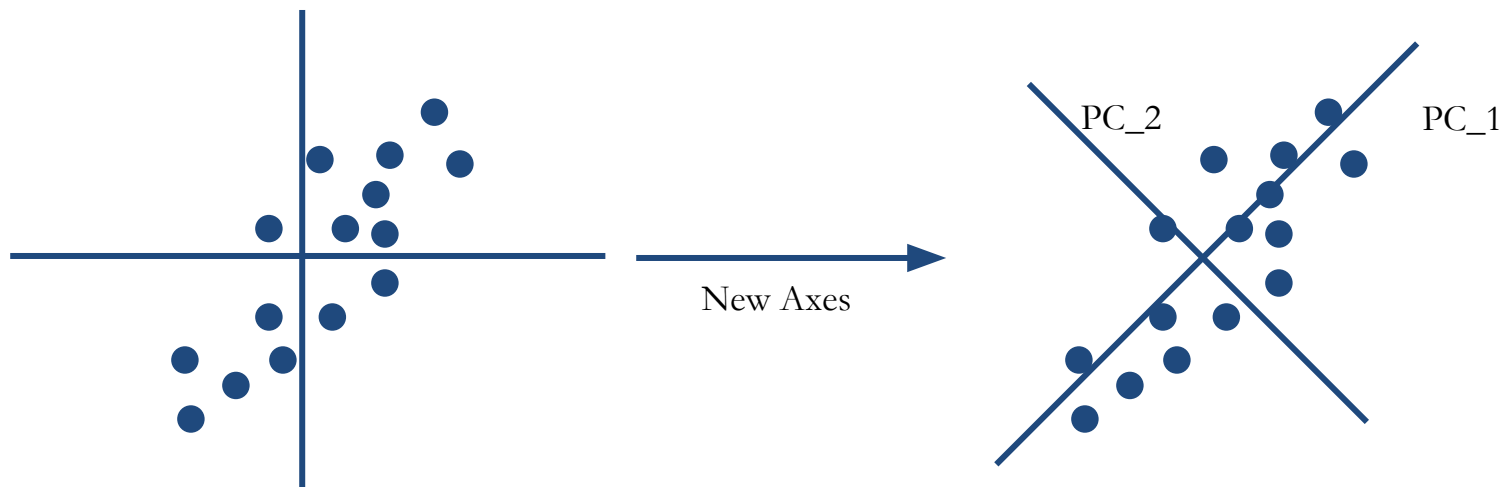
# PCA with SNP data:

- An excellent way to visualise diversity, and
- An efficient mathematical way to specify population structure



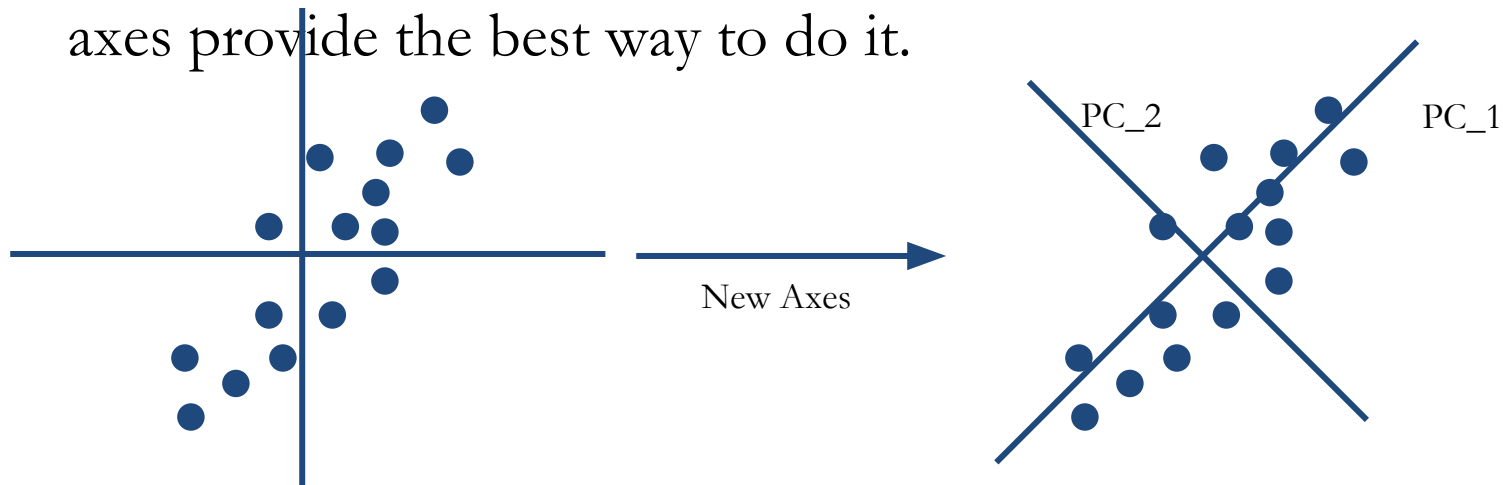
# PCA

- A way of specifying new “axes” to the data, so that the new axes express the variation in the data best.



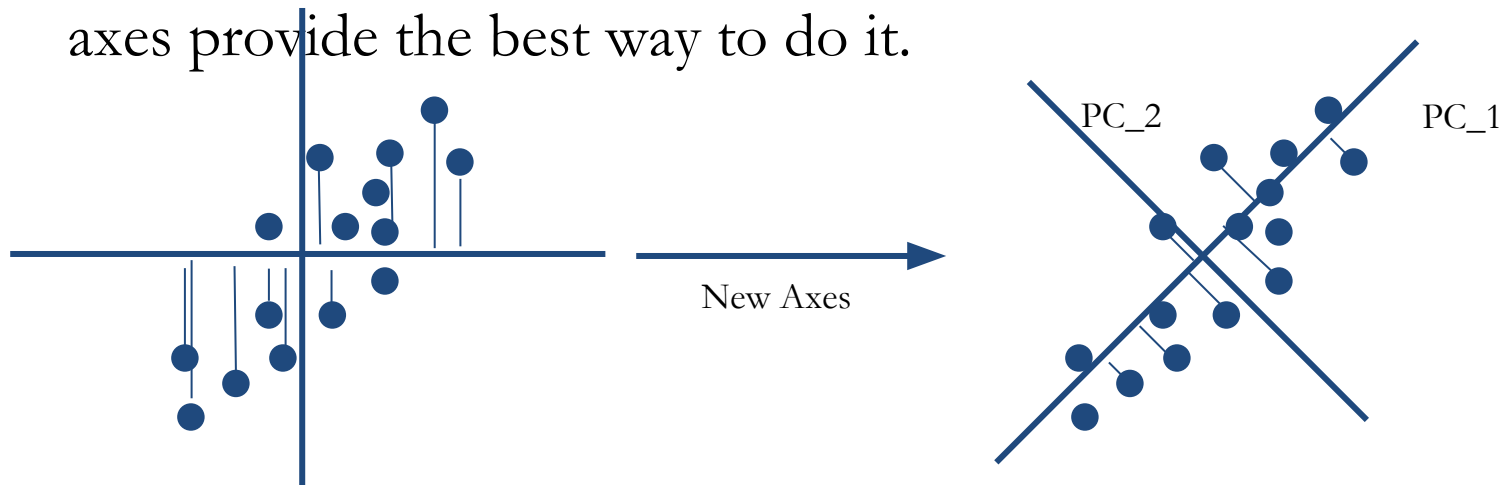
# PCA

- A way of specifying “new axes” for the data, so that the new axes (or Principal Components) capture the highest possible variation in the data.
- If we need to describe the data using fewer dimensions, the new axes provide the best way to do it.



# PCA

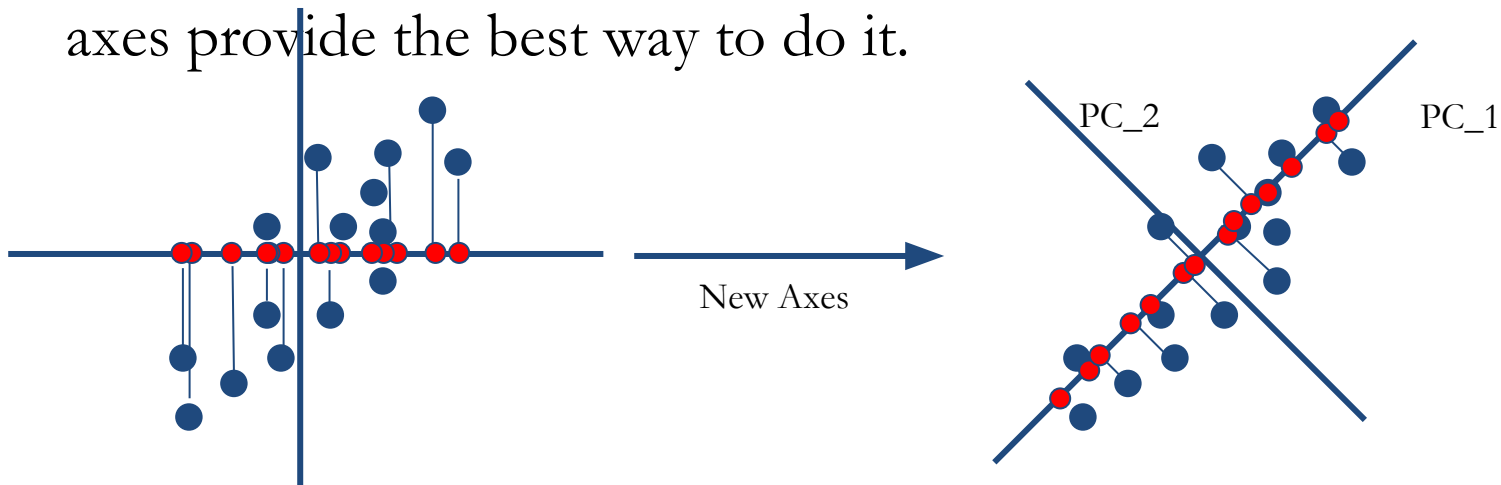
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From 2D to 1D:

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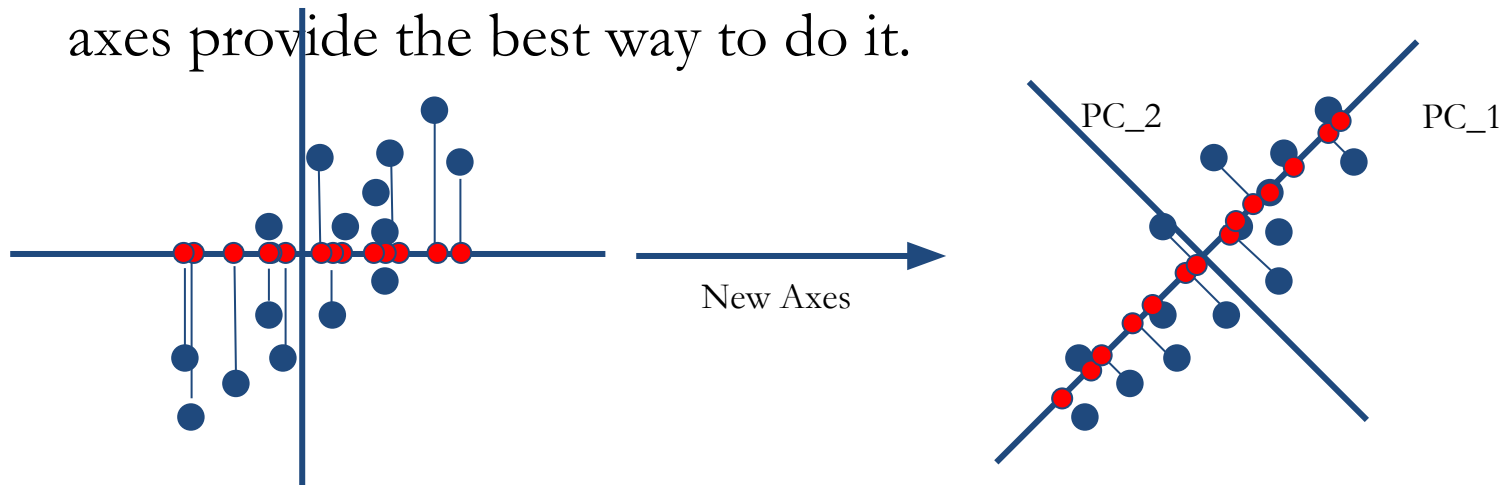


From 2D to 1D:

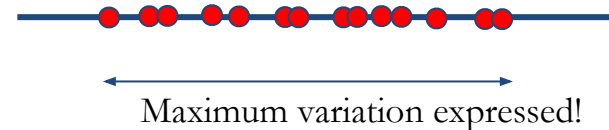
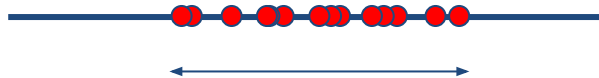


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- From 3D to 2D:

[https://www.google.com/search?biw=1440&bih=767&tbm=isch&sa=1&ei=cw2cXLOzAZGblwT-o6TQCQ&q=eigenvectors+3d+gif&oeq=eigenvectors+3d+gif&gs\\_l=img.3...551553.556272..556385...0.0..0.84.386.6.....1....1..gws-wiz-img.2TdLFyVmTjY#imgsrc=30k1xua4SqZHkM:](https://www.google.com/search?biw=1440&bih=767&tbm=isch&sa=1&ei=cw2cXLOzAZGblwT-o6TQCQ&q=eigenvectors+3d+gif&oeq=eigenvectors+3d+gif&gs_l=img.3...551553.556272..556385...0.0..0.84.386.6.....1....1..gws-wiz-img.2TdLFyVmTjY#imgsrc=30k1xua4SqZHkM:)

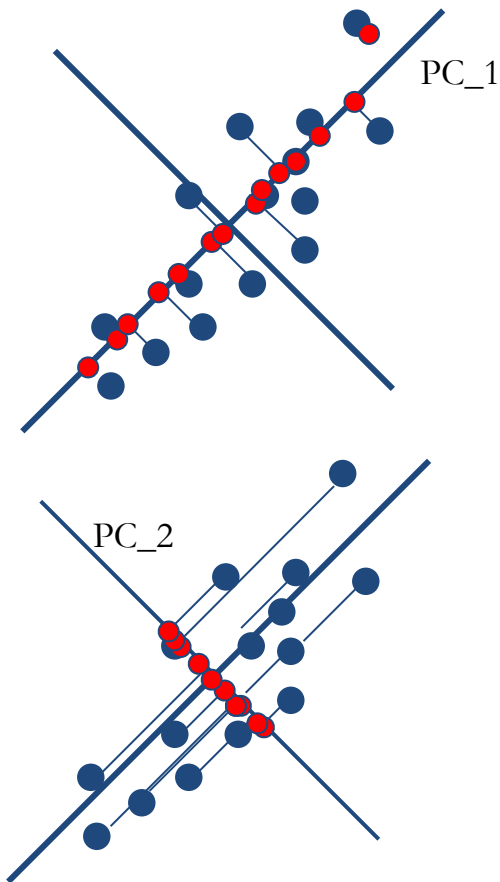


# PCA

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- If we need to describe the data using fewer dimensions, the new axes provide the best way to do it.
- From 3D to 2D
- A SNP dataset has as many “dimensions” as there are SNPs.
  - And the values in it are discrete (e.g., 0, 1, and 2)

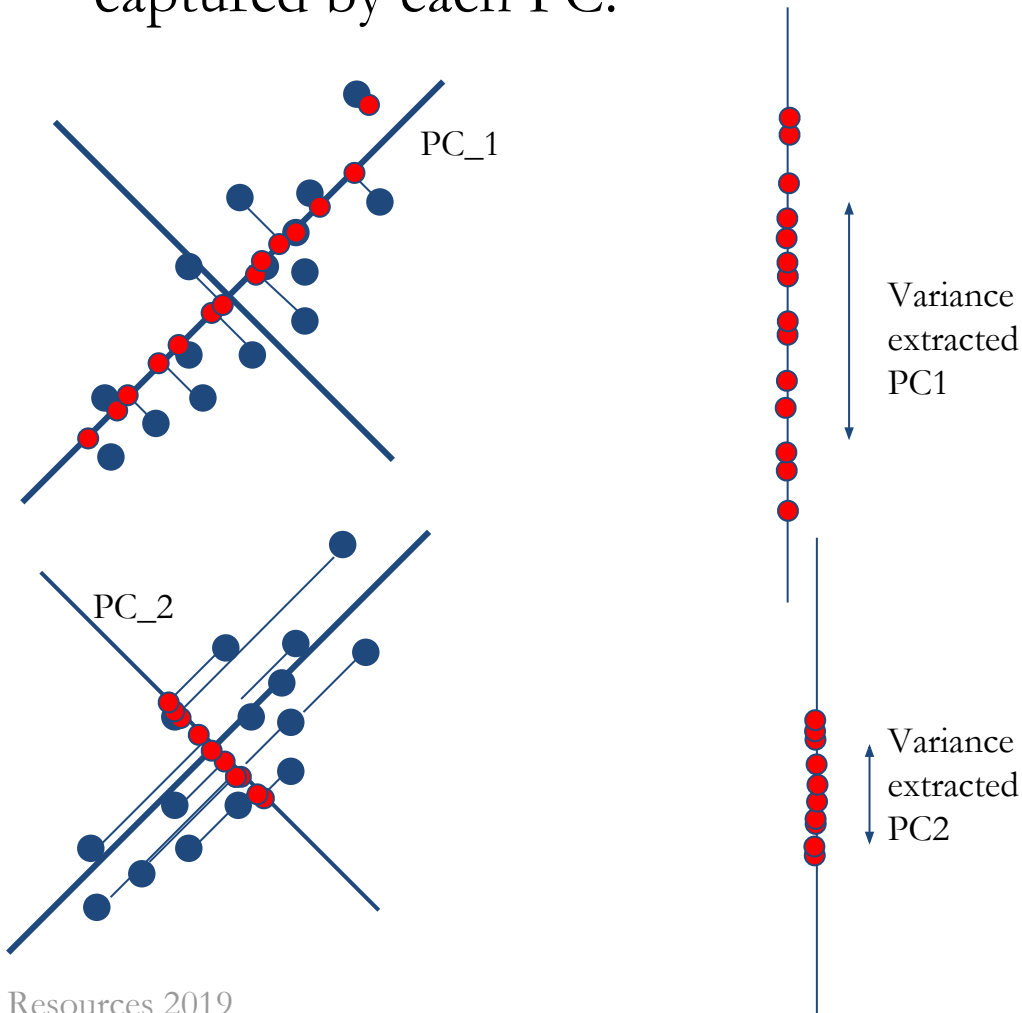
# PCA

- A “scree plot” shows how much of the variation in the data is captured by each PC.



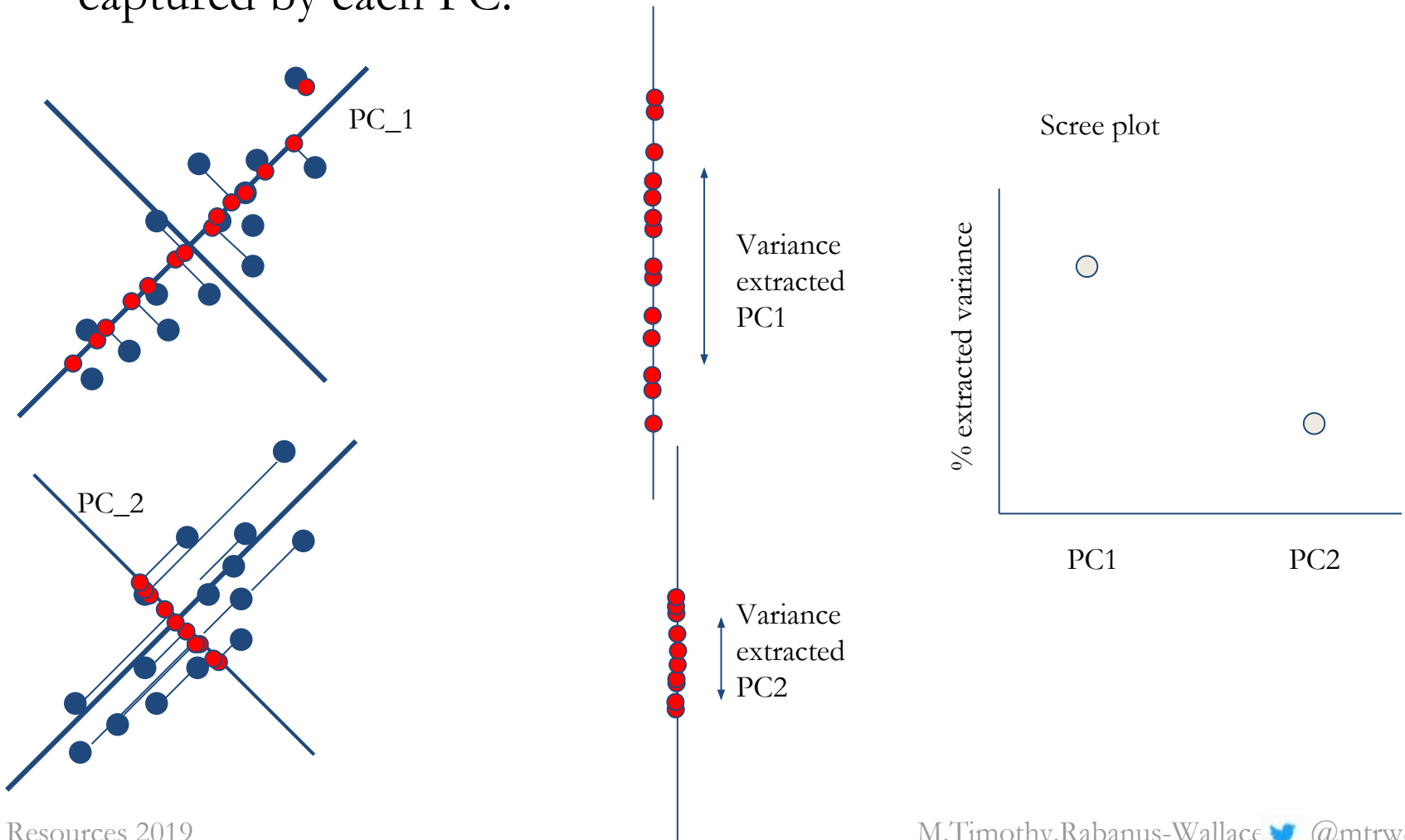
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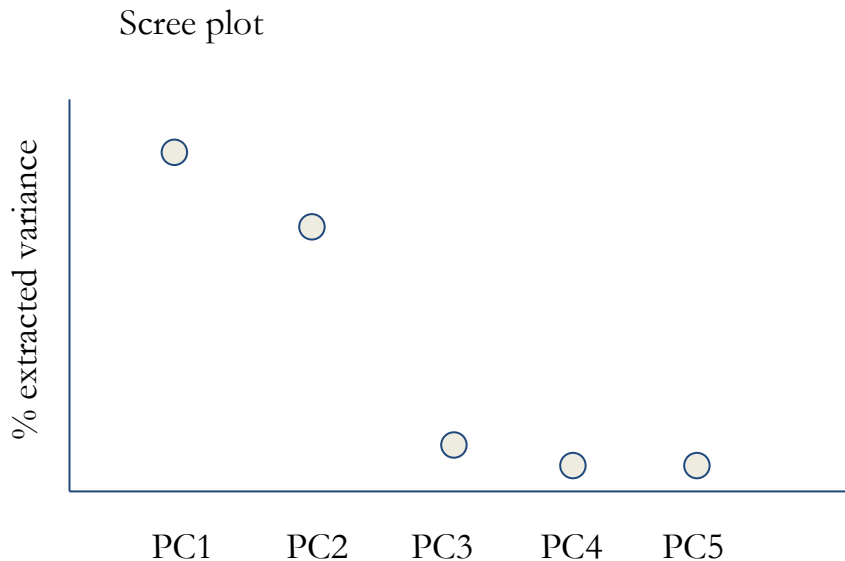
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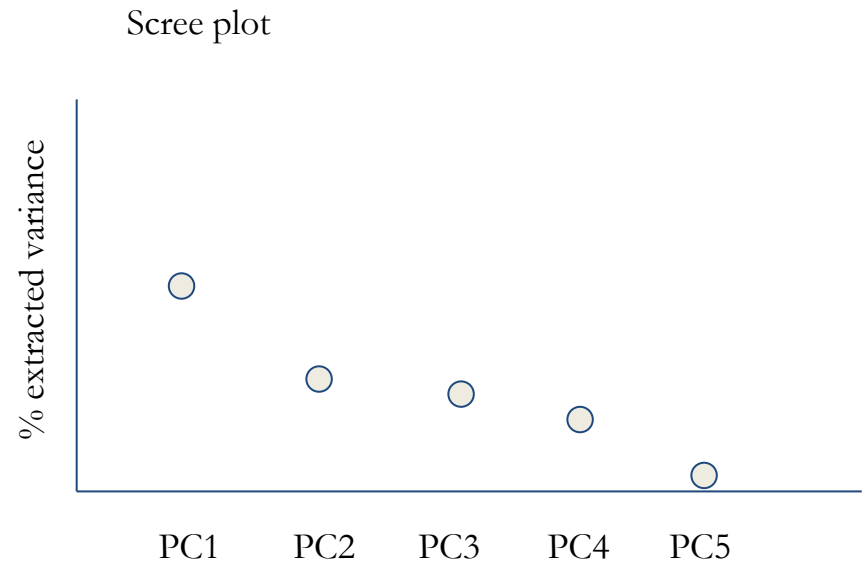


# PCA

- A “scree plot” shows how much of the variation in the data is captured by each PC.
  - Interpreting scree plots



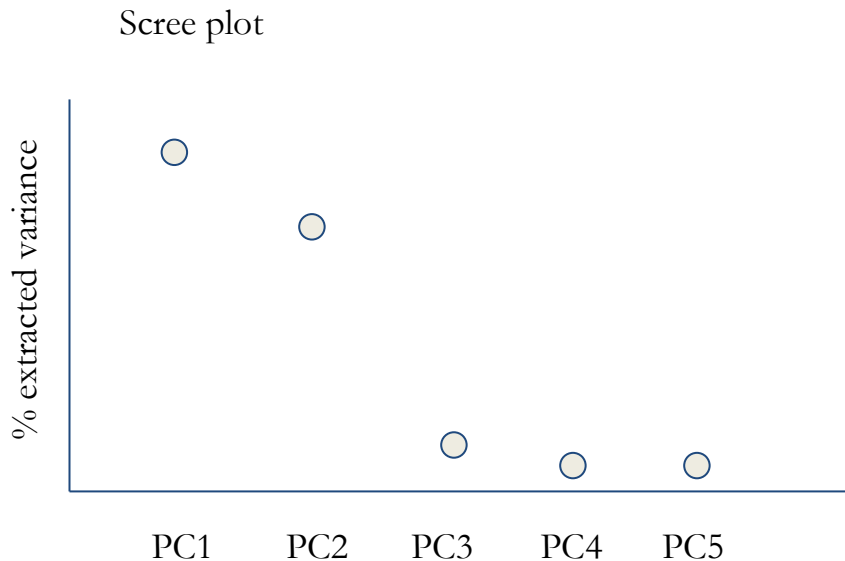
PCs 1 and 2 can be used to describe the dataset very well, because they explain most of the variance!



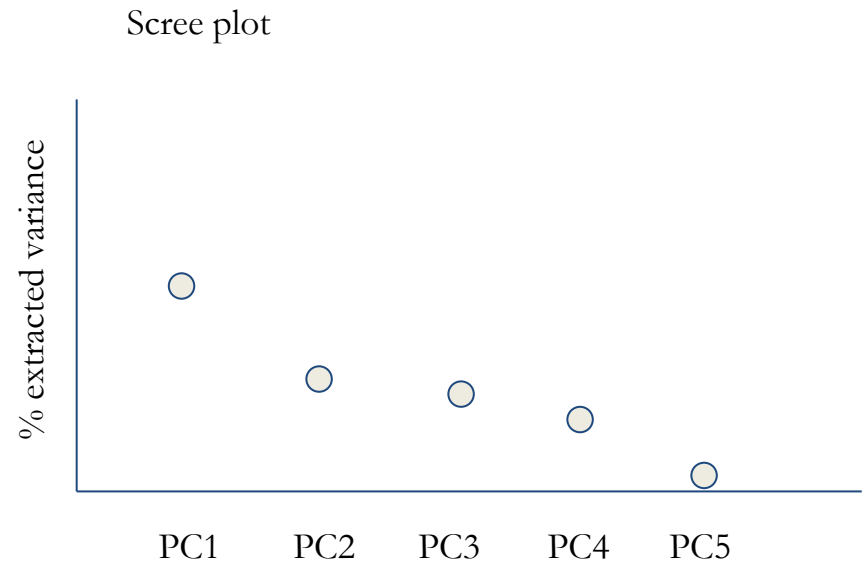
Need more PCs to describe most of the variation in the data. Use PCs 1--4?

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PCs 1 and 2 can be used to describe the dataset very well, because they explain most of the variance!



Need more PCs to describe most of the variation in the data. Use PCs 1--4?

A geneticist might use a rule like “use as many PCs as needed to describe 95% of the variation”.

# Genetic Associations

- Testing whether genetic markers (SNPs in our case) are associated with a phenotype.
  - That's 'associated with' ... not 'cause'!

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# Genetic Associations

- Testing whether genetic markers (SNPs in our case) are associated with a phenotype.
  - That's 'associated with' ... not 'cause'!
  - Association suggests *linkage to* the cause of the phenotype
  - Means the SNP **may** be genetically near a gene that causes the phenotype
  - Means the SNP allele can be used as a marker to screen for the (probable) presence of the causal gene(s)

# Genetic Associations








Intuition

Phenotype	Genotype
	2
	0
	2
	2
	0
	0
	0

Strong association!








# Genetic Associations

Intuition

Phenotype	Genotype	
	0	
	0	
	2	Weak / no association
	0	
	0	
	2	
	0	

# Genetic Associations

Intuition

Phenotype	Genotype
	2
	0
	2
	2
	0
	2
	0



Maybe associated .... ?

But how do we judge  
what is significant?

# Genetic Associations

Any appropriate statistical test can be used to judge whether a SNP is likely associated with a phenotype, e.g.:

## Chi squared

	Phenotype	
	2	0
Phenotype	 20	52
	 32	32

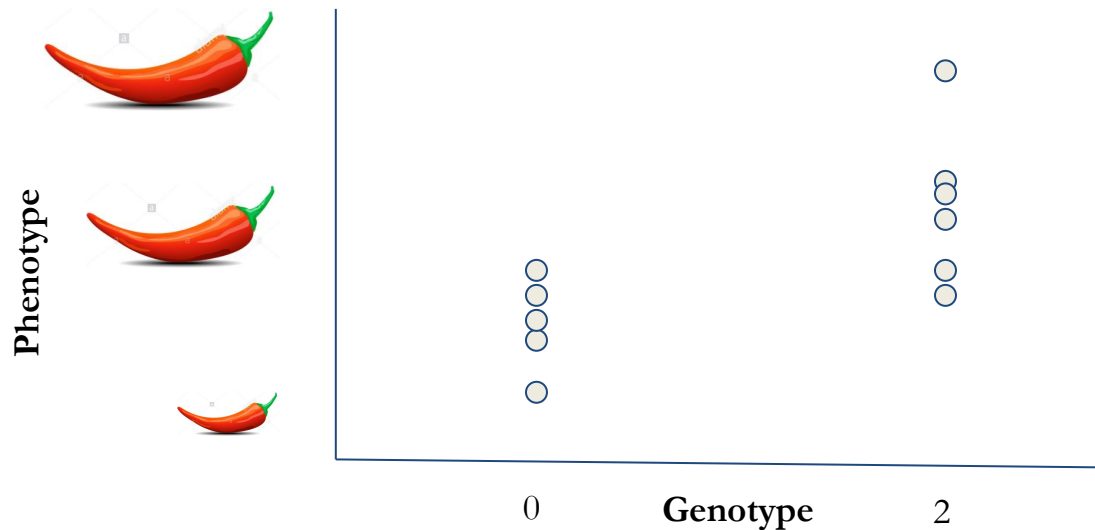
Null hypothesis: The genotype and the phenotype are independent

... generate a p-value ...

# Genetic Associations

Any appropriate statistical test can be used to judge whether a SNP is likely associated with a phenotype, e.g.:

## t-test



Null Hypothesis: The mean sizes of plants of the two genotypes are equal

... generate a p-value ....

# Genetic Associations

Any appropriate statistical test can be used to judge whether a SNP is likely associated with a phenotype, e.g.:

## **We will use a linear regression**

- Fast
- Helps account for population structure
- *You are not required to know details*, just:
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Genome Wide Association Study (GWAS)

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## Genome Wide Association Study (GWAS)

(we just use chromosome 1H)

# Associations and population structure

```
CGATTCGTGCGGGGCTCCTCTCAGGATGCTTAAA  
CGATTCGTGCGGGGCTCCTCTCAGGATGCTTAAA  
CGATTCGTGCGGGGCTCCTCTCAGGATGCTTAAA  
CGATTCGTGCGGGGCTCCTCTCAGGATGCTTGAA  
CGATTCGTGCGGGGCTCCTCTCAGGATGCTTGAA  
CGATTCGCGCGGGGCTCCTCTCAGGATGCTTGAA  
CGATTCGCGCGGGGCTCCTCTCAGGATGCTTGAA  
CGATTCGCGCGGGGCTCCTCTCAGGATGCTTGAA  
CGATTCGCGCGGGGCTCCTCTCAGGATGCTTGAA  
CGATTCGCGCGGGGCTCCTCTCAGGATGCTTGAA
```



Does either SNP associate with fruit size?

# Associations and population structure

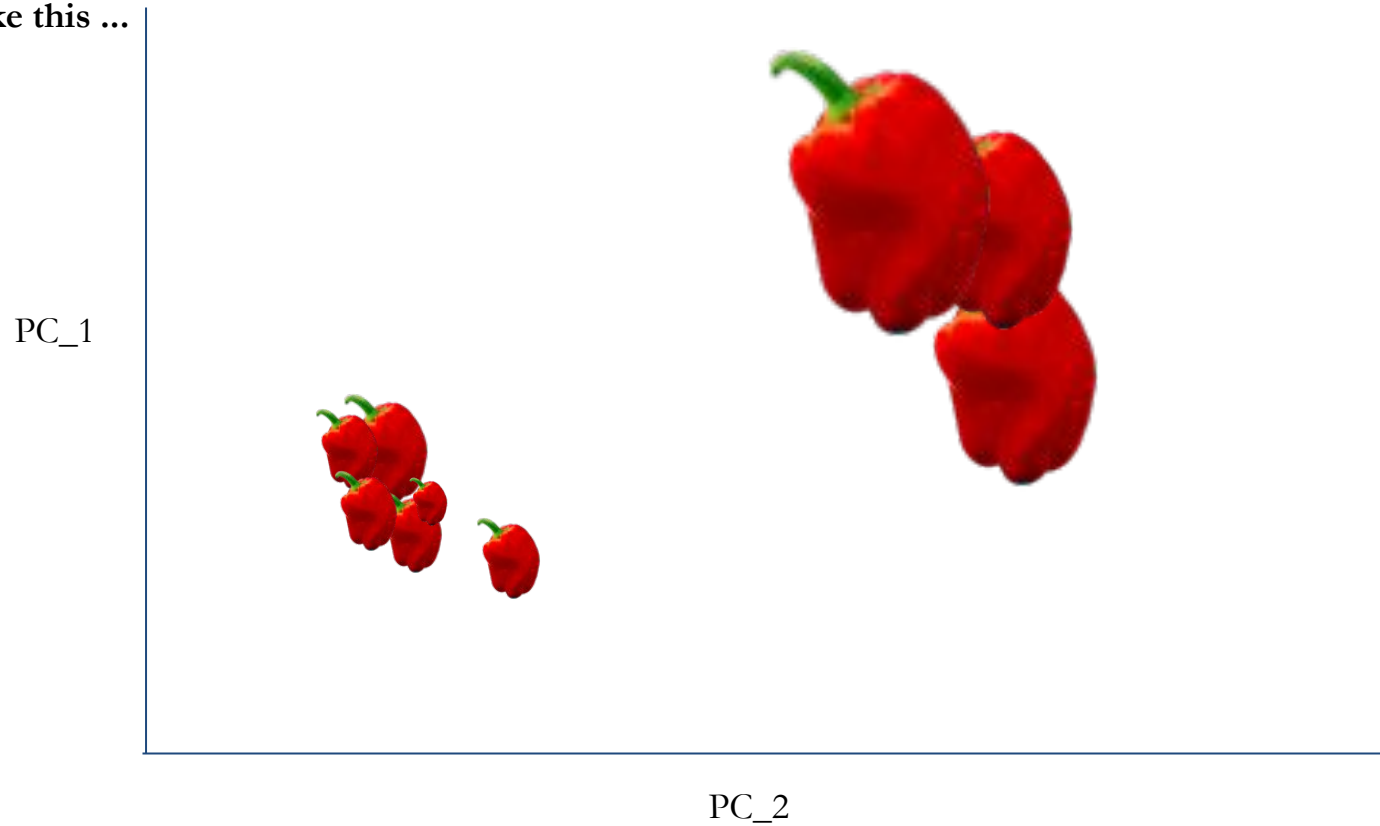
AGCCCTGTCTCTAGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTAAA  
AGCCCTGTCTCTAGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTAAA  
AGCCCTGTCTCTAGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTAAA  
AGCCCGTCTCTGGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTGAA  
AGCCCGTCTCTGGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTGAA  
AGCCCGTCTCTGGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTGAA  
AGCCCGTCTCTGGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTGAA  
AGCCCGTCTCTGGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTGAA  
AGCCCGTCTCTGGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTGAA  
AGCCCGTCTCTGGGCTCTCGATTCTGCGGGGCTCCTCTCAGGATGCTTGAA



What about now?

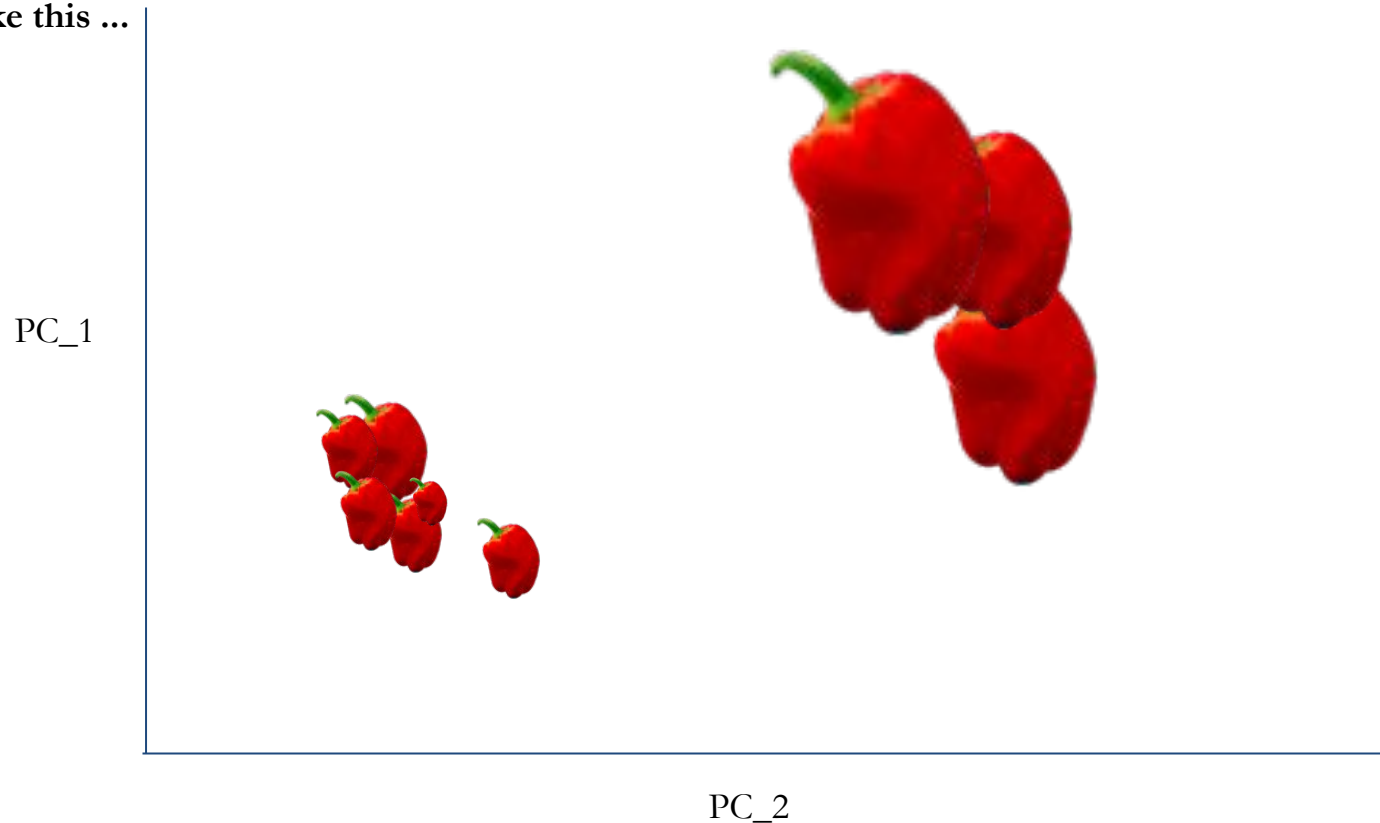
# Associations and population structure

A PCA plot would look a bit  
like this ...



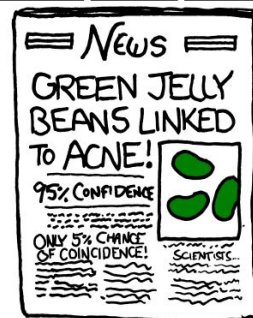
# Associations and population structure

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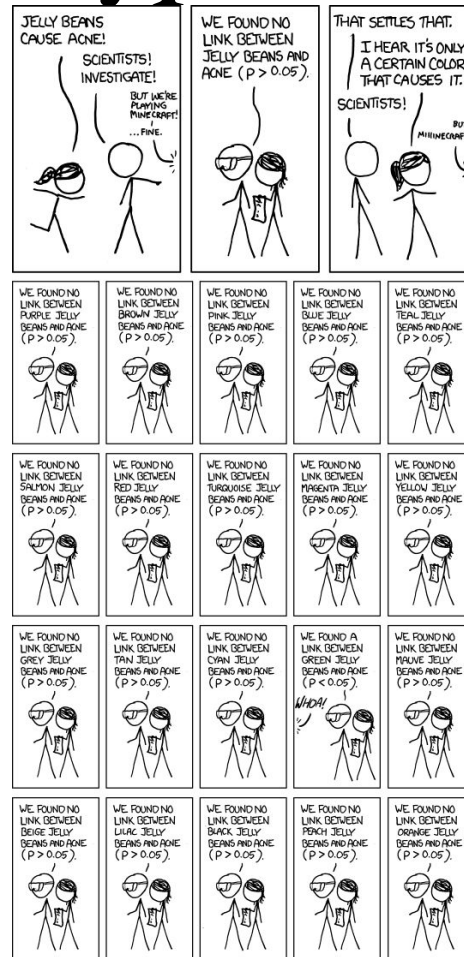


- The principal components are able to predict the phenotype!
  - i.e., population structure is a strong influence
- We can control for this in the linear model
  - The model will test how much extra predictive power the SNP allele gives us, when the population structure (summarised by the PCs) are also used to predict the phenotype.

A three-panel comic strip featuring stick figures. In the first panel, a female stick figure runs while holding a bowl of jelly beans, with speech bubbles saying 'JELLY BEANS CAUSE ACNE!' and 'SCIENTISTS! INVESTIGATE!'. A male stick figure responds with 'BUT I'VE BEEN PLAYING MINECRAFT! ...FINE.'. In the second panel, the two figures walk together; the male figure holds a clipboard and says 'WE FOUND NO LINK BETWEEN JELLY BEANS AND ACNE ( $p > 0.05$ ).'. In the third panel, the female figure says 'THAT SETTLES THAT.' and 'I HEAR IT'S ONLY A CERTAIN COLOR THAT CAUSES IT.', while the male figure responds with 'SCIENTISTS! BUT MINECRAFT!'.



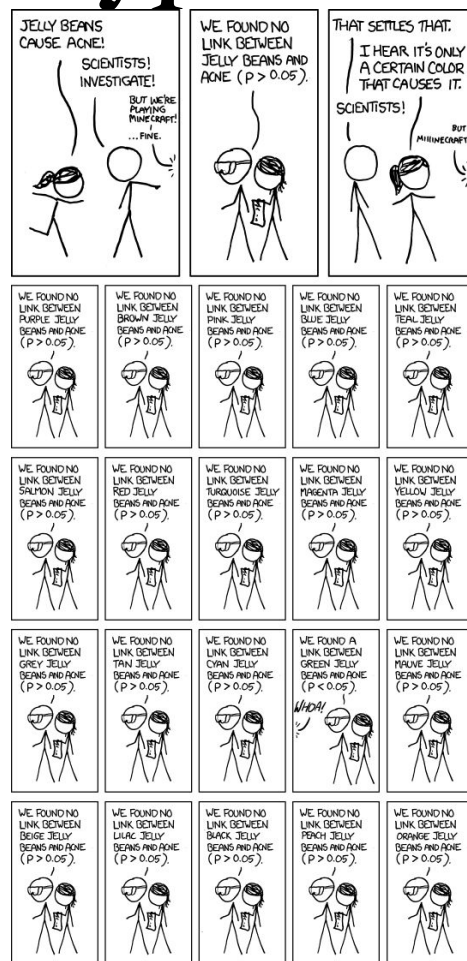
# Multiple hypothesis testing ...



- The normal “significance threshold” of  $p\text{-value} = 0.05$  causes false positives when we test many hypotheses



# Multiple hypothesis testing ...



- The normal “significance threshold” of  $p\text{-value} < 0.05$  causes false positives when we test many hypotheses.
- We correct for this by setting the threshold much more stringently.
- The “Bonferroni correction” involves simply dividing the  $p\text{-value}$  significance threshold (0.05) by the number of tests.
- The number of tests is the number of SNPs.

# Association testing in this session

Test for differences in row type  
(6-rowed vs 2-rowed)

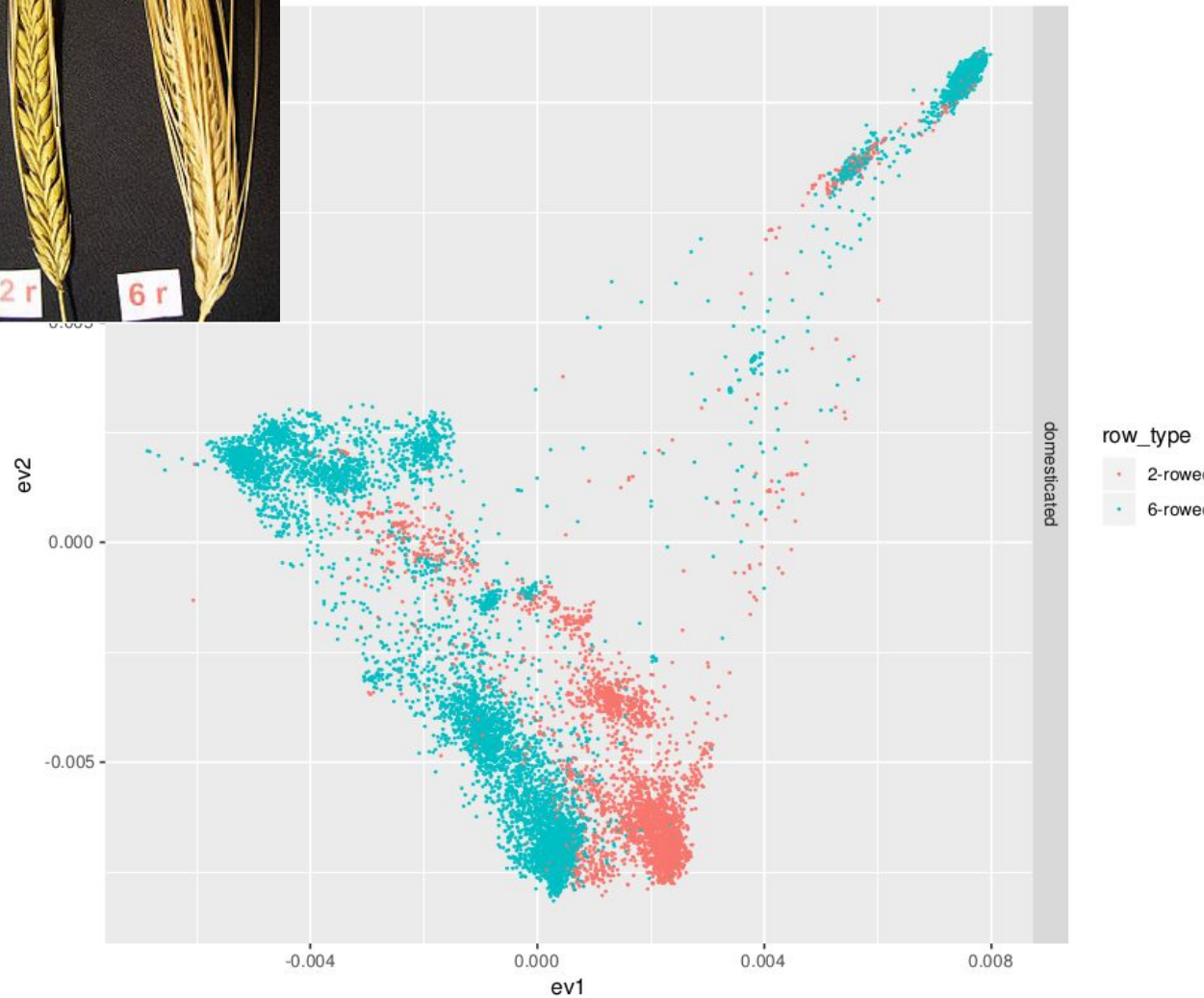


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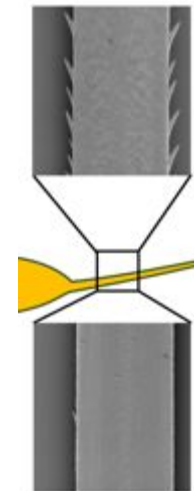
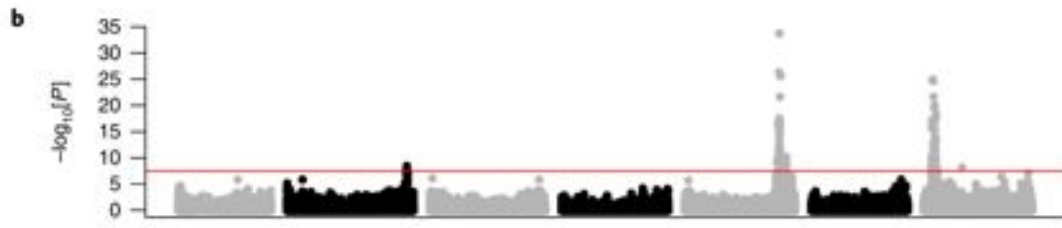
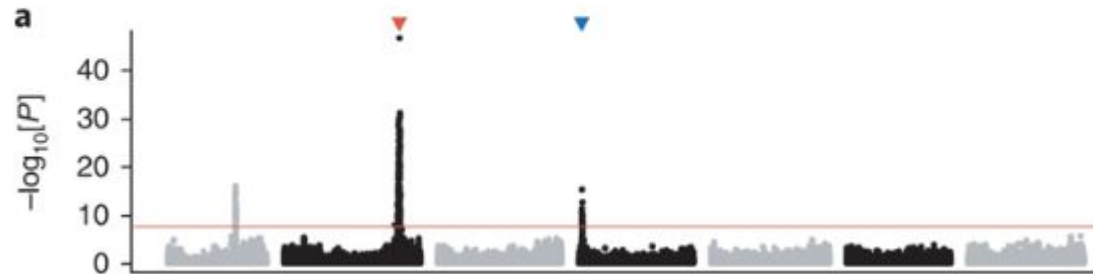
The collection our sample came from shows some relationship between row-type and population structure!



# Association testing in this session

Previous GWAS results show genetic associations with awn barbs and row type

**Fig. 3: Genome-wide association scans for morphological characters.**

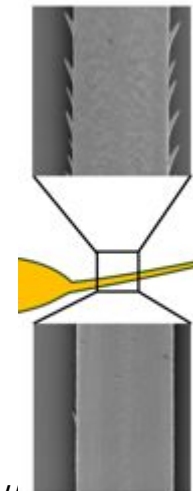
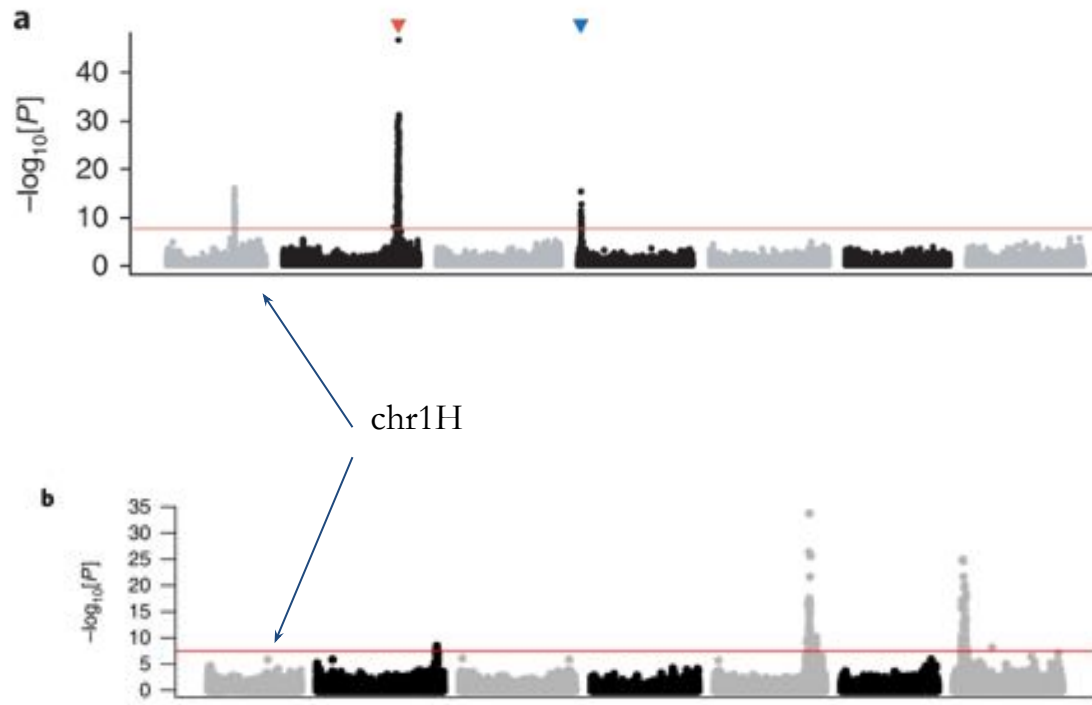


<https://www.nature.com/articles/s41588-018-0266-x>

# Association testing in this session

Previous GWAS results show genetic associations with row type (and also awn barbs, below)

**Fig. 3: Genome-wide association scans for morphological characters.**

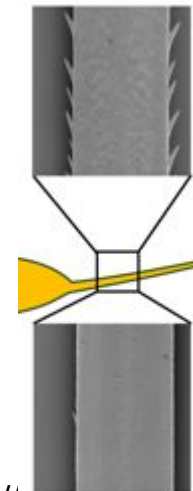
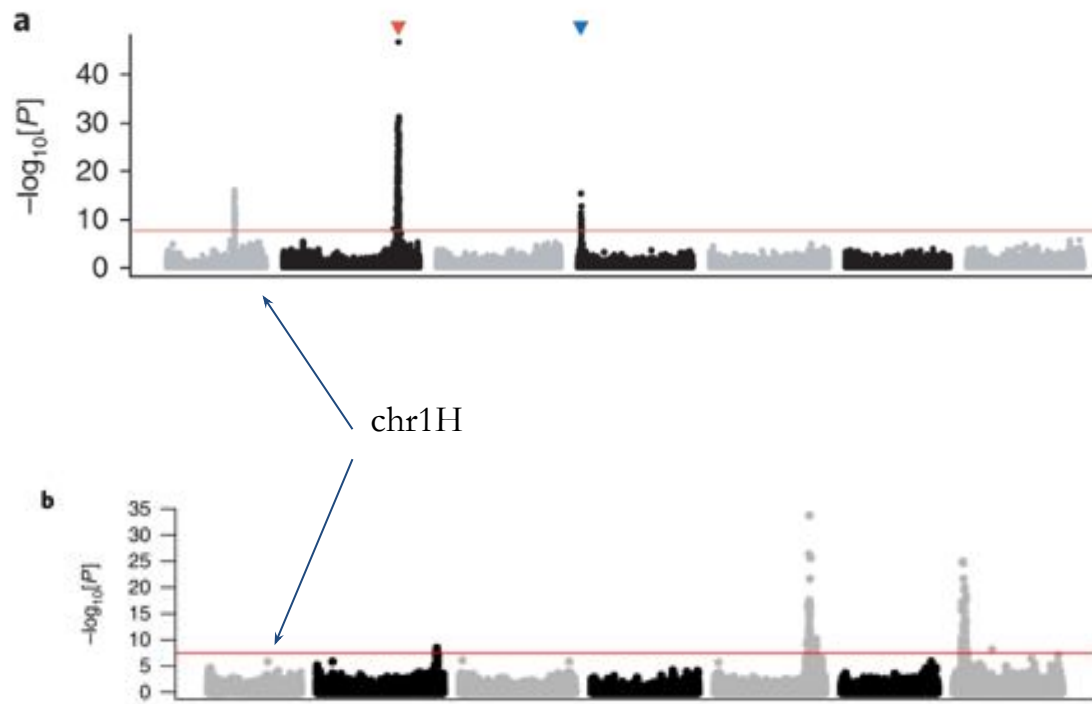


<https://www.nature.com/articles/s41588-018-0266-x>

# Association testing in this session

Previous GWAS results show genetic associations with row type (and also awn barbs, below)

**Fig. 3: Genome-wide association scans for morphological characters.**



We are unlikely to find any strong correlations owing to small sample size ...

<https://www.nature.com/articles/s41588-018-0266-x>



# Association testing in this session

So ... primary aims:

- Load our cleaned SNP data into R
- Create a PCA to summarise the population structure between samples
  - Plot a PCA plot!
- Link it to phenotype data from a database
  - Using a new data.table trick ...
  - More PCA plots ...
- Link three datasets: **The PCs** that summarise the population structure, **the SNPs**, and **the phenotype data**
- Run a GWAS to test associations at each SNP
- Plot the GWAS results as a Manhattan Plot with the significance threshold shown on the plot.