

Define these words that we'll need to understand population genetics:

**Allele**

**Biallelic**

**Homozygous**

**Heterozygous**

**Dominant**

**Recessive**

**Penetrance**

**Polygenic trait**

**Ancestry**

**Genetic locus**

**Recombination**

**Allele Frequency**

**Haplotype**

**Linkage (genetic)**

**Linkage disequilibrium**

**Neutral mutation**

| Gene     | Allele Frequencies |     |               |     |
|----------|--------------------|-----|---------------|-----|
|          | Population I       |     | Population II |     |
|          | 1                  | 2   | 1             | 2   |
| <i>A</i> | 0.8                | 0.2 | 0.2           | 0.8 |
| <i>B</i> | 0.8                | 0.2 | 0.2           | 0.8 |
| <i>C</i> | 0.8                | 0.2 | 0.2           | 0.8 |

Given this population data on these three alleles, how would you go about identifying which population a person most likely belonged to? What do you predict would happen in a person from population I and a person from population II had a child?

These are the results of a testcross.

In cross 1: you cross female heterozygotes of gene *A*, *B*, and *C* with homozygous recessive males.

You get the following flies:

| Genotype                       | Number of flies |
|--------------------------------|-----------------|
| <i>A</i> • <i>B</i> • <i>C</i> | 625             |
| <i>a</i> • <i>b</i> • <i>c</i> | 620             |
| <i>A</i> • <i>B</i> • <i>c</i> | 5               |
| <i>A</i> • <i>b</i> • <i>C</i> | 76              |
| <i>A</i> • <i>b</i> • <i>c</i> | 45              |
| <i>a</i> • <i>B</i> • <i>C</i> | 40              |
| <i>a</i> • <i>B</i> • <i>c</i> | 73              |
| <i>a</i> • <i>b</i> • <i>C</i> | 7               |

Draw a map with the appropriate distances between *A*, *B*, and *C*.

In cross 2: you cross female heterozygotes of gene *A*, *B*, and *D* with homozygous recessive males.

You get the following flies:

| Genotype | Number of flies |
|----------|-----------------|
| A•B•D    | 527             |
| a•b•d    | 528             |
| A•B•d    | 530             |
| a•b•D    | 525             |
| A•b•D    | 97              |
| A•b•d    | 99              |
| a•B•D    | 98              |
| a•B•d    | 99              |

Add gene *D* to your map from the 1<sup>st</sup> cross.

| SNP number |     |     |        |        |
|------------|-----|-----|--------|--------|
| 1          | 2   | 3   | 4      | 5      |
| --A-----   | T-- | G-- | T----- | T----- |
| --T-----   | T-- | G-- | T----- | T----- |
| --A-----   | A-- | G-- | T----- | A----- |
| --T-----   | T-- | G-- | T----- | A----- |
| --A-----   | T-- | G-- | T----- | A----- |
| --T-----   | T-- | C-- | A----- | T----- |
| --A-----   | A-- | C-- | A----- | A----- |
| --T-----   | A-- | C-- | A----- | A----- |
| --A-----   | T-- | C-- | A----- | T----- |
| --T-----   | A-- | C-- | A----- | A----- |

For 1,2 and 2,3:  
Determine |D'|