Exercises for Lectures 12-13

1. Assuming the red flower colour is a dominant trait versus white flower colour, and the two alleles affecting flower color are *A* and *a*. Red individuals in an F_2 population can have genotype *AA* or *Aa*. F_3 families are needed to determine the genotype of red-flower individuals. When no segregation for flower color is observed in an F_3 family, the F3 family is said to be derived from the homozygous genotype *AA*. In contrast, when segregation is observed, the F3 family is said from the heterozygous genotype *Aa*.

- If one F_2 individual has the genotype *Aa*, and 5 individuals from the selfed seed are grown in the following F_3 family, what is the probability that the F_2 individual will be *AA*?
- If we wish the error probability to be below 0.05, how many F_3 individuals should be grown?
- If we wish the error probability to be below 0.01, how many F_3 individuals should be grown?

2. Assume at one locus the two alleles are A and a, and at the other locus the two alleles are B and b. Genotype of two parents are AABB and aabb. Sample sizes of the 4 identifiable genotypes in an DH population are given in the following table.

Genotype	AABB	AAbb	aaBB	aabb
Sample size	64	8	7	61

(1) Test if genotypes AA and aa can be fitted by the 1:1 segregation ratio.
(2) Test if genotypes BB and bb can be fitted by the 1:1 segregation ratio.
(3) Test if locus Aa and Bb are linked.
(4) Work out the recombination frequency between the two loci.

3. Assume at one locus allele A is dominant to allele a, and at the other locus allele B is dominant to b. Genotype of two parents are AABB and aabb. Sample sizes of the 4 identifiable genotypes in an F2 population are given in the following table. Work out the recombination frequency between the two loci.

Genotype	A_B_	A_bb	aaB_	aabb
Sample size	1733	25	14	569

(1) Test if genotypes A_ and aa can be fitted by the 3:1 segregation ratio.
(2) Test if genotypes B_ and bb can be fitted by the 3:1 segregation ratio.
(3) Test if locus Aa and Bb are linked.
(4) Work out the recombination frequency between the two loci.

4. Assume at one locus allele A is co-dominant to allele a, and at the other locus allele B is dominant to b. Genotype of two parents are AABB and aabb. Sample sizes of the 6 identifiable genotypes in an F2 population are given in the following table. Work out the recombination frequency between the two loci.

Genotype	AAB_	AAB_	AaB_	Aabb	aaB_	aabb
Sample size	572	3	1161	22	14	569

(1) Test if genotypes AA, Aa and aa can be fitted by the 1:2:1 segregation ratio.

(2) Test if genotypes B_ and bb can be fitted by the 3:1 segregation ratio.

(3) Test if locus Aa and Bb are linked.

(4) Work out the recombination frequency between the two loci.

5. Use the barley DH population (…\Examples\MAP\BarleyDH.map, BarleyDH.xls or BarleyDH.xlsx) to construct the genetic linkage maps.

- Construct the seven linkage maps of barley
- Output the seven barley linkage maps
- Split one chromosome into two at the largest marker interval
- Identify the segregation distortion loci in this population

6. Use the rice F2 population (…\Examples\MAP\RiceF2.map, RiceF2.xls or RiceF2.xlsx) to construct the genetic linkage map.

- Construct the 12 rice linkage maps
- Output the 12 rice linkage maps
- Split one chromosome into two at the largest marker interval
- Identify the segregation distortion loci in this population