Exercises for Lectures 14-15

1. The following table gives the frequency distributions on flower length (mm) of tobacco in two fixed parental lines P_1 and P_2, and their F_1 and F_2 generations (East 1913). Assuming P_1 has all the alleles increasing flower length, P_2 has all the alleles reducing flower length.

- Estimate the effective number of genes on flower length.
- Estimate the gene effect under the polygene hypothesis.

Pop.	Size	Flower length (mm)																						
		34	37	40	43	46	49	52	55	58	61	64	67	70	73	76	79	82	85	88	91	94	97	100
P_1	211	1	21	140	49																			
F_1	98									4	10	41	40	3										
P_2	168																				13	45	91	19
F_2	444							3	9	18	47	55	93	75	60	43	25	7	8	1				

2. Use the barley DH population (…\Examples\BIP\BarleyDH.bip, BarleyDH.xls or BarleyDH.xlsx) to conduct QTL mapping.

- Find additive QTLs controlling kernel weight by using Interval Mapping and ICIM, and determine the source of the QTL allele that increases kernel weight.
- Compare the mapping results from different mapping parameters.
- Find the largest interaction from ICIM epistatic mapping

3. Use the rice F2 population (…\Examples\BIP\ RiceF2.bip, RiceF2.xls or RiceF2.xlsx) to conduct QTL mapping.

- Find additive and dominance QTL controlling the resistance by using Interval Mapping and ICIM. For the identified QTLs, determine the source of the allele that reduces the resistance.
- Compare the mapping results from different mapping parameters.

4. Compare two mapping methods by simulation using RIL populations with a size of 200: Assume there are 5 chromosomes, each of 150 cM, and evenly distributed with 16 markers. Two traits of interest are plant height and grain yield.

Plant height has a heritability of 0.7, and is controlled by 3 independent QTLs, located at 18 cM, 55 cM, and 101 cM on chromosomes 1, 2, and 3, respectively. Additive effects of the three QTL are 10 cm, 4 cm, and -6 cm, and the population mean is 100 cm. Dominance and gene interaction are not considered.

Grain yield has a heritability of 0.5, and is controlled by 7 QTLs. One QTL is located at 25 cM on chromosome 1; two are located at 35 cM and 73 cM on chromosome 2; two are located at 18 cM, and 55 cM on chromosome 3; and two are located at 39 cM and 131 cM on chromosome 4. Additive effects of the 7 QTL are 1 t/ha, -1 t/ha, 1 t/ha, 1 t/ha, 1 t/ha, -1 t/ha, and 1 t/ha, respectively, and the population mean is 3 t/ha. Dominance and gene interaction are not considered.

Assume the support interval is 10 cM, i.e., in a simulated population one predefined QTL is declared to be correctly identified if there is a significant peak in a chromosomal interval of 10 cM. The true QTL location is at the center of the support interval. One hundred populations are simulated.

- Draw the average LOD profile of IM and ICIM for plant height and grain yield
- Find out the detection power of IM and ICIM for each plant height and grain yield QTL
- Find out the false discovery rate of IM and ICIM for plant height and grain yield
- What else can you find from the power simulation?