Name:

Graded by: Instructor

**TOTAL POINTS: /100**

Problem 1: Sample 10 SNPs as QTNs out of the available SNPs. Simulate QTN effects from a standard normal distribution. Assign genetic effects for each of the individuals. Simulate normally distributed residual effects with appropriate variance to have a heritability of 0.75. Add residual effects to genetic effects to create phenotypes. You can either use the G2P R function or code everything by yourself. Describe the distribution of genetic effects, residual effects, and phenotypes, and explore the relationships among them (20 points).

* Describe the distribution of genetic effects (2 points), residual effects (2 points), and phenotypes (2 points)

Full Points

* Describe the pair-wise relationships among genetic effects, residual effects, and phenotypes (each pair 2 points, 6 points in total)

Full Points

* Commenting (2 pts)
* Full Points
* Result interpretation (4 points)

Full Points

* Bug-free (2 pts)

Full Points

Comments:

POINTS: 20

Problem 2: Perform GWAS by using the correlation method. You can either use the GWASbyCor R function or code everything by yourself. Create a Manhattan plot and label the positions of the QTNs (20 points).

* Manhattan plot (4 pts)

Full Points

* QTN positions (4 pts)

Full Points

* Commenting (4 pts)
* Full Points
* Result interpretation (4 points)

Full Points

* Bug-free (4 pts)

Full Points

Comments:

POINTS: 20

Problem 3: Find the number of QTNs among the top ten associated SNPs (20 points).

* Label the top ten associated SNPs (4 pts)

Full Points

* Label the QTNs matched (4 pts)

Full Points

* Commenting (4 pts)
* Full Points
* Result interpretation (4 points)

Full Points

* Bug-free (4 pts)

Full Points

Comments:

POINTS: 20

Problem 4: Count the number of SNPs with P values smaller than the P value of the seventh significant QTN (20 points).

* Label the 7th QTN and its P value (4 pts)

Full Points

* Correctly count the number of SNPs with P values smaller than the P value of the seventh significant QTN (4 pts)

Full Points

* Commenting (4 pts)
* Full Points
* Result interpretation (4 points)

Full Points

* Bug-free (4 pts)

Full Points

Comments:

POINTS: 20

Problem 5: Redo (3-4) for 100 replicates. Report the averages and standard deviations (20 points).

* Conduct the replicates correctly (3 pts)

Full Points

* Calculate the average correctly (3 pts)

Full Points

* Calculate the standard deviations correctly (3 pts)

Full Points

* Commenting (3 pts)
* Full Points
* Result interpretation (5 points)

Full Points

* Bug-free (3 pts)

Full Points

Comments:

POINTS: 20

Problem 6 (**Extra Credit**): Simulate phenotypes from genotypes so that the phenotypes with skewed normal distribution due to genetic effect with a long tail on the right (25 points).

* A: Genetic effect has skewed and continuous distribution (10 pts)

Full Points

* B: Commenting (5 pts only if full credit on A)
* Full Points
* Result interpretation (5 points)

Full Points

* C: Bug-free (5 pts only if full credit on A)

Full Points