

- Exams in this class ask you to demonstrate your knowledge of the subject matter that we have been discussing in class and you have been working on by going over the material and doing practice problems.
- The exam will consist of short answer questions and problems similar to the suggested problems/homework. None of the problems will be a surprise. They are all similar to things you have already worked on. The exam is the same length as the previous exams. *If you have prepared for the exam, the 3 hours provided will be more than ample time to finish the exam.* You will be able to complete it in the normally scheduled class period of 1 hour.
- This is not an exhaustive review sheet. It only outlines ideas that you should be familiar with.
- The best way to prepare is:
 - Do and understand all of the suggested problems in the book where appropriate
 - Do and understand the QTL project
 - Understand the concepts listed below

Multifactorial Traits

- *What is the difference between Discontinuous vs Continuous Traits (Quantitative)*
- *What ways do geneticists use twins to determine the heritability of multifactorial traits?*
- *What is concordance in twins and how is it used to determine heritability? (see suggested problems in the chapter)*
- *What is a Genome Wide Association Study and how is it done?*
- *What is a population? What is a sample?*
- *What is a Tag SNP and how is it used in Genome Wide Association Studies?*

Quantitative Traits and Phenotypic Variance

- *What are the components of Phenotypic Variance? Be comfortable with the basic equation (see the suggested problems)*
- *What is the difference between Broad-sense and Narrow-sense Heritability? Be comfortable with the basic equation (see the suggested problems)*
- *What variability do we hope to control for or eliminate in our olfactory bulb QTL work?*
- *What are recombinant inbred strains and how are they generated?*

QTL Analysis-Olfactory Bulb Volume Calculations

- *How do we calculate the shrunken olfactory bulb area for each mouse?*
- *When we determine the volume of our olfactory bulb, why do we multiply the area by 0.3 mm?*
- *How do we calculate the shrunken brain area for each mouse?*
- *When we determine the volume of our brain, why do we multiply the area by 0.3 mm?*
- *How and why do we have to calculate the unshrunk brain volume for our analysis?*

QTL Analysis- Regression Analysis

- *What does a regression line tell you about your two variables?*
- *What does the R^2 value tell you?*
- *What is a residual value?*
- *Which variables if any contributed the most to our Unshrunk OB Volume variation: sex, age, body weight, brain weight?*
- *How will we use the residual values to map our QTLs?*

QTL Analysis- QTL Mapping

- *What is the difference between a high LRS value for a marker and a low LRS value?*
- *What kind of variation do you find at SNPs?*
- *At the end, why did we look at regions that have high SNP density when picking a genome region to further analyze?*

QTL Analysis-Microarrays

- *What is a physical map of the genome? How is it different from a genetic map?*
- *How does a gene expression microarray work? What do you hybridize to the chip?*
- *How was the Mouse GNF Expression Atlas Data generated?*
- *Why did we choose genes that were highly expressed in the olfactory bulb?*

QTL Analysis-Allen Brain Atlas

- *What is the basic idea behind in situ hybridization?*
- *What are the major layers of the Olfactory Bulb?*