

Name: \_\_\_\_\_

Group #: \_\_\_\_\_

Section #: \_\_\_\_\_

Assessing the influence of environment on morphology in rainbow trout (*Oncorhynchus mykiss*)

**Introduction:** For scientists, data analysis skills are critical. In order to summarize data and interpret their results, scientists need to know which statistical tests to use. Today we will be performing a T-test (Equation 1) to compare the data we collected in Lab 13. The T-test is a relatively simple test that is used to compare means from two categories of data and is appropriate to use when data consists of one categorical variable and one continuous variable. For us, our categorical variable is rearing environment (hatchery and wild), and our continuous variables are: heart mass, liver mass, and pyloric caeca number. We will be performing a T-test for each continuous variable and interpreting the results.

**Objectives:** We will be analyzing the data we collected last week to determine if we found differences between the wild and hatchery raised trout. We will then create figures, interpret our results, and answer a series of questions related to our findings.

**Instructions:** One student from each group needs to log into their university email account and download the spreadsheet with the data from last week's lab. As a class we will work through the data analysis and as a group you will create figures and answer questions 4-8. Copy and paste the figures into a Word document along with your answers to questions 4-8 and email the document to your instructor. Be sure to include the names of all of your group members in the document.

$$t = \frac{(\bar{x}_1 - \bar{x}_2)}{\left( \sqrt{\frac{s_1^2}{n_1}} + \sqrt{\frac{s_2^2}{n_2}} \right)}$$

Equation 1: The T-test compares means ( $\bar{x}_1, \bar{x}_2$ ) of two sample populations by taking the difference of the two means ( $\bar{x}_1 - \bar{x}_2$ ) and dividing it by the sum of the standard errors from the two sample populations. The standard error is an estimate of where the true mean of the population lies given the data and is calculated by taking the square root of the squared standard error ( $s^2$ ) divided by the sample size ( $n$ ).

Example figure with caption:

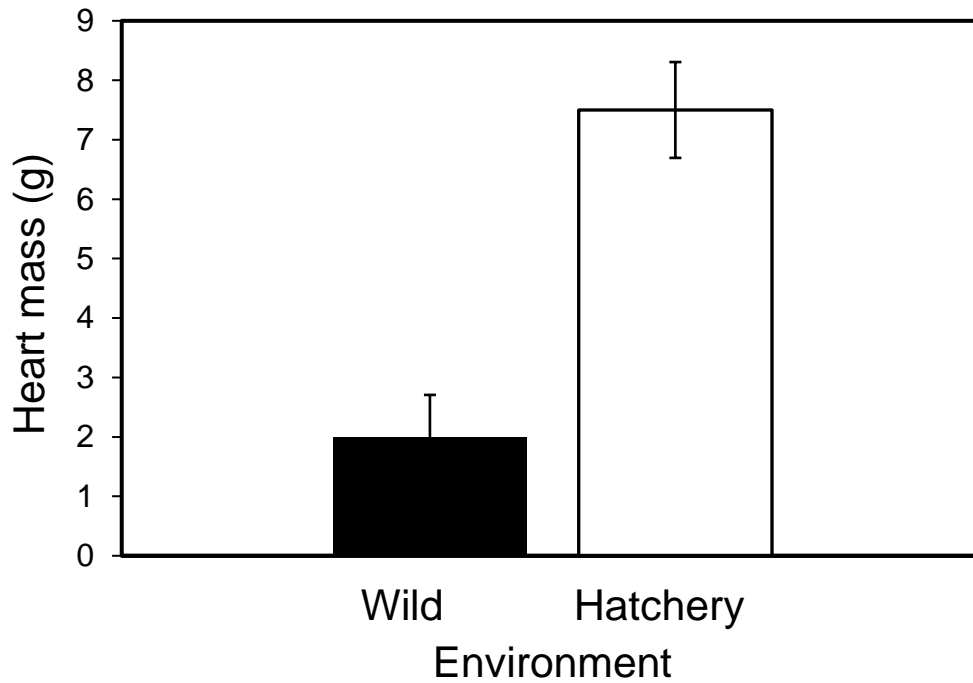


Figure 1: Mean heart mass ( $\pm 1$  SE) of wild ( $N = 10$ ) and hatchery raised ( $N = 10$ ) rainbow trout.

1. Does the data support or refute your hypothesis? (Be specific. How does it support or not?)

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2. What are some additional features of the hatchery environment that could influence a trout's phenotype?

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3. What are some ways we could improve our study to provide more robust conclusions?

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## Part 2

**Discuss** the following questions as a group and type your answers (full sentences) in the Word document with your figures. Do not use the examples provided here or examples from the readings. Instead, discuss with your group and think of examples we have not considered during lab (there are many). These questions will be graded for both content and completeness. When you are done email them to the instructor. Be sure to include the full name of everyone in your group

4. Explain how gene-by-environment interaction fits into our current understanding of evolution?
5. On a molecular level, how does an organism adapt to its environment? How might some adaptations become permanent in a population?
6. A population of fish becomes isolated in a cave and over time loses the use of their eyes. Discuss the interaction between evolutionary, environmental, and genetic factors that cause this to happen.
7. How might natural selection or other evolutionary forces (i.e. gene flow, genetic drift, mutation, non-random mating) interact with variation of gene expression within populations?
8. What are some ways the modern human environment might influence our phenotypes? What could be some consequences of this over time?