1. In yet another chapter of your dissertation on the evolution of body size in the Cutthroat trout in the Selway-Bitteroot Wilderness lakes, you raised a question about how the Cutthroats were able to expand their range into lakes with different prey items. You realized that the majority of lakes in the wilderness are below treeline, where fish are larger and have access to large prey items such as fish and crustaceans. Your previous work showed that smaller body size was an adaptation to peripheral higher elevation lakes where fish have access to smaller prey like insects.

a. Imagine a founding population of Cutthroats from a low elevation lake, with body size equal to the metapopulation mean, arriving in a high elevation lake. Assuming no evolution, what is the expected fitness of fish from the core populations in peripheral habitats? Does the core population grow or shrink in the peripheral habitat? (Are the peripheral habitats sink populations?)

You already have data from a fully reciprocal transplant study which you used (or can use, see hint below) to estimate $\theta$ for high elevation peripheral lakes 1 and 2 ("RT _Data.csv"), and you have an estimate (Lakes 3 and 4) of the mean and variance for body size for the core population from the sample of 400 low elevation fish from the RT experiment.

2. You found that some high elevation lakes were not stocked, but are linked by streams to low elevation lakes. These lakes were colonized via migration along the streams. Hence, some founding populations that colonized along streams have grown, become established, and the niche must have evolved in response to local selection. Of course, occupation and adaptation of peripheral habitats can be thwarted by continued migration from the core populations.

You begin to wonder how cutthroat populations were able to expand their range to these lakes, given the level of migration that must occur via streams and the low fitness that larger fish must experience in these higher lakes.

You decide to use molecular markers to estimate $m$, the migration rate, between 4 pairs of low elevation “core” lakes and their connected high elevation lakes. The core lakes are assumed to have an optimal and observed body size equal to the metapopulation average. You obtained the following migration rates between low and high lakes, respectively:

- Lake Fir-Lake Lupine: 0.0001
- Lake Forest-Lake Alpine: 0.01
- Lake Humic-Lake Clearwater: 0.1
- Lake Fishy-Lake Buggy: 0.5

a. For each of the four high elevation lake populations, what is the expected value for body size at the equilibrium? How does this compare with the optimum, $\theta$, that you calculated for high elevation lakes? In other words, how far is the expected body size from the optimal body size at equilibrium between selection and gene flow? Is maladaptation weak or strong, and why?

b. For each of the four high elevation lake populations, determine if the level of adaptation is sufficient for the population to survive. Is the mean fitness greater than 1? Do you think any of
these populations are sinks and persist only by immigration? Be ready to explain the results.

**Hints:**

*You already have all the data you need from the previous two problem sets.*

To estimate absolute fitness, we will assume that \( W_{\text{max}} \) is a measure of reproductive success. Assume that \( W_{\text{max}} = 1.1 \), suggesting that the reproductive rate of each individual slightly exceeds the replacement rate.

The variance in high elevation lakes can be estimated from the sample of 400 fish that were captured in Lakes 1 and 2 for the RT experiment, and the same for low elevation lakes. \( G \) for high elevation lakes was provided (0.71).

*SEE Scott’s sheet on the webpage for details on quadratic regression. Note that \( \gamma \) should be used as a positive number.*

Assume that all low elevation lakes have a common value for \( \theta_c = z_c \), and all high elevation lakes have the same value for \( \theta_p \), which are the averages of the values from Problem Set 4.