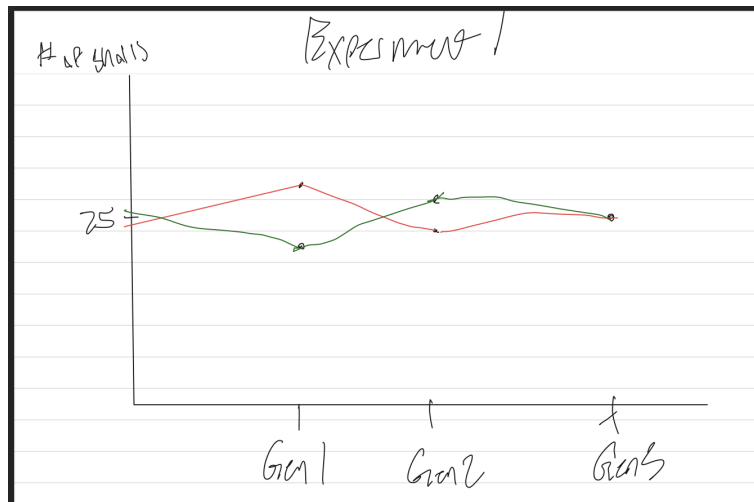


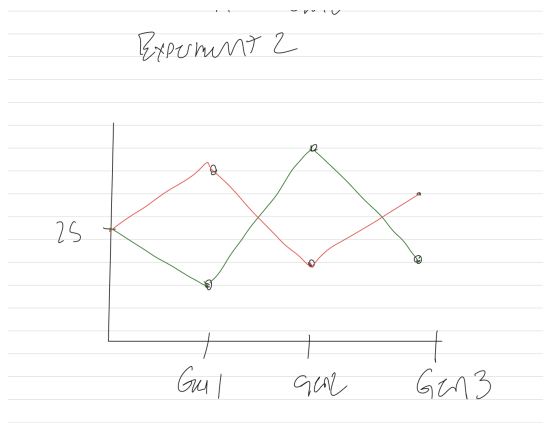
Jacob Aleixo  
BIO II

0) Pre-Lab Predictions (hand-drawn)

0A.



0B.



My prediction is that oystercatchers will eat the more noticeable snails, so red decreases and white increases, while the drifting log kills at random, so any color differences will be small and inconsistent.

## A) Hypotheses

I predict that in Experiment 1 the oystercatchers will target the snails that stand out the most, so one color will consistently drop while the other increases. In Experiment 2, the drifting log kills snails randomly, so any difference between colors will be due to chance and hard to predict or measure consistently.

### Experiment 1 — Oystercatcher (Selection)

- $H_0$ :  $\mu_{\text{red}} = \mu_{\text{white}}$  at generation 3.
- $H_a$  (directional):  $\mu_{\text{red}} < \mu_{\text{white}}$  at generation 3 (predation prefers red).

### Experiment 2 — Drifting Logs (Drift)

- $H_0$ :  $\mu_{\text{red}} = \mu_{\text{white}}$  at generation 3.
- $H_a$  (nondirectional):  $\mu_{\text{red}} \neq \mu_{\text{white}}$  at generation 3 (random differences possible).

## B) Tables & Figures (class data)

Figure 1. Mean snail counts ( $\pm$ SD) over generations after oystercatcher predation ( $n = 6$  groups). Lines connect means for each color; greater separation indicates stronger color-biased selection.

Table 1. Oystercatcher (Exp 1) class summary by generation and color (means, SD;  $n = 6$  groups).

Generation	Snail color	Mean	SD
0	red	25	0
0	white	25	0
1	red	19.7	1.51
1	white	30.3	1.51
2	red	15	3.95
2	white	35	3.95
3	red	11.3	11.6
3	white	38.7	11.6

Figure 1. Mean snail counts ( $\pm$ SD) across generations after oystercatcher predation ( $n = 6$  groups). Lines connect the mean for each color at each generation; increasing separation between white and red indicates color-biased selection.

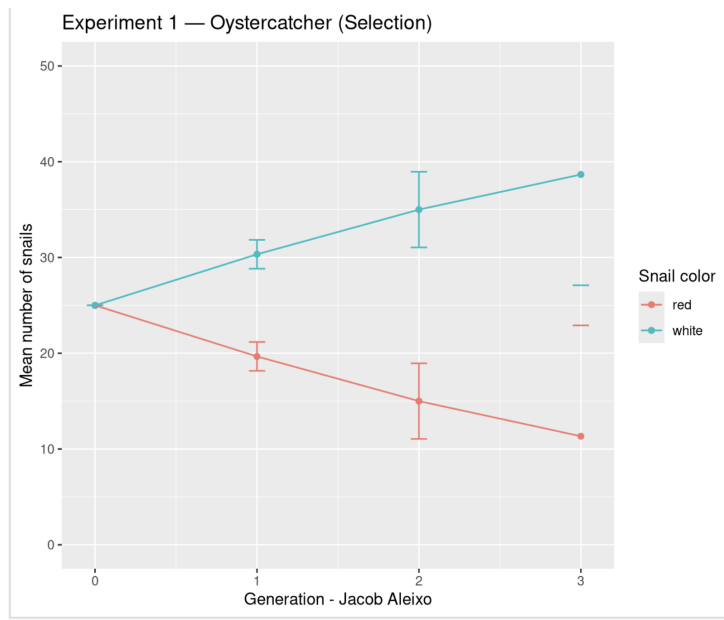
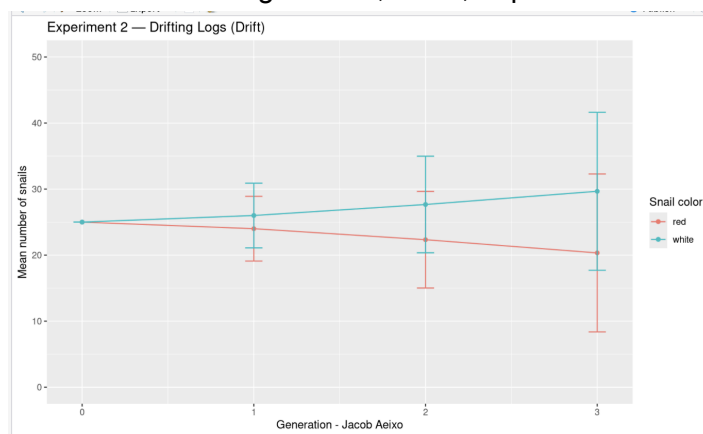


Table 2. Drifting Logs (Exp 2) class summary by generation and color (means, SD; n = 6 groups).

Generation	Snail color	Mean	SD
0	red	25	0
0	white	25	0
1	red	24	4.9
1	white	26	4.9
2	red	22.3	7.31
2	white	27.7	7.31
3	red	20.3	12
3	white	29.7	12

Figure 2. Mean snail counts ( $\pm$ SD) over generations after drifting-log mortality (n = 6 groups). Lines are for visual guidance; small, unpredictable shifts are consistent with random drift.



### C) Results

1. Experiment 1 (Oystercatcher). We compared generation-3 red vs. white with an independent-samples t-test. Red mean = 11.33 (SD = 11.57); White mean = 38.67 (SD = 11.57);  $t(10) = -4.09$ ,  $p = 0.00217$ . We reject  $H_0$  ( $\alpha = 0.05$ ): oystercatcher predation produced a color-biased difference consistent with selection.
2. Experiment 2 (Drifting Logs). We compared generation-3 red vs. white with an independent-samples t-test. Red mean = 20.33 (SD = 11.96); White mean = 29.67 (SD = 11.96);  $t(10) = -1.35$ ,  $p = 0.206$ . We fail to reject  $H_0$  ( $\alpha = 0.05$ ): differences were not statistically detectable and are consistent with random drift.

#### D) Discussion

$H_0$  decisions. For Experiment 1 we reject  $H_0$  ( $p = 0.00217$ ): red and white counts differ at generation 3, with white higher. For Experiment 2 we fail to reject  $H_0$  ( $p = 0.206$ ): the color means are not detectably different.

Mechanisms (brief defs). Natural selection is a non-random change in trait frequencies caused by differential survival or reproduction. Genetic drift is a random change in trait frequencies due to chance.

Map results → mechanisms. Experiment 1 shows a clear, directional pattern—white increases while red decreases—matching predation that favors one color, so the evidence supports selection. Experiment 2 shows small, inconsistent shifts with overlapping SD bars and no significant difference, which fits drift (random mortality by the log).

Notes on variation/limits. Our class means use a small number of groups, so SD bars are wide, especially by gen 3. Counting error and initial composition differences between groups can add noise. Despite this, Exp 1's directional separation is strong, while Exp 2 remains near-parallel with stochastic wiggles.

#### E)

Our class results support our predictions: with oystercatchers (Experiment 1), white snails ended higher and red lower, giving a significant color difference that indicates natural selection against the more conspicuous snails. With drifting logs (Experiment 2), red and white means at generation 3 were not significantly different, consistent with genetic drift where mortality is random. Overall, selection produced a clear, directional change, while drift produced small, unpredictable shifts without a consistent color bias.

## F) Appendix — R Code

# Jacob Aleixo — BIO104 A2: line graphs + t-tests in R

# 1) Packages

```
library(ggplot2)
```

```
library(gsheet)
```

```
library(dplyr)
```

# 2) Import class data

```
url <-
```

```
"https://docs.google.com/spreadsheets/d/1QhfezUHodqtNOnJGOnqA62mSfhJUtlItoJQUUYpuC  
YE/edit?gid=0#gid=0"
```

```
snail_data <- gsheets2tbl(url)
```

# 3) Clean types (protect against sheet weirdness)

```
snail_data <- snail_data %>%
```

```
  mutate(
```

```
    exp      = as.integer(exp),
```

```
    generation = as.integer(generation),
```

```
    snailcolor = as.factor(snailcolor),
```

```
    snails     = as.numeric(snails)
```

```
  )
```

# 4) Group summaries (means + SD) for plotting

```
n_exp1 <- snail_data |> dplyr::filter(exp==1, generation==3) |> dplyr::count(group) |> nrow()
```

```
n_exp2 <- snail_data |> dplyr::filter(exp==2, generation==3) |> dplyr::count(group) |> nrow()
```

```
snail_means_sd <- snail_data %>%
```

```
  group_by(exp, generation, snailcolor) %>%
```

```
  summarise(mean = mean(snails, na.rm = TRUE),
```

```
            stdev = sd(snails, na.rm = TRUE),
```

```
            .groups = "drop")
```

# ----- PLOTS -----

# 5) EXPERIMENT 1: Oystercatcher (selection)

```
exp1 <- filter(snail_means_sd, exp == 1)
```

```
p1 <- ggplot(exp1, aes(x = generation, y = mean, color = snailcolor, group = snailcolor)) +
```

```
  geom_point() +
```

```
  geom_line() +
```

```
  geom_errorbar(aes(ymin = mean - stdev, ymax = mean + stdev), width = 0.1) +
```

```

  scale_x_continuous(name = "Generation - Jacob Aleixo", breaks =
sort(unique(exp1$generation))) +
  scale_y_continuous(name = "Mean number of snails", limits = c(0, 50)) +
  labs(title = "Experiment 1 — Oystercatcher (Selection)", color = "Snail color")
print(p1)

```

```

# 6) EXPERIMENT 2: Drifting logs (drift)
exp2 <- filter(snail_means_sd, exp == 2)
p2 <- ggplot(exp2, aes(x = generation, y = mean, color = snailcolor, group = snailcolor)) +
  geom_point() +
  geom_line() +
  geom_errorbar(aes(ymin = mean - stdev, ymax = mean + stdev), width = 0.1) +
  scale_x_continuous(name = "Generation - Jacob Aeixo", breaks =
sort(unique(exp2$generation))) +
  scale_y_continuous(name = "Mean number of snails", limits = c(0, 50)) +
  labs(title = "Experiment 2 — Drifting Logs (Drift)", color = "Snail color")
print(p2)

```

```

table_exp1
table_exp2

```

# ----- TABLES FOR YOUR REPORT -----

# 7) Table skeletons (means/SD by generation & color) you can paste into Sheets

```

table_exp1 <- snail_means_sd %>% filter(exp == 1) %>%
  arrange(generation, snailcolor)
table_exp2 <- snail_means_sd %>% filter(exp == 2) %>%
  arrange(generation, snailcolor)

```

# View in console

```

table_exp1
table_exp2

```

# ----- T-TESTS AT GENERATION 3 -----

# 8) Subsets for gen 3

```

Red1 <- filter(snail_data, exp == 1, generation == 3, snailcolor == "red")
White1 <- filter(snail_data, exp == 1, generation == 3, snailcolor == "white")

```

```

Red2 <- filter(snail_data, exp == 2, generation == 3, snailcolor == "red")
White2 <- filter(snail_data, exp == 2, generation == 3, snailcolor == "white")

```

# 9) Run tests

```

tt1 <- t.test(Red1$snails, White1$snails)
tt2 <- t.test(Red2$snails, White2$snails)

```

# 10) Pretty print for your Results section

```
fnt <- function(tt, red, white) {  
  paste0(  
    "Red mean = ", round(mean(red, na.rm = TRUE), 2), " (SD = ", round(sd(red, na.rm =  
TRUE), 2), "); ",  
    "White mean = ", round(mean(white, na.rm = TRUE), 2), " (SD = ", round(sd(white, na.rm =  
TRUE), 2), "). ",  
    "t(", round(tt$parameter, 0), ") = ", round(tt$statistic, 2),  
    ", p = ", signif(tt$p.value, 3)  
  )  
}
```

```
cat("\nExperiment 1 (gen 3) — Oystercatcher:\n", fnt(tt1, Red1$snails, White1$snails), "\n", sep  
= "")
```

```
cat("Experiment 2 (gen 3) — Drift:\n",      fnt(tt2, Red2$snails, White2$snails), "\n", sep = "")
```

#Experiment 1 (gen 3) — Oystercatcher:

#Red mean = 11.33 (SD = 11.57);

#White mean = 38.67 (SD = 11.57).

#t(10) = -4.09, p = 0.00217

# Experiment 2 (gen 3) — Drift:

#Red mean = 20.33 (SD = 11.96);

#White mean = 29.67 (SD = 11.96).

#t(10) = -1.35, p = 0.206