05\_Class\_Activity

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# In-Class Activity 5: Probability and Statistical Inference

## What did we do last time?

In our previous activity, we:

* Created and interpreted frequency distributions (histograms)
* Compared data between groups using side-by-side histograms
* Explored how sample size affects our understanding of populations
* Created density plots and calculated probabilities

## Today’s focus:

Today we’ll focus on:

* Student’s t-distribution and when to use it
* Calculating and interpreting standard error
* Creating confidence intervals
* Conducting one-sample and two-sample t-tests
* Understanding statistical assumptions and their importance

# Setup

First, let’s load the packages and data we’ll be using:

# Load required packages  
library(tidyverse) # For data manipulation and visualization  
library(patchwork) # For combining plots  
library(car) # For diagnostic tests (QQ plots)  
  
# Read in the data files  
grayling\_df <- read\_csv("data/gray\_I3\_I8.csv")   
pine\_df <- read\_csv("data/pine\_needles.csv")  
  
  
# Look at the first few rows of each dataset  
head(grayling\_df)

# A tibble: 6 × 5  
 site lake species length\_mm mass\_g  
 <dbl> <chr> <chr> <dbl> <dbl>  
1 113 I3 arctic grayling 266 135  
2 113 I3 arctic grayling 290 185  
3 113 I3 arctic grayling 262 145  
4 113 I3 arctic grayling 275 160  
5 113 I3 arctic grayling 240 105  
6 113 I3 arctic grayling 265 145

head(pine\_df)

# A tibble: 6 × 6  
 date group n\_s wind tree\_no length\_mm  
 <chr> <chr> <chr> <chr> <dbl> <dbl>  
1 3/20/25 cephalopods n lee 1 20  
2 3/20/25 cephalopods n lee 1 21  
3 3/20/25 cephalopods n lee 1 23  
4 3/20/25 cephalopods n lee 1 25  
5 3/20/25 cephalopods n lee 1 21  
6 3/20/25 cephalopods n lee 1 16

# Part 1: Exploring the Data

Before conducting statistical tests, it’s important to understand your data.

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| Practice Exercise 1: Creating Histograms |
| Let’s create histograms of fish lengths from each lake to visualize their distributions.  # Create a histogram for Lake I3 i3\_hist <- grayling\_df %>%   filter(lake == "I3") %>%  ggplot(aes(length\_mm)) +   geom\_histogram(binwidth = 10, fill = "blue", alpha = 0.7) +  labs(title = "Lake I3 Fish Lengths",  x = "Length (mm)",  y = "Count")  # Create a histogram for Lake I8 i8\_hist <- grayling\_df %>%   filter(lake == "I8") %>%  ggplot(aes(length\_mm)) +   geom\_histogram(binwidth = 10, fill = "darkgreen", alpha = 0.7) +  labs(title = "Lake I8 Fish Lengths",  x = "Length (mm)",  y = "Count")  # Display the histograms side by side using patchwork i3\_hist + i8\_hist    # CAN YOU THINK OF AN EASIER WAY? |

## Now, let’s calculate summary statistics for each lake:

# Calculate summary statistics for both lakes  
grayling\_summary <- grayling\_df %>%   
 group\_by(lake) %>%  
 summarize(  
 mean\_length = mean(length\_mm, na.rm = TRUE),  
 sd\_length = sd(length\_mm, na.rm = TRUE),  
 n = sum(!is.na(length\_mm)),  
 se\_length = sd\_length / sqrt(n),  
 .groups = "drop"  
 )  
  
# Display the summary statistics  
grayling\_summary

# A tibble: 2 × 5  
 lake mean\_length sd\_length n se\_length  
 <chr> <dbl> <dbl> <int> <dbl>  
1 I3 266. 28.3 66 3.48  
2 I8 363. 52.3 102 5.18

# Part 3: Testing Assumptions

Before conducting a t-test, we need to check if our data meets the necessary assumptions:

1. **Normality**: The data should be approximately normally distributed
2. **Independence**: Observations should be independent
3. **No extreme outliers**: Outliers can heavily influence t-test results

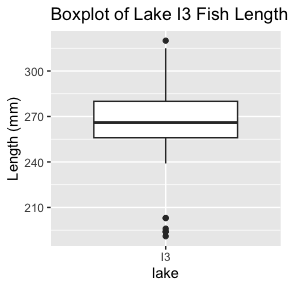
Let’s check the normality assumption for Lake I3 fish lengths:

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| Practice Exercise 2: Checking Normality |
| # Filter for Lake I3 fish i3\_df <- grayling\_df %>% filter(lake == "I3")  # Create a QQ plot to check normality # QQ plots compare our data to a theoretical normal distribution # Points should roughly follow the line if data is normally distributed qqPlot(i3\_df$length\_mm,   main = "QQ Plot for Lake I3 Fish Lengths",  ylab = "Sample Quantiles")    [1] 53 35 |

# Also perform a formal test of normality using the Shapiro-Wilk test  
# Null hypothesis: Data is normally distributed  
# If p > 0.05, we don't reject the assumption of normality  
shapiro\_test <- shapiro.test(i3\_df$length\_mm)  
print(shapiro\_test)

Shapiro-Wilk normality test  
  
data: i3\_df$length\_mm  
W = 0.91051, p-value = 0.0001623

# Check for outliers using a boxplot  
i3\_df %>%   
 ggplot(aes(x = lake, y = length\_mm)) +  
 geom\_boxplot() +  
 labs(title = "Boxplot of Lake I3 Fish Lengths",  
 y = "Length (mm)")



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| Tip |
| How to interpret these results:   * The QQ plot: Points should follow the straight line if data is normally distributed * Shapiro-Wilk test: If p > 0.05, we don’t reject the assumption of normality * Boxplot: Look for points beyond the whiskers as potential outliers |

# Part 4: One-Sample t-Test

A one-sample t-test compares a sample mean to a specific value.

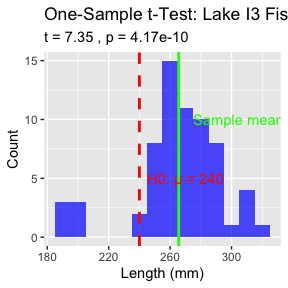
Let’s test if the mean fish length in Lake I3 differs from 240mm:

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| Practice Exercise 3: One-Sample t-Test |
| # Calculate the mean of I3 fish i3\_mean <- mean(i3\_df$length\_mm, na.rm = TRUE) cat("Mean fish length in Lake I3:", round(i3\_mean, 1), "mm\n")  Mean fish length in Lake I3: 265.6 mm |

# Perform a one-sample t-test  
# H0: μ = 240 (The mean fish length is 240mm)  
# H1: μ ≠ 240 (The mean fish length is not 240mm)  
t\_test\_result <- t.test(i3\_df$length\_mm, mu = 240)  
  
# Display the test results  
t\_test\_result

One Sample t-test  
  
data: i3\_df$length\_mm  
t = 7.3497, df = 65, p-value = 4.17e-10  
alternative hypothesis: true mean is not equal to 240  
95 percent confidence interval:  
 258.6481 272.5640  
sample estimates:  
mean of x   
 265.6061

# Create a visualization of the test  
i3\_df %>%  
 ggplot(aes(x = length\_mm)) +  
 geom\_histogram(binwidth = 10, fill = "blue", alpha = 0.7) +  
 geom\_vline(xintercept = 240, color = "red", linetype = "dashed", linewidth = 1) +  
 geom\_vline(xintercept = i3\_mean, color = "green", linewidth = 1) +  
 annotate("text", x = 240, y = 5, label = "H0: μ = 240", color = "red", hjust = -0.1) +  
 annotate("text", x = i3\_mean, y = 10, label = paste("Sample mean =", round(i3\_mean, 1)),   
 color = "green", hjust = -0.1) +  
 labs(title = "One-Sample t-Test: Lake I3 Fish Lengths",  
 subtitle = paste("t =", round(t\_test\_result$statistic, 2),   
 ", p =", format.pval(t\_test\_result$p.value, digits = 3)),  
 x = "Length (mm)",  
 y = "Count")



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| Tip |
| Interpret the results:   1. What was the null hypothesis? H0: μ = 240mm 2. What was the alternative hypothesis? H1: μ ≠ 240mm 3. What does the p-value tell us? (Is it < 0.05?) 4. Should we reject or fail to reject the null hypothesis? 5. What is the practical interpretation for biologists? |

# Part 5: Confidence Intervals

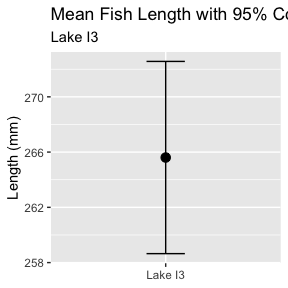
A confidence interval gives us a range of plausible values for the population mean.

For a 95% confidence interval using the t-distribution:

Where: - is the sample mean - is the sample standard deviation - is the sample size - is the critical t-value with n-1 degrees of freedom

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| Practice Exercise 4: Calculating Confidence Intervals |
| Let’s calculate the 95% confidence interval for Lake I3 fish lengths:  # Extract sample statistics i3\_stats <- grayling\_summary %>% filter(lake == "I3") i3\_mean <- i3\_stats$mean\_length i3\_se <- i3\_stats$se\_length i3\_n <- i3\_stats$n  # Find the critical t-value for 95% confidence with n-1 degrees of freedom # qt(0.975, df) gives the t-value for a 95% confidence interval (two-tailed) t\_critical <- qt(0.975, df = i3\_n - 1) cat("Critical t-value for", i3\_n-1, "degrees of freedom:", round(t\_critical, 3), "\n")  Critical t-value for 65 degrees of freedom: 1.997  # Calculate the confidence interval i3\_ci\_lower <- i3\_mean - t\_critical \* i3\_se i3\_ci\_upper <- i3\_mean + t\_critical \* i3\_se  # Display the confidence interval cat("95% Confidence Interval for Lake I3 fish mean length:",   round(i3\_ci\_lower, 1), "to", round(i3\_ci\_upper, 1), "mm\n")  95% Confidence Interval for Lake I3 fish mean length: 258.6 to 272.6 mm  # Compare this to a confidence interval using the normal approximation (z = 1.96) z\_ci\_lower <- i3\_mean - 1.96 \* i3\_se z\_ci\_upper <- i3\_mean + 1.96 \* i3\_se  cat("95% CI using normal approximation:",   round(z\_ci\_lower, 1), "to", round(z\_ci\_upper, 1), "mm\n")  95% CI using normal approximation: 258.8 to 272.4 mm |

# Visualize the confidence interval  
ggplot() +  
 geom\_errorbar(aes(x = "Lake I3",   
 ymin = i3\_ci\_lower,   
 ymax = i3\_ci\_upper),  
 width = 0.2) +  
 geom\_point(aes(x = "Lake I3", y = i3\_mean), size = 3) +  
 labs(title = "Mean Fish Length with 95% Confidence Interval",  
 subtitle = "Lake I3",  
 x = NULL,  
 y = "Length (mm)")



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| Tip |
| Interpretation:   * We are 95% confident that the true population mean fish length in Lake I3 falls within this interval * Note the small difference between using the t-distribution vs. normal approximation |

# Part 6: Two-Sample t-Test

A two-sample t-test compares means from two independent groups.

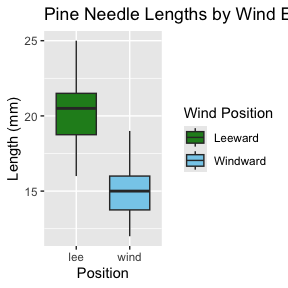
Let’s compare pine needle lengths between windward and leeward sides:

# Summarize pine needle data by wind exposure  
pine\_summary <- pine\_df %>%  
 group\_by(wind) %>%  
 summarize(  
 mean\_length = mean(length\_mm),  
 sd\_length = sd(length\_mm),  
 n = n(),  
 se\_length = sd\_length / sqrt(n)  
 )  
  
# Display the summary statistics  
print(pine\_summary)

# A tibble: 2 × 5  
 wind mean\_length sd\_length n se\_length  
 <chr> <dbl> <dbl> <int> <dbl>  
1 lee 20.4 2.45 24 0.500  
2 wind 14.9 1.91 24 0.390

## Look a the plot of pine needles

# Create a boxplot to visualize the data  
pine\_df %>%  
 ggplot(aes(x = wind, y = length\_mm, fill = wind)) +  
 geom\_boxplot() +  
 labs(title = "Pine Needle Lengths by Wind Exposure",  
 x = "Position",  
 y = "Length (mm)",  
 fill = "Wind Position") +  
 scale\_fill\_manual(values = c("lee" = "forestgreen", "wind" = "skyblue"),  
 labels = c("lee" = "Leeward", "wind" = "Windward"))



Before conducting the t-test, we should check the assumptions:

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| Practice Exercise 5: Check Assumptions for Two-Sample t-Test |
| # Separate data by groups windward\_data <- pine\_df %>% filter(wind == "wind") leeward\_data <- pine\_df %>% filter(wind == "lee")  # 1. Check for normality in each group using QQ plots  qqPlot(windward\_data$length\_mm, main = "QQ Plot: Windward Needles")    [1] 21 22  qqPlot(leeward\_data$length\_mm, main = "QQ Plot: Leeward Needles")    [1] 4 16  # 2. Check for equal variances using Levene's test # H0: Variances are equal # H1: Variances are not equal levene\_result <- leveneTest(length\_mm ~ wind, data = pine\_df) print("Levene's Test for Homogeneity of Variance:")  [1] "Levene's Test for Homogeneity of Variance:"  print(levene\_result)  Levene's Test for Homogeneity of Variance (center = median)  Df F value Pr(>F) group 1 1.2004 0.2789  46 |

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| Tip |
| Interpreting the assumption checks:   * QQ plots: Do points approximately follow the line for both groups? * Levene’s test: If p > 0.05, we don’t reject the assumption of equal variances |

## Now let’s conduct the two-sample t-test:

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| Practice Exercise 6: Two-Sample t-Test |
| # Perform a two-sample t-test # H0: μ1 = μ2 (The mean needle lengths are equal) # H1: μ1 ≠ μ2 (The mean needle lengths are different)  # var.equal=TRUE uses the standard t-test (pooled variance) # var.equal=FALSE uses Welch's t-test (for unequal variances) t\_test\_result <- t.test(length\_mm ~ wind, data = pine\_df, var.equal = TRUE)  # Display the test results print(t\_test\_result)  Two Sample t-test  data: length\_mm by wind t = 8.6792, df = 46, p-value = 3.01e-11 alternative hypothesis: true difference in means between group lee and group wind is not equal to 0 95 percent confidence interval:  4.224437 6.775563 sample estimates:  mean in group lee mean in group wind   20.41667 14.91667  # Calculate the mean difference mean\_diff <- pine\_summary$mean\_length[pine\_summary$wind == "lee"] -   pine\_summary$mean\_length[pine\_summary$wind == "wind"] cat("Mean difference (lee - wind):", round(mean\_diff, 2), "mm\n")  Mean difference (lee - wind): 5.5 mm  # Visualize the results with a mean and error bar plot ggplot(pine\_summary, aes(x = wind, y = mean\_length, fill = wind)) +  geom\_bar(stat = "identity", alpha = 0.7) +  geom\_errorbar(aes(ymin = mean\_length - se\_length,   ymax = mean\_length + se\_length),  width = 0.2) +  scale\_fill\_manual(values = c("lee" = "forestgreen", "wind" = "skyblue"),  labels = c("lee" = "Leeward", "wind" = "Windward")) +  labs(title = "Pine Needle Lengths by Wind Exposure",  subtitle = paste("t =", round(t\_test\_result$statistic, 2),   ", p =", format.pval(t\_test\_result$p.value, digits = 3)),  x = "Position",  y = "Mean Length (mm)",  fill = "Wind Position")    Interpret the results:   1. What was the null hypothesis? 2. What was the alternative hypothesis? 3. What does the p-value tell us? 4. Should we reject or fail to reject the null hypothesis? 5. What is the practical interpretation for botanists? |

# Part 7: Comparing Fish Lengths Between Lakes

Let’s apply what we’ve learned to compare fish lengths between Lakes I3 and I8:

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| Practice Exercise 7: Comparing Lakes |
| # Perform a two-sample t-test comparing I3 and I8 # First check assumptions (variances) levene\_lakes <- leveneTest(length\_mm ~ lake, data = grayling\_df) print("Levene's Test for Lakes:")  [1] "Levene's Test for Lakes:"  print(levene\_lakes)  Levene's Test for Homogeneity of Variance (center = median)  Df F value Pr(>F)  group 1 13.705 0.0002907 \*\*\*  166  --- Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  # Perform the t-test with appropriate variance setting lakes\_t\_test <- t.test(length\_mm ~ lake, data = grayling\_df,   var.equal = (levene\_lakes$`Pr(>F)`[1] > 0.05))  # Display the results print(lakes\_t\_test)  Welch Two Sample t-test  data: length\_mm by lake t = -15.532, df = 161.63, p-value < 2.2e-16 alternative hypothesis: true difference in means between group I3 and group I8 is not equal to 0 95 percent confidence interval:  -109.32342 -84.66053 sample estimates: mean in group I3 mean in group I8   265.6061 362.5980  # Create a visualization ggplot(grayling\_df, aes(x = lake, y = length\_mm, fill = lake)) +  geom\_boxplot(alpha = 0.7) +  labs(title = "Comparison of Fish Lengths Between Lakes",  subtitle = paste("t =", round(lakes\_t\_test$statistic, 2),   ", p =", format.pval(lakes\_t\_test$p.value, digits = 3)),  x = "Lake",  y = "Length (mm)")    Write your interpretation of the results:   1. Is there a significant difference in fish lengths between lakes? 2. Which lake has longer fish on average? 3. How would you report this result in a scientific paper? |

# Part 8: Communicating Statistical Results

In scientific writing, it’s important to report statistical results clearly and consistently.

Here’s a standard format for reporting t-test results:

For a one-sample t-test: “A one-sample t-test showed that the mean fish length in Lake I3 (M = [mean], SD = [sd]) was [significantly/not significantly] different from 240 mm, t([df]) = [t-value], p = [p-value].”

For a two-sample t-test: “A two-sample t-test revealed that pine needle lengths on the leeward side (M = [mean1], SD = [sd1]) were [significantly/not significantly] [longer/shorter] than on the windward side (M = [mean2], SD = [sd2]), t([df]) = [t-value], p = [p-value].”

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| Practice Exercise 8: Writing Statistical Results |
| Write properly formatted statements reporting the results of: 1. The one-sample t-test comparing Lake I3 fish to 240mm 2. The two-sample t-test comparing pine needle lengths 3. The two-sample t-test comparing fish lengths between lakes  Remember to include: - Means and standard deviations for each group - The t-value with degrees of freedom - The p-value and whether the result is significant |

# Reflection Questions

1. How does the t-distribution differ from the normal distribution, and why does this matter for small samples?
2. What assumptions must be met to use a t-test, and what alternatives exist if these assumptions are violated?
3. What is the difference between statistical significance and practical importance?
4. How would the confidence interval change if we used a 99% confidence level instead of 95%?
5. How would you explain the concept of a p-value to someone with no statistical background?