

Final Lab Report Horsetooth Reservoir

Group 1

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2024-10-18

Introduction

Horsetooth reservoir is a mesotrophic temperate reservoir located in Fort Collins, Colorado (Stevens, 2000). The reservoir was planned as part of the Colorado Big Thompson project in 1933, but construction of the reservoir itself didn't begin until 1946, completing 10 years later (Blumhardt et al., 2022) with a maximum capacity of 193,329,488 m³ (Northern Water). The reservoir was constructed over the former town of Stout which boasted a population of 900 at its peak, but became fully abandoned by the year 1900 (Blumhardt et al.). Today, the reservoir generates \$103 million annually through visitor expenditures (Madsen et al., 2020), and visitors can enjoy a myriad of recreational activities such as hiking, fishing, boating, swimming, and camping. The reservoir experiences annual water level fluctuations of about 40-60 feet between each summer and winter (Hawley et al., 2013). During the winter months, water is drained away for agricultural use in eastern Colorado (G. Nugent, personal communication, 2024), and to make room for the spring filling season (USBR). In the summer, the reservoir experiences highest dissolved oxygen levels between 7 and 15 meters of depth, and chlorophyll-a concentrations are highest in the top 10 meters, with values varying between 0.6 and 11 ug/L (Hawley et al.). Horsetooth reservoir stratifies strongly in the summer months, experiencing turnover in the fall. The reservoir experiences a low homogenized temperature of 5°C in April, up from 8.5°C in November. When stratified in summer, the epilimnion reaches temperatures between 20-23°C, and the hypolimnion between 5-7°C (Hawley et al.). The reservoir is stocked with a variety of fish species including large and smallmouth bass, bluegill, carp, crappie, walleye, and 4 kinds of trout (Colorado Fishing Atlas).

Methods

a.

This study involved a comprehensive sampling effort designed to assess various water quality parameters, biological communities, and chemical profiles. Sampling was conducted to achieve a detailed understanding of the ecosystem by using the following protocols:

Secchi Depth Measurement

Secchi depth was measured to estimate water clarity, an important indicator of turbidity and light penetration. Each group member measured the Secchi depth individually, ensuring multiple observations. These were averaged to provide a robust representation of visibility at the site.

Depth Profile Measurements

A depth profile was established by measuring temperature, pH, conductivity, salinity, dissolved oxygen (percent and concentration), and chlorophyll a at 1-meter increments, beginning at the surface. Stabilization of parameters was ensured before recording, allowing for precise characterization of vertical changes in water chemistry and stratification.

Algae and Zooplankton Sampling

To analyze the biological components, algae and zooplankton samples were collected using a plankton net. The net was deployed to a depth of 1 meter and carefully raised to avoid contamination. Samples were rinsed into Falcon tubes, preserved with Lugol's solution, and labeled appropriately. This method provided material for the identification and quantification of phytoplankton and zooplankton communities.

Water Chemistry Analysis

Water samples were collected at two distinct depths: the epilimnion (1 meter) and 1 meter below the thermocline. Using a Van Dorn sampler, water was collected for various analyses, including total phosphorus, NH₄/NO₃, and dissolved organic carbon. Samples were prepared by rinsing collection containers, filtering water through GFF filters, and properly labeling for subsequent laboratory analysis. This approach aimed to capture both surface and deeper water chemical profiles to evaluate nutrient levels and organic content.

Chlorophyll a Analysis

Filters from the water chemistry sampling were prepared for chlorophyll a analysis. Filters were folded, wrapped in aluminum foil, labeled, and stored in a cooler. These samples were collected to measure chlorophyll a concentration as an indicator of primary productivity.

Overview of Sampling Efforts

This sampling protocol was designed to collect data on physical, chemical, and biological aspects of the aquatic system. Secchi depth measurements provided insight into light availability and turbidity. Depth profiles captured vertical gradients of water quality parameters, while algae and zooplankton sampling allowed for biodiversity assessments. Chemical analysis at distinct depths enabled nutrient profiling and assessment of organic matter. Finally, chlorophyll a measurements informed the productivity of the system. Collectively, these efforts provided a holistic view of the ecosystem's health and functioning.

b.

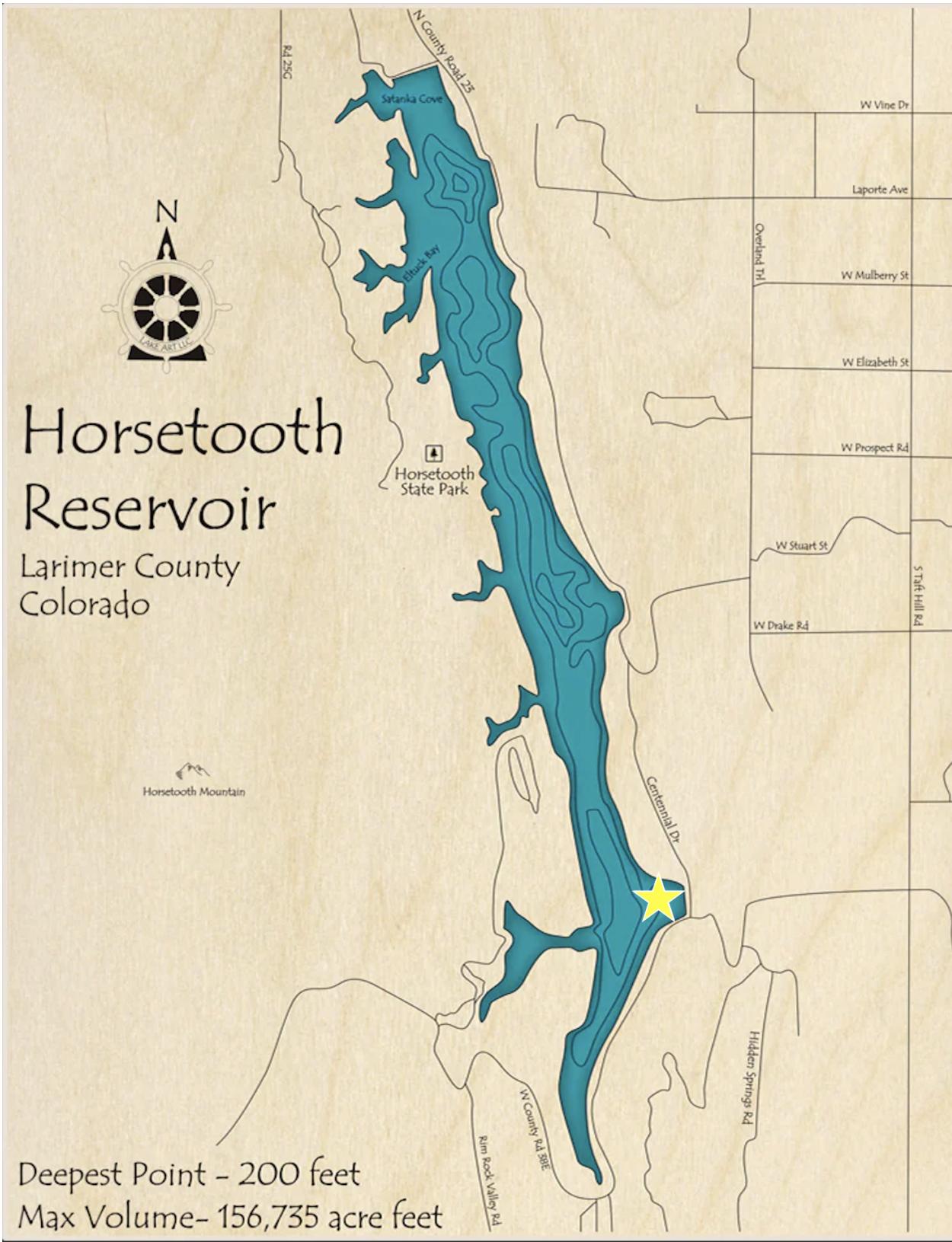


Figure 1: Horsetooth Reservoir map with sampling location marked with yellow star

Results

1.

```
###  
#1#  
###  
G01 <- read_csv("Group01_09062024_profiledata.csv")  
G01 %>%  
  filter(!is.na(do_percent) & !is.na(do_mgL)) %>%  
  ggplot() +  
  geom_point(aes(x = do_mgL, y = z_m, color = "DO (mg/L)"), size = 3) +  
  geom_point(aes(x = do_percent, y = z_m, color = "DO (%)"), size = 4) +  
  theme_few() +  
  labs(  
    title = "Oxygen Profile with DO percent and mg/L",  
    x = 'DO (mg/L)',  
    y = 'Depth (m)',  
    color = NULL  
) +  
  scale_y_reverse(expand = c(0.015, 0)) +  
  theme(text = element_text(size = 10))
```

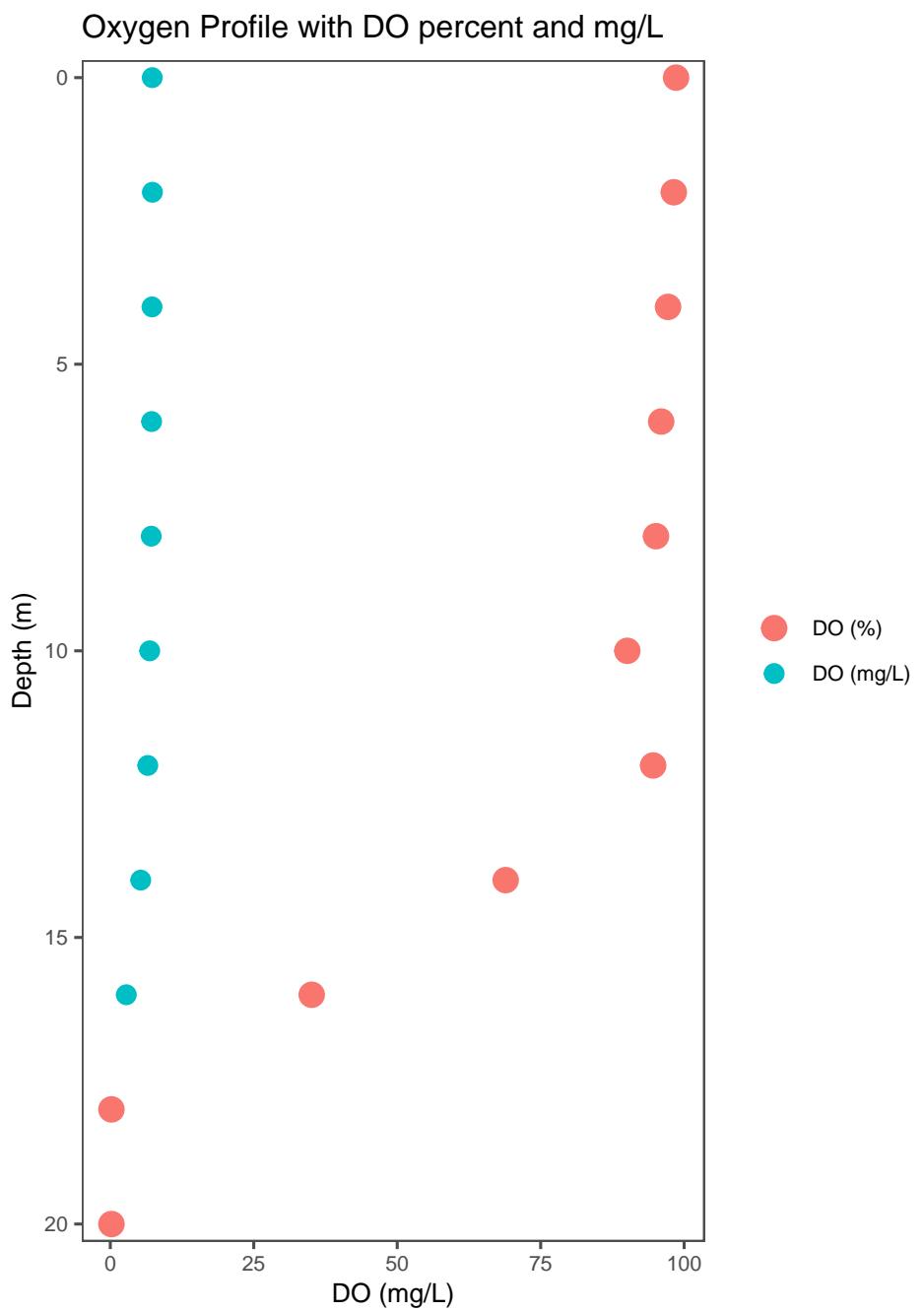


Figure 2: An oxygen profile, containing both the DO (percent) and DO (mg/L).

2.

```
###  
#2#  
###  
G01 <- read_csv("Group01_09062024_profiledata.csv")  
  
G01 %>%  
  filter(!is.na(temp_c) & !is.na(z_m) & group == "Group_1") %>%  
  ggplot(aes(x = temp_c, y = z_m)) +  
  geom_point(size = 4, color = "lightblue") +  
  theme_few() +  
  labs(  
    x = 'Temperature (°C)',  
    y = 'Depth (m)',  
    title = "Temperature Profile in Horsetooth Reservoir"  
) +  
  scale_y_reverse(expand = c(0.015, 0)) +  
  theme(text = element_text(size = 10))
```

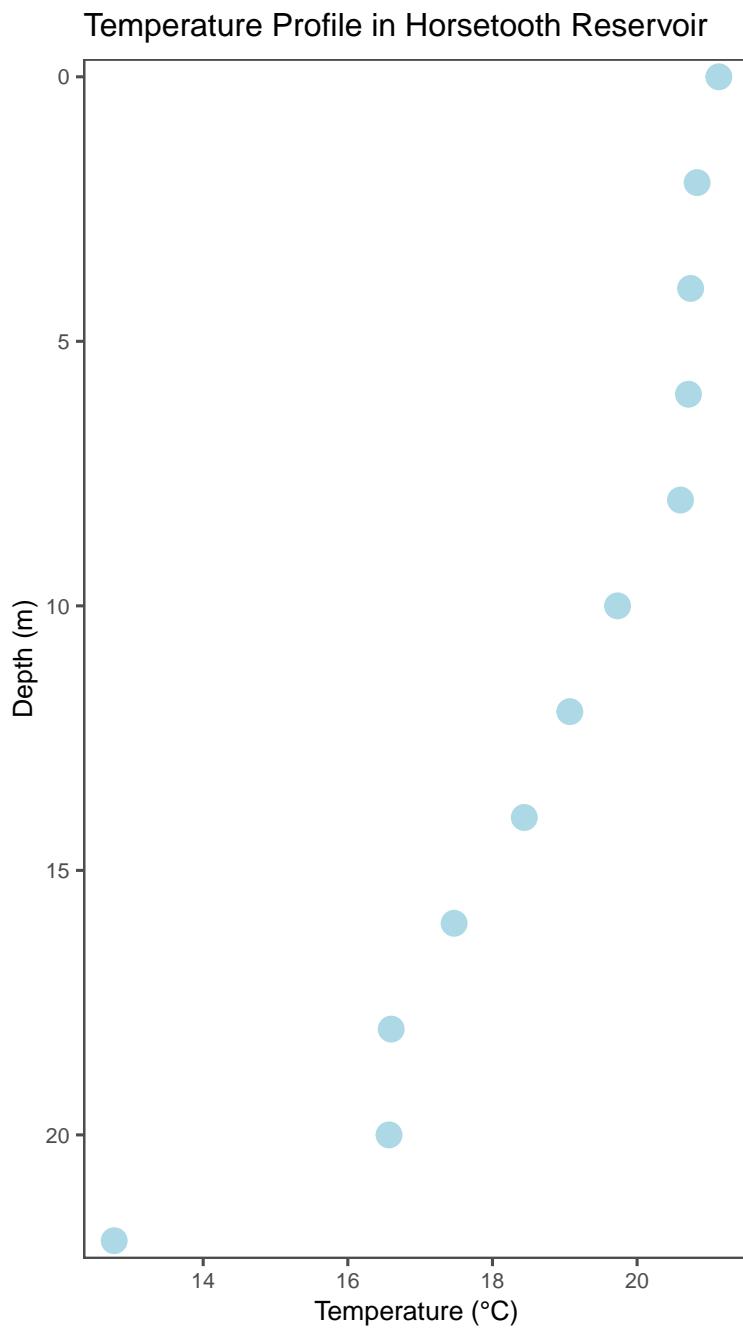


Figure 3: Temperature profile illustrating variations in temperature ($^{\circ}\text{C}$) with depth in Horsetooth Reservoir.

3.

```
###  
#3#  
###  
G01 <- read_csv("Group01_09062024_profiledata.csv")  
  
G01 %>%  
  filter(!is.na(ph) & !is.na(z_m) & group == "Group_1") %>%  
  ggplot(aes(x = ph, y = z_m)) +  
  geom_point(size = 4, color = "lightgreen") +  
  theme_few() +  
  labs(  
    x = 'PH',  
    y = 'Depth (m)', title = "pH Profile of Horsetooth Reservoir") +  
  scale_y_reverse(expand = c(0.015, 0)) +  
  theme(text = element_text(size = 10))
```

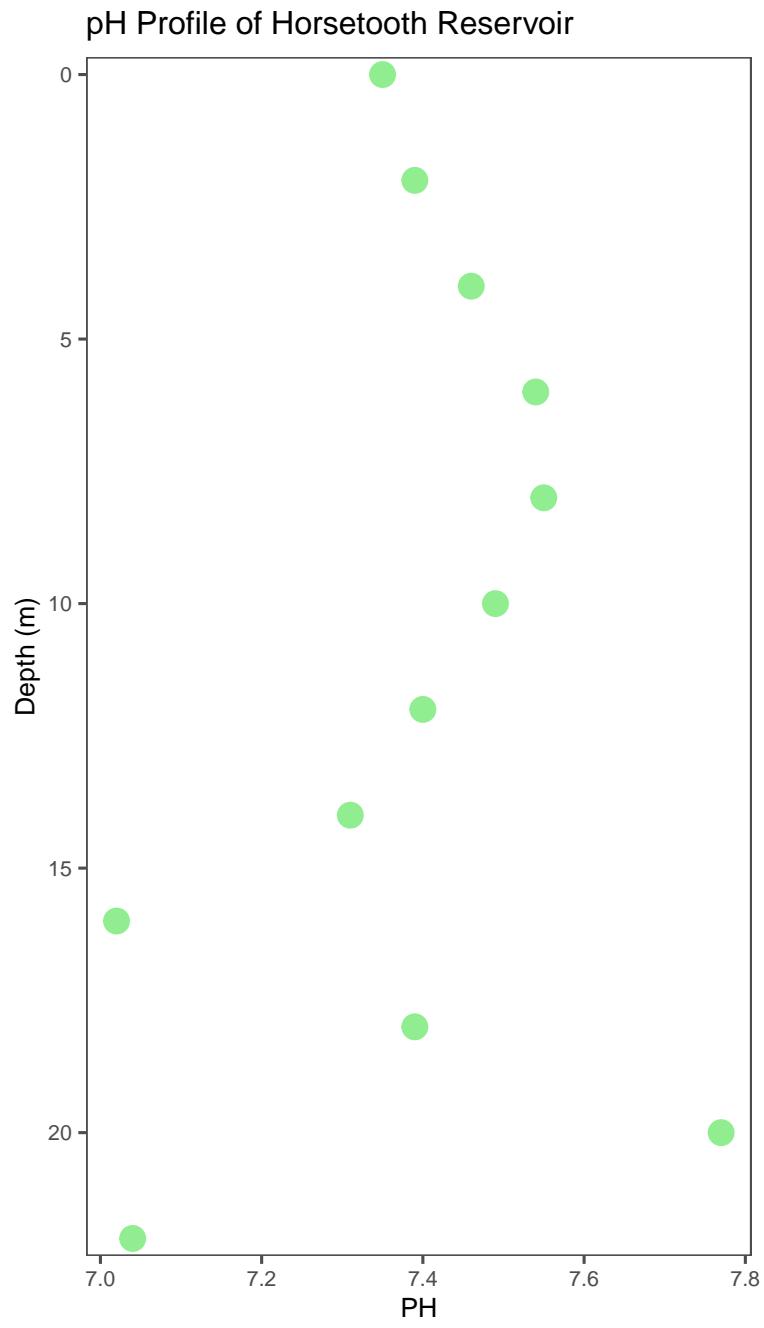


Figure 4: pH profile showing pH values across various depths in Horsetooth Reservoir.

4.

```
###  
##  
###  
  
StandardData <- read_csv("ESS474Fall2024stdcurvedata-2.csv")  
G1Epi <- read_csv("Group1Epi.csv")  
G1Hypo <- read_csv("Group1Hypo.csv")  
  
combined_dt <- rbind(  
  mutate(StandardData, source = "original"),  
  mutate(G1Epi, source = "newepi"),  
  mutate(G1Hypo, source = "newhypo")  
)  
  
ggplot(combined_dt, aes(x=mg_L_TN, y=Area)) +  
  ggtitle("Total Nitrogen and Area Standard Curve") +  
  coord_cartesian(xlim = c(0, 0.25), ylim = c(0, 6.485)) +  
  stat_poly_line(source = "original") +  
  stat_poly_eq(use_label(c("eq", "R2"))) +  
  geom_point(data = subset(combined_dt, source == "original")) +  
  geom_smooth(method=lm, color="red", se=FALSE) +  
  
  geom_point(data = subset(combined_dt, source == "newepi"), color = "black",  
             shape = 23, size = 4, fill = "yellow") +  
  geom_text(data = G1Epi, aes(label = "Epilimnion"), hjust = -0.1, vjust = 1.2) +  
  
  geom_point(data = subset(combined_dt, source == "newhypo"), color = "black",  
             shape = 23, size = 4, fill = "yellow") +  
  geom_text(data = G1Hypo, aes(label = "Hypolimnion"), hjust = -0.1, vjust = -0.5) +  
  
  xlab("Total Nitrogen (mg/L)") +  
  ylab("Area")
```

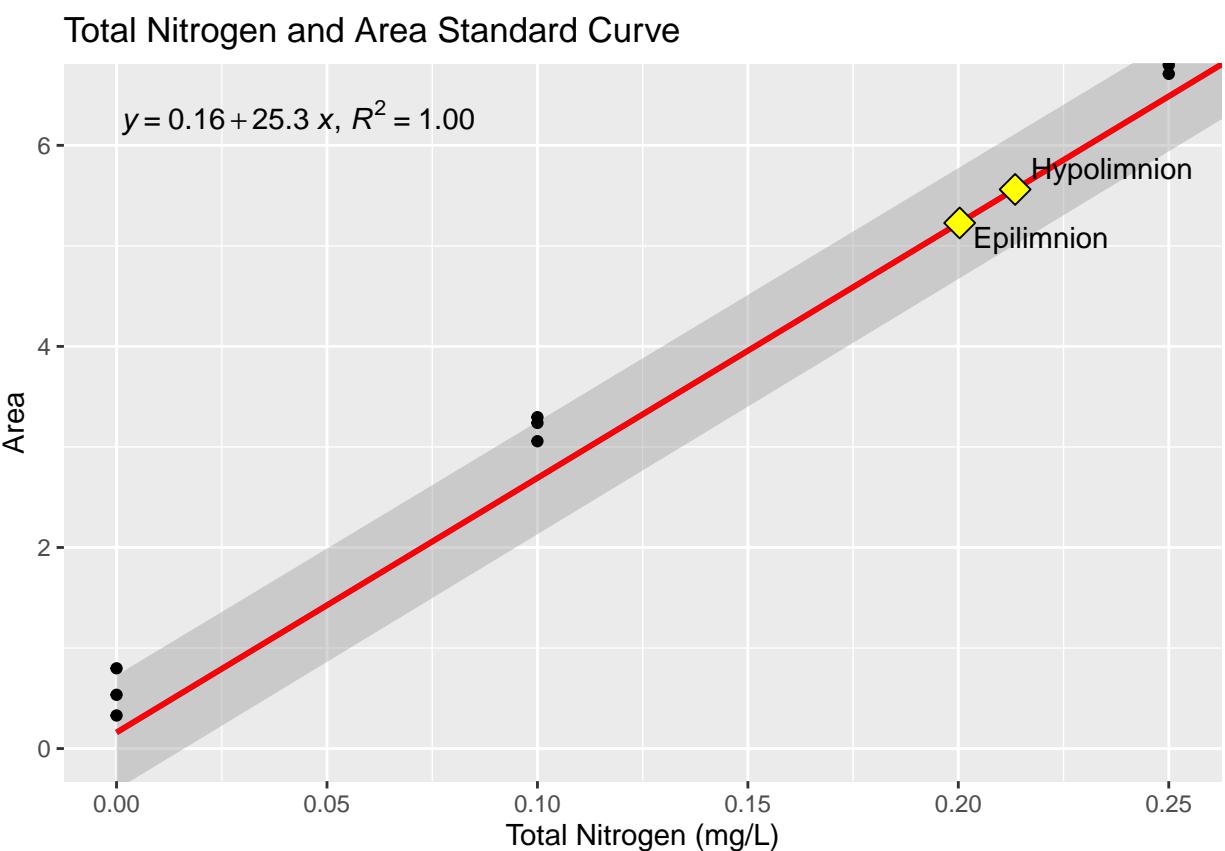


Figure 5: Standard curve of area to TN relationship with epilimnion and hypolimnion values. Yellow diamonds represent mean epilimnion and hypolimnion values for group 1

4b.

```
ggplot(combined_dt, aes(x=mg_L_TN, y=Area)) +  
  ggtitle("Total Nitrogen and Area Standard Curve") +  
  stat_poly_line(source = "original") +  
  stat_poly_eq(use_label=c("eq", "R2")) +  
  geom_point(data = subset(combined_dt, source == "original")) +  
  geom_smooth(method=lm , color="red", se=FALSE) +  
  
  geom_point(data = subset(combined_dt, source == "newepi"), color = "black",  
             shape = 23, size = 4, fill = "yellow") +  
  geom_text(data = G1Epi, aes(label = "Epilimnion"), hjust = -0.1, vjust = 1.2) +  
  
  geom_point(data = subset(combined_dt, source == "newhypo"), color = "black",  
             shape = 23, size = 4, fill = "yellow") +  
  geom_text(data = G1Hypo, aes(label = "Hypolimnion"), hjust = -0.1, vjust = -0.5) +  
  
  xlab("Total Nitrogen (mg/L)") +  
  ylab("Area")
```

Total Nitrogen and Area Standard Curve

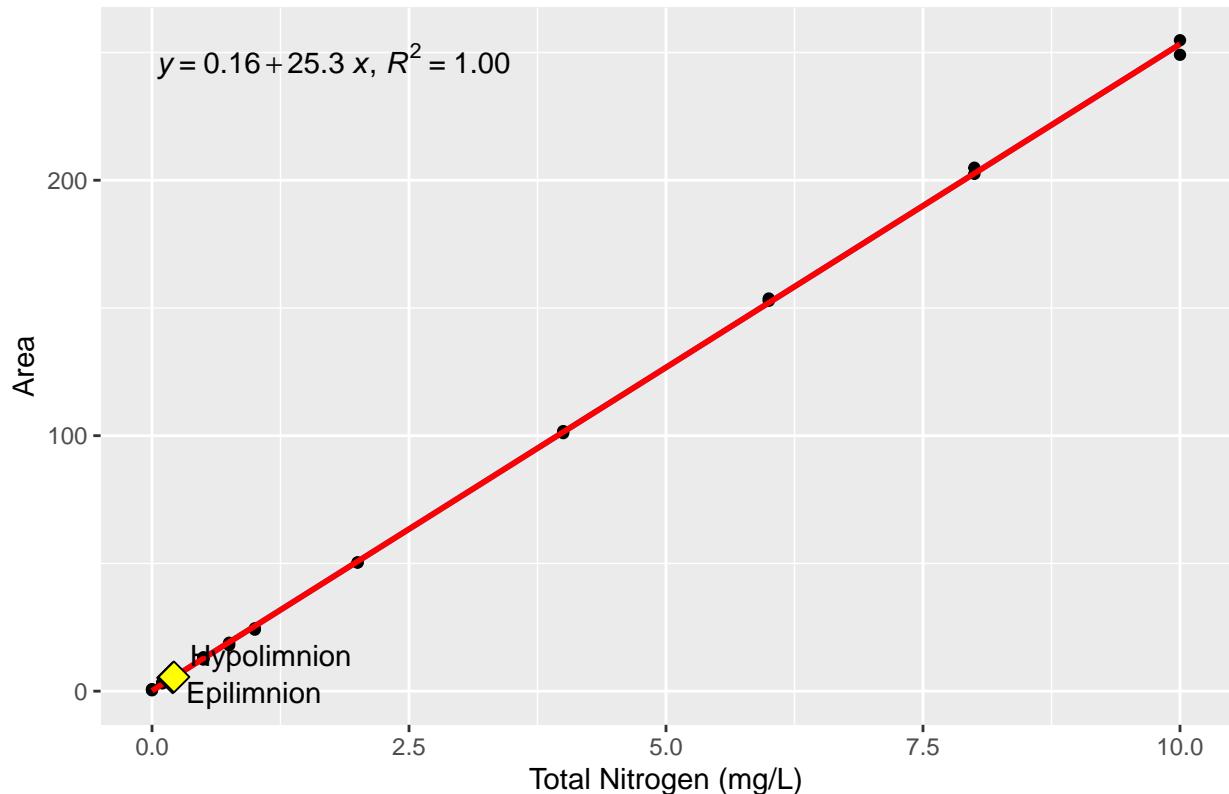


Figure 6: Standard curve of Area to total nitrogen relationship with epilimnion and hypolimnion values, data range restricted for clarity.

5.

```
###  
#5#  
###
```

```

F5allsynth <- read_csv("ALLTNsynth.csv")

colors <- c("Hypolimnion" = "blue", "Epilimnion" = "green")

ggplot(F5allsynth, aes(x = placeholder)) +
  ggtitle("Total Nitrogen Comparison Between Strata") +
  geom_line(aes(y = TNmgLhypo, color = "Hypolimnion"), size = 1) +
  geom_line(aes(y = TNmgLepi, color = "Epilimnion"), size = 1) +
  labs(x = "Cumulative Probability",
       y = "Total Nitrogen (mg/L)",
       color = "Legend") +
  scale_color_manual(values = colors) +
  theme(axis.text.x = element_blank())

```

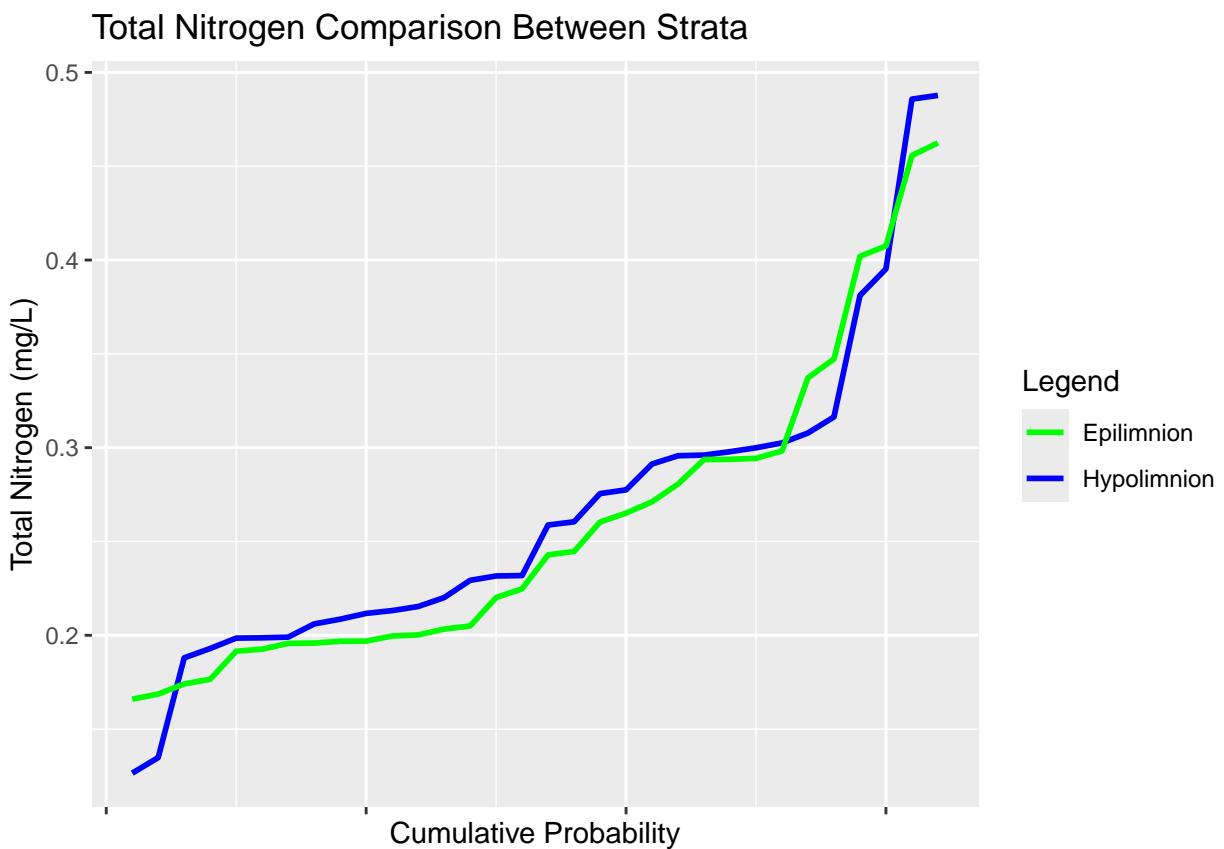


Figure 7: Comparison of total nitrogen between the epilimnion and hypolimnion depths

```

#theme(legend.position = "bottom")

```

6.

```

###  
#6#  
###  
Chla<-read.csv("Horsetooth_Chla_data_2024.csv")  
Chla <- Chla %>% filter(!is.na(Chla_ug_per_Liter))  
mean_Chla<-mean(Chla$Chla_ug_per_Liter)

```

```

Chla_Fig<-ggplot(Chla, aes(x = Chla_ug_per_Liter)) +
  geom_histogram(binwidth = 0.05, color = "black", fill = "skyblue") +
  geom_vline(aes(xintercept = mean_Chla), color = "red3", linetype = "dashed", linewidth = 1) +
  labs(
    title = "Distribution of Epilimnion Chlorophyll a Values", x = "Chlorophyll a (ug/L)", y = "Frequency"
  )
  theme_bw()
Chla_Fig

```

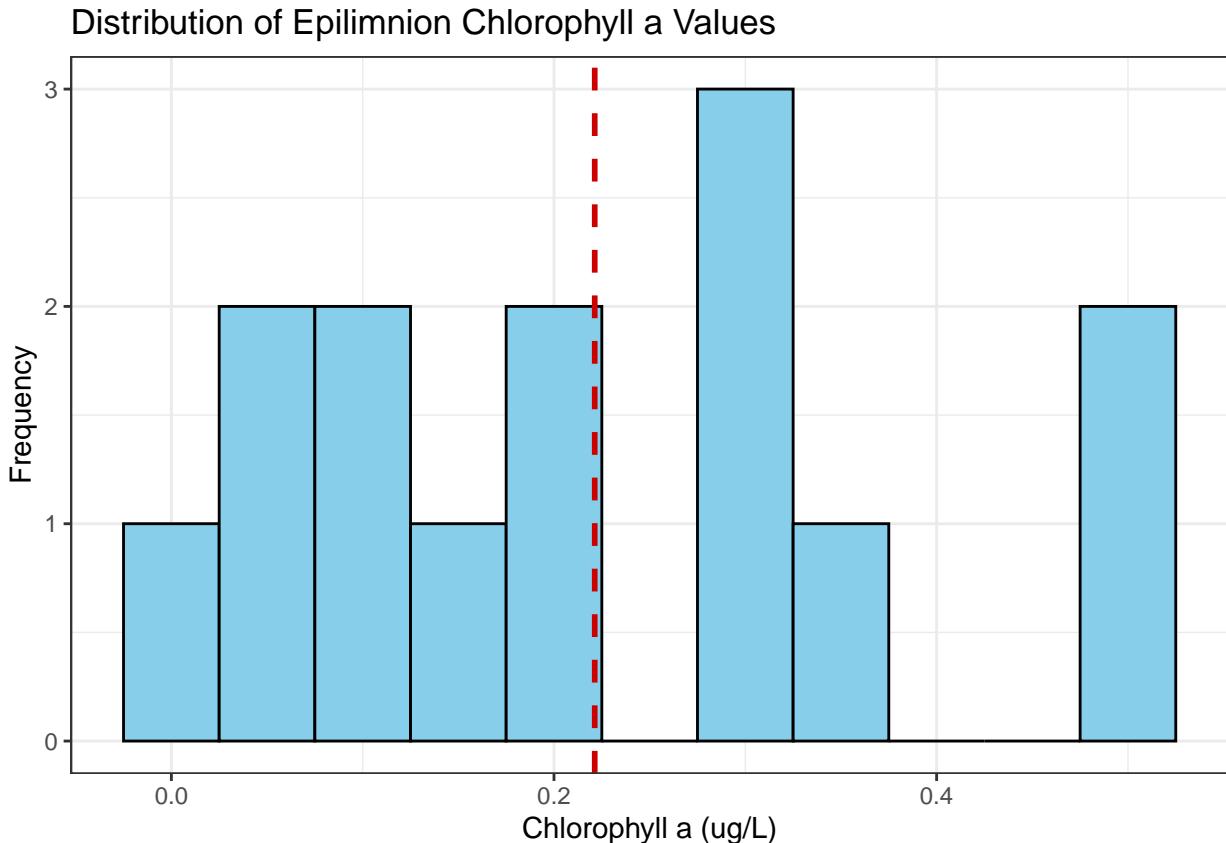


Figure 8: Distribution of chlorophyll a values, measured in ug/L, in the epilimnion for Horsetooth Reservoir 2024. Mean chlorophyll a demonstrated by the red line.

7.

```

#####
#7#
#####
DOC<-read.csv("Revised2_DOC_2024.csv")
DOC_no_outlier <- DOC[DOC$DOC != -0.8245, ]

DOC_Plot<-ggplot(DOC_no_outlier, aes(x = depth, y = DOC, fill = depth)) +
  geom_boxplot()+
  labs(title = "DOC Levels in Epilimnion vs Hypolimnion", x="Depth", y="Dissolved Organic Carbon (mg/L)")
  scale_fill_manual(values = c("coral3", "cornflowerblue")) +theme_bw()
DOC_Plot

```

8.

DOC Levels in Epilimnion vs Hypolimnion

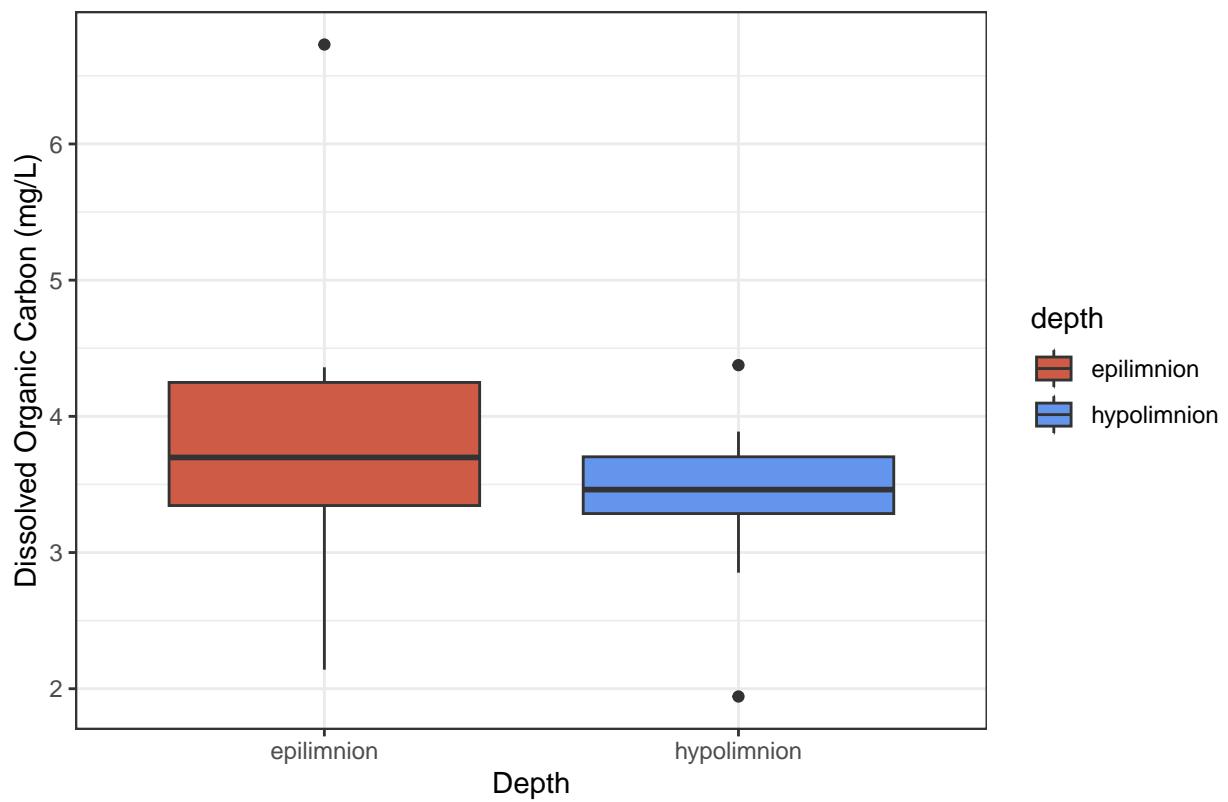


Figure 9: Dissolved organic carbon levels in the hypolimnion and epilimnion for Horsetooth Reservoir in 2024.

```

df <- read.csv("Phytoplankton.csv")
total_row <- df %>% filter(Slide == "TOTAL:")
df <- df %>% filter(Slide != "TOTAL:")
shannon_diversity <- function(counts) {
  proportions <- counts / sum(counts)
  proportions <- proportions[proportions > 0]
  -sum(proportions * log(proportions))
}
simpsons_index <- function(counts) {
  proportions <- counts / sum(counts)
  1 - sum(proportions^2)
}
results <- df %>%
  rowwise() %>%
  mutate(
    Shannon_Index = shannon_diversity(c_across(Diatoms:Unidentified.Phytoplankton)),
    Simpsons_Index = simpsons_index(c_across(Diatoms:Unidentified.Phytoplankton))
  ) %>%
  ungroup()
total_indices <- total_row %>%
  rowwise() %>%
  mutate(
    Shannon_Index = shannon_diversity(c_across(Diatoms:Unidentified.Phytoplankton)),
    Simpsons_Index = simpsons_index(c_across(Diatoms:Unidentified.Phytoplankton))
  )
combined_results <- bind_rows(results, total_indices)
plot_data <- combined_results %>%
  select(Slide, Shannon_Index, Simpsons_Index) %>%
  pivot_longer(cols = c(Shannon_Index, Simpsons_Index), names_to = "Index", values_to = "Value")

plot_data$Index <- recode(plot_data$Index,
                           "Shannon_Index" = "Shannon Index",
                           "Simpsons_Index" = "Simpson's Index")

ggplot(plot_data, aes(x = Slide, y = Value, fill = Index)) +
  geom_bar(stat = "identity", position = "dodge") +
  theme_minimal() +
  labs(
    title = "Phytoplankton Diversity Indices",
    x = "Slide",
    y = "Index Value",
    fill = "Index Type") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

```

9.

```

###  

#9#  

###  

secchi<-read.csv("HorsetoothSampling_SecchiDepth_2024.csv")
mean_depth<-mean(secchi$depth_m)
secchi$group_number <- str_replace(secchi$group_number, "Group_|group_|Group ", "")  

secchi_fig<-ggplot(secchi, aes(x = "", y = depth_m)) +  

  geom_boxplot(fill = "cadetblue3", color = "black") +

```

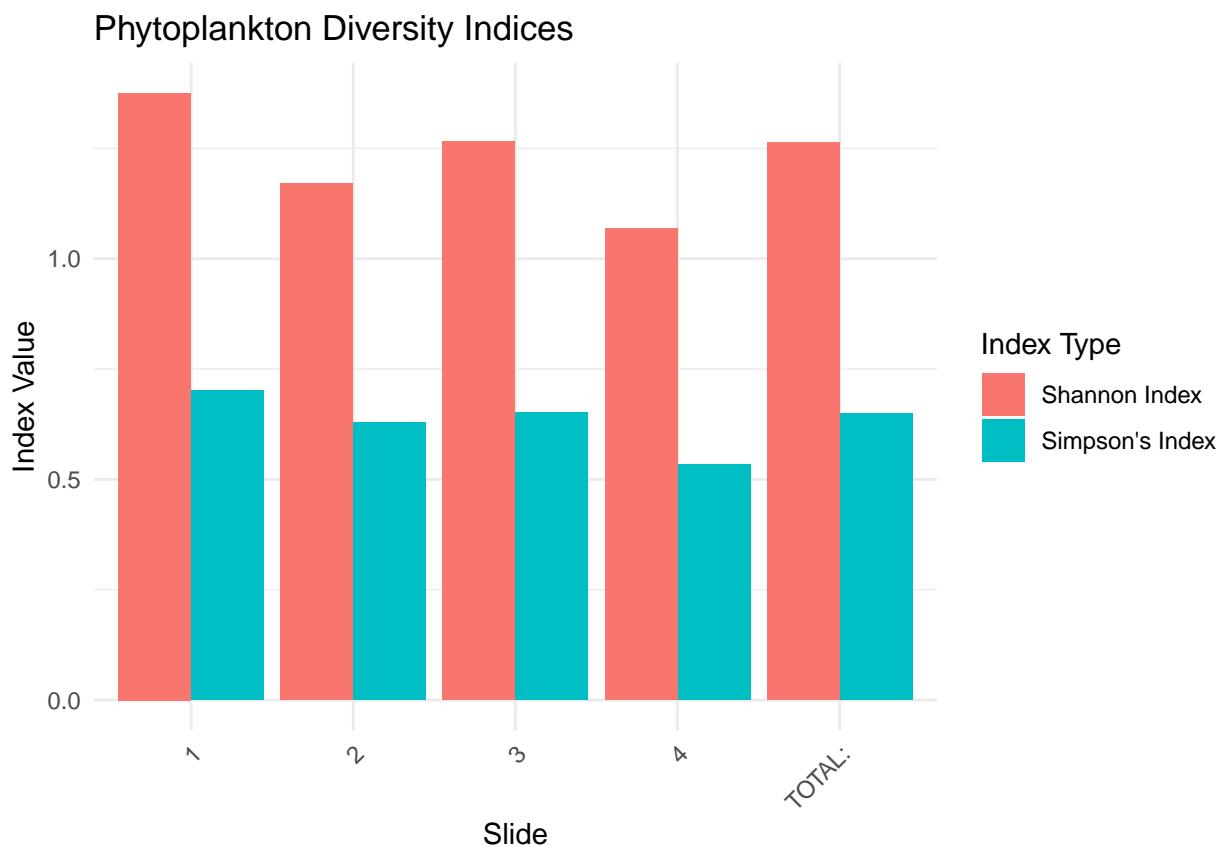


Figure 10: Phytoplankton diversity indices for Horsetooth Reservoir sample slides, including the total indices for all organisms counted.

```

geom_hline(aes(yintercept = mean_depth), color = "red2", linetype = "dashed", linewidth = 1) +
scale_y_reverse() +
labs(title = "Distribution of Secchi Depth", x = NULL,y = "Depth Below Surface (m)") +
theme_bw() +
theme(axis.ticks.x = element_blank(), axis.text.x = element_blank())

secchi_fig

```

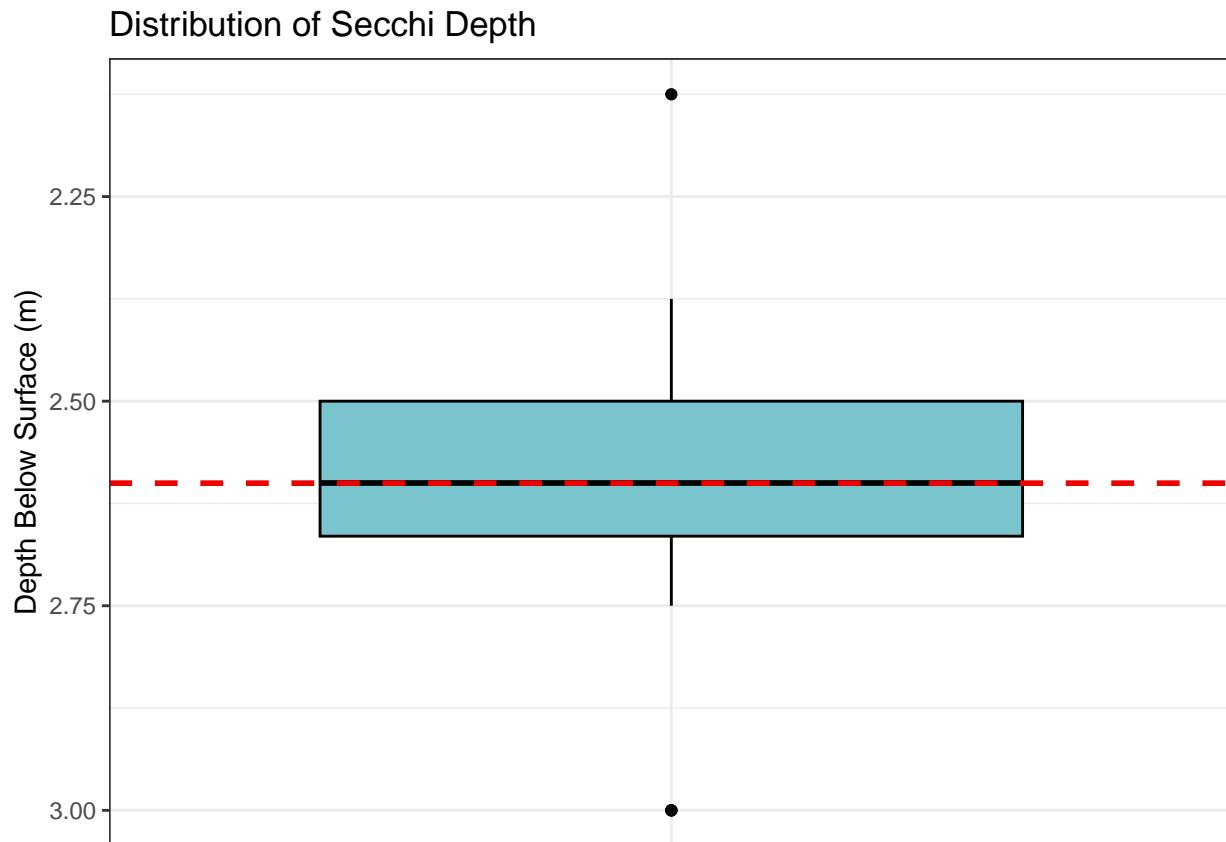


Figure 11: Secchi depth for Horsetooth Reservoir in 2024. Red dashed line representing mean secchi depth for all groups.

Results Interpretation

a.

1.

Figure 2 presents dissolved oxygen (DO) measured in both mg/L and percentage plotted against depth. The data points in green represent DO in mg/L, while those in blue show DO as a percentage. Both datasets exhibit a slight decline in DO with increased depth, indicative of lesser oxygen replenishment and reduced photosynthetic activity in deeper waters. This trend suggests a well-oxygenated environment near the surface with a gradual decrease downwards, yet the levels remain relatively high throughout, suggesting good overall water quality.

2.

Figure 3 shows the temperature profile against depth, marked by light blue points that denote temperature

in degrees Celsius. A noticeable trend is the thermal stratification, where surface temperatures are higher, gradually decreasing with depth—a typical pattern during warmer months in stratified bodies of water. This thermal layering is significant as it influences the mixing of water layers and the biological processes within the reservoir.

3.

Figure 4 maps pH values against depth, depicted with light green points. The pH levels are relatively stable across different depths, starting slightly neutral to alkaline at the surface and increasing marginally deeper down. The slight increase in pH with depth could be related to decreasing photosynthetic activity or the dissolution of minerals from sediments. The stability in pH values indicates a well-buffered system that does not experience drastic fluctuations, which is beneficial for maintaining a stable aquatic environment.

4.

Figure 5 and 6 describe the average Total Nitrogen for both epilimnion and hypolimnion collected by our group as determined by the Area Under Curve. These datum are shown plotted on the original standard curve ($R^2 = \sim 1$) used to identify the values, and show a slightly greater TN in the hypolimnion when compared to the epilimnion. The standard curve was created using a wide range of data, so the figure was restricted in range to provide visibility of the relevant data points.

5.

Figure 7 shows the overall difference between the total nitrogen of all collected epilimnion and hypolimnion values across all groups, sorted by value. With all runs flagged as non-synonymous or a calibration removed, the data trends show that the hypolimnion is most likely richer in total nitrogen. While the data range is extremely broad, suggesting a lot of error, the majority of the data points still describe a clear increase in TN in the hypolimnion. The discrepancies in the readings may have been due to different depths taken between groups, or error loading the tubes in the same way.

6.

Figure 8 shows chlorophyll a and has values ranging from 0.001 to 0.514 ug/L. The range for this data makes it difficult to conclude on any relationship with chlorophyll a. The mean value from all observations was 0.22 ug/L. It is possible that some of these measurements were impacted by the amount of time the chlorophyll was exposed to light. If the samples were exposed to light the chlorophyll would degrade possibly explaining the large range of chlorophyll a observed in the figure.

7.

Figure 9 displays dissolved organic carbon values for the epilimnion and hypolimnion. DOC values for the epilimnion trended higher than the hypolimnion. Additionally, the epilimnion had a greater range of DOC measurements when comparing to the hypolimnion. In the original data there was an outlier of -0.8245 which was excluded because it makes little sense in the context of measuring DOC.

8.

Figure 10 the diversity of phytoplankton sampled from Horsetooth Reservoir, represented through the Shannon Diversity Index and Simpson's 1-D Index for individual slides and a combined "TOTAL" value that included every organism counted between all slides. Both indices highlight key aspects of phytoplankton diversity, with Shannon focusing on richness and evenness, while Simpson's Index emphasizes the dominance of certain groups. Across individual slides, diversity values vary, suggesting heterogeneity in phytoplankton composition. Some slides show higher diversity, indicative of an even distribution of species, while others exhibit lower values, reflecting dominance by specific phytoplankton groups.

9.

Figure 11 shows the distribution of secchi depth across different groups. All observations appear to be within ~ 0.5 m of the calculated mean, 2.6 m. Based on the plot similar measurements of depth were observed across groups resulting in a trend of secchi depth around 2.6 m.

b. Comment on the phytoplankton diversity value calculated

For some slides, the Simpson Index is notably higher than Shannon's, suggesting the presence of a few dominant phytoplankton groups skewing the overall diversity. The combined "TOTAL" row represents the diversity of all organisms counted and demonstrates relatively balanced diversity indices, indicating a stable overall ecosystem diversity in the reservoir.

The calculated diversity indices reveal moderate Shannon values across slides, suggesting a reasonably diverse phytoplankton community, albeit with some species potentially dominating the ecosystem. Similarly, the relatively high Simpson values indicate that dominant species play a significant role in shaping the community structure. The observed variability across slides may reflect localized environmental factors or sampling differences. Overall, the diversity indices point to a dynamic and moderately diverse phytoplankton ecosystem within Horsetooth Reservoir, with potential implications for its ecological health and stability.

Discussion

a.

There appears to be differences in dissolved organic carbon (DOC) between the hypolimnion and epilimnion. As Figure 9 demonstrates, the epilimnion had a greater variability of dissolved organic carbon values and this layer also trended higher in terms of mg/L of DOC. According to Houser, Bade, and Cole (2003), these higher values of DOC are due to terrestrial inputs running into the reservoir and the biological activity occurring in this layer (225). The epilimnion is warmer and receives more sunlight resulting in microbial activity that can break down carbon and more photosynthesis occurs here. The hypolimnion can have lower values of DOC because organisms use it as it sinks in the water column and as it reaches the lower depths, the carbon can undergo sedimentation. There were some outlier values still included in this graph because they may represent natural variability within the sampled environment or reflect specific events such as episodic inputs from surface runoff, biological activity, or sediment interactions. Including these values yields a better understanding of the reservoir and the measurement techniques used to gather the data.

b.

The conclusion drawn from Fig 5 is that the hypolimnion was recorded to have higher TN concentrations on average. While many of these data points were likely erroneous due to many potential factors, the trend appears largely consistent. The hypolimnion would be more likely to contain higher dissolved inorganic nitrogen, as the nitrogen in the mixed layer will be consumed by phytoplankton, and any remaining DIN will sink to the hypolimnion, where there are no phytoplankton to utilize it until the next turnover.

c.

Horsetooth Reservoir, located near Fort Collins, Colorado, exhibits water quality parameters that are generally consistent with other reservoirs in the Colorado Front Range. Horsetooth Reservoir maintains high dissolved oxygen levels, often exceeding 95% saturation near the surface, which is typical for well-oxygenated reservoirs in the region. Surface water temperatures in the reservoir during late summer can reach around 21°C, similar to other reservoirs in the area. The pH levels in Horsetooth Reservoir range from 7.3 to 7.5, indicating neutral to slightly alkaline conditions, which is common among reservoirs in the Colorado Front Range. Conductivity measurements are approximately 70 µS/cm, reflecting low to moderate mineral content, comparable to other regional reservoirs. Chlorophyll-a concentrations, indicative of algal biomass, are generally low in Horsetooth Reservoir, suggesting oligotrophic to mesotrophic conditions, similar to other reservoirs in the area.

Overall, Horsetooth Reservoir's water quality parameters align closely with those of other reservoirs in the Colorado Front Range, reflecting similar environmental conditions and management practices.

d.

The similarities in water quality between Horsetooth Reservoir and other nearby reservoirs can be traced back to some common limnological characteristics. These reservoirs are all influenced by the same general climate, with similar rainfall patterns, sunlight, and temperatures, which play a major role in regulating water

quality. The geology of the area is another big factor: the streams and rivers feeding these reservoirs carry minerals and nutrients from similar types of rocks and soils, resulting in comparable pH and conductivity levels. The shared nutrient inputs, whether they're from natural sources or human activities like agriculture and urban runoff, contribute to the somewhat uniform chlorophyll-a concentrations, which suggest moderate algal growth.

On the other hand, some differences in water quality parameters, like how temperature and oxygen levels change with depth, can be explained by physical factors such as the size and shape of the reservoirs. Deeper reservoirs tend to have more pronounced temperature layering, while shallower ones might mix more evenly. The time water spends in a reservoir, known as residence time, also matters—a shorter residence time means nutrients get flushed out faster, potentially lowering algal growth. Human activities around each reservoir, like how land is used or developed, can also vary, leading to different levels of nutrients and minerals being washed into the water. All these factors combine to create both the similarities and the unique characteristics we see in different reservoirs.

e.

Our group (group 1) had many limitations when it came to our samples and measurements from them. These issues speak to the need for labels to be durable in a water environment and sufficiently labeled in terms of writing and content clarity. Although this was different in a class setting, it would also be important to track your samples from lake to lab to make sure all necessary samples were tested. This could have avoided some of the confusion our group experienced. Additionally, when our data is missing or unclear because of labeling mistakes, the quality of whole class data decreases when applicable.

In many of the samples, there were outlier points, some of which had to be removed based on the context of what was being measured. An example was in dissolved organic carbon where a negative value was removed. Some of these outliers could also speak to a reservoir not acting like a traditional lake. There may be unexpected measurements due to anthropogenic influences, the shape of the reservoir, and operational management choices. The stratification of the lake, which can change based on wind events and shifts in temperature, also can affect these readings, especially when comparing epilimnion to hypolimnion. If this stratification is not strong then measurement readings can be less significant.

More likely, wide data ranges could be due to user errors in field equipment. When each person does something slightly different than the next, or if they don't recalibrate equipment—such as rinsing equipment from the last group—data can become questionable in its accuracy. In our reservoir sampling, the boat we were on was moving around. This shifting impacted each group's measurements which most likely were taken at slightly different areas. An additional sampling error was in the chlorophyll samples where samples are very sensitive to light. These samples should have been folded and protected from the light, but many were not. Further, more water could have been pushed through the filter. With practice and more time to sample, equipment issues could easily be amended for future sampling campaigns.

Conclusion

Based on the information gathered from Horsetooth Reservoir the trophic state appears to be mesotrophic. The observed secchi depth mean for the class is 2.6 m. According to New Hampshire Department of Environmental Services (2019, p.12) this mean value corresponds to a mesotrophic lake where 1.8-4 m secchi depth is categorized as a mesotrophic lake. Further, the bottom of the lake has dissolved oxygen levels of 0.01-0.02 mg/L indicating anoxic conditions at the bottom of the lake while the top of the lake had levels around 7 mg/L. The stratification of the lake indicates that species are using the oxygen for respiration pointing to a lake that is more productive. This supports the conclusion of the lake being mesotrophic.

The nitrogen levels observed for our group were around 0.2 mg/L. According to the Massachusetts Water Watch Partnership <0.3 mg/L is associated with an oligotrophic lake (2016). Due to the lack of high levels of nitrogen in this reservoir, this suggests a healthier lake. If more nitrogen was present the lake would be eutrophic indicating higher productivity possibly in the form of harmful algal growth. This lower amount of nitrogen allows productivity, without it becoming harmful to the lake ecosystem. The chlorophyll a level was low when considering lake ecosystems pointing to an oligotrophic lake, but these values observed should be

taken with skepticism due to errors in sampling techniques and exposure to light. Even so, the chlorophyll a level tells there is not an overabundance of phytoplankton in the water providing support that this reservoir is relatively healthy. The health of this ecosystem is supported through the thriving communities of zooplankton and phytoplankton captured. Species of daphnia, rotifers, and copepods were spotted showing that one species does not dominate the water. Moreover, zooplankton are sensitive to pollutants, particularly excess nutrients. A diverse community suggests a variety of food sources, proper nutrient cycling, and a stable food web.

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Contribution Roles

Ben: Introduction; Results: d 4,5; Discussion 5 b

Alexia: Methods a; Results: d 1,2,3,8; 4b; Discussion 5: c,d

Maisie: Methods b; Results: d 6, 7, 9; Discussion 5 a, e; Conclusion

Appendix

```
knitr::opts_chunk$set(echo = TRUE)
library(knitr)
library(tidyverse)
library(broom)
library(dplyr)
library(stringr)
library(ggplot2)
library(ggthemes)
library(readr)
library(ggpmisc)

####
#1#
###
G01 <- read_csv("Group01_09062024_profiledata.csv")
G01 %>%
  filter(!is.na(do_percent) & !is.na(do_mgL)) %>%
  ggplot() +
  geom_point(aes(x = do_mgL, y = z_m, color = "DO (mg/L)", size = 3) +
  geom_point(aes(x = do_percent, y = z_m, color = "DO (%)", size = 4) +
  theme_few() +
  labs(
    title = "Oxygen Profile with DO percent and mg/L",
    x = 'DO (mg/L)',
    y = 'Depth (m)',
    color = NULL
  ) +
  scale_y_reverse(expand = c(0.015, 0)) +
  theme(text = element_text(size = 10))

###
#2#
###
G01 <- read_csv("Group01_09062024_profiledata.csv")

G01 %>%
  filter(!is.na(temp_c) & !is.na(z_m) & group == "Group_1") %>%
  ggplot(aes(x = temp_c, y = z_m)) +
  geom_point(size = 4, color = "lightblue") +
  theme_few() +
  labs(
    x = 'Temperature (°C)',
    y = 'Depth (m)',
    title = "Temperature Profile in Horsetooth Reservoir"
  ) +
  scale_y_reverse(expand = c(0.015, 0)) +
  theme(text = element_text(size = 10))

###
```

```

#3#
###  

G01 <- read_csv("Group01_09062024_profiledata.csv")  

G01 %>%
  filter(!is.na(ph) & !is.na(z_m) & group == "Group_1") %>%
  ggplot(aes(x = ph, y = z_m)) +
  geom_point(size = 4, color = "lightgreen") +
  theme_few() +
  labs(
    x = 'PH',
    y = 'Depth (m)', title = "pH Profile of Horsetooth Reservoir")+
  scale_y_reverse(expand = c(0.015, 0)) +
  theme(text = element_text(size = 10))  

###  

#4#
###  

StandardData <- read_csv("ESS474Fall2024stdcurvedata-2.csv")
G1Epi <- read_csv("Group1Epi.csv")
G1Hypo <- read_csv("Group1Hypo.csv")  

combined_dt <- rbind(
  mutate(StandardData, source = "original"),
  mutate(G1Epi, source = "newepi"),
  mutate(G1Hypo, source = "newhypo"))
)  

ggplot(combined_dt, aes(x=mg_L_TN, y=Area)) +
  ggtitle("Total Nitrogen and Area Standard Curve") +
  coord_cartesian(xlim = c(0, 0.25), ylim = c(0, 6.485))+
  stat_poly_line(source = "original") +
  stat_poly_eq(use_label(c("eq", "R2")))) +
  geom_point(data = subset(combined_dt, source == "original")) +
  geom_smooth(method=lm , color="red", se=FALSE) +  

  geom_point(data = subset(combined_dt, source == "newepi"), color = "black",
             shape = 23, size = 4, fill = "yellow")+
  geom_text(data = G1Epi, aes(label = "Epilimnion"), hjust = -0.1, vjust = 1.2)+  

  geom_point(data = subset(combined_dt, source == "newhypo"), color = "black",
             shape = 23, size = 4, fill = "yellow")+
  geom_text(data = G1Hypo, aes(label = "Hypolimnion"), hjust = -0.1, vjust = -0.5)+  

  xlab("Total Nitrogen (mg/L)")+
  ylab("Area")  

ggplot(combined_dt, aes(x=mg_L_TN, y=Area)) +
  ggtitle("Total Nitrogen and Area Standard Curve") +
  stat_poly_line(source = "original") +

```

```

stat_poly_eq(use_label(c("eq", "R2")))+  

geom_point(data = subset(combined_dt, source == "original"))+  

geom_smooth(method=lm , color="red", se=FALSE) +  

geom_point(data = subset(combined_dt, source == "newepi"), color = "black",  

shape = 23, size = 4, fill = "yellow") +  

geom_text(data = G1Epi, aes(label = "Epilimnion"), hjust = -0.1, vjust = 1.2) +  

geom_point(data = subset(combined_dt, source == "newhypo"), color = "black",  

shape = 23, size = 4, fill = "yellow") +  

geom_text(data = G1Hypo, aes(label = "Hypolimnion"), hjust = -0.1, vjust = -0.5) +  

xlab("Total Nitrogen (mg/L)") +  

ylab("Area")  

###  

#5#  

###  

F5allsynth <- read_csv("ALLTNsynth.csv")  

colors <- c("Hypolimnion" = "blue", "Epilimnion" = "green")  

ggplot(F5allsynth, aes(x = placeholder)) +  

ggtitle("Total Nitrogen Comparison Between Strata") +  

geom_line(aes(y = TNmgLhypo, color = "Hypolimnion"), size = 1) +  

geom_line(aes(y = TNmgLepi, color = "Epilimnion"), size = 1) +  

  labs(x = "Cumulative Probability",  

       y = "Total Nitrogen (mg/L)",  

       color = "Legend") +  

  scale_color_manual(values = colors) +  

theme(axis.text.x = element_blank())  

#theme(legend.position = "bottom")  

###  

#6#  

###  

Chla<-read.csv("Horsetooth_Chla_data_2024.csv")  

Chla <- Chla %>% filter(!is.na(Chla_ug_per_Liter))  

mean_Chla<-mean(Chla$Chla_ug_per_Liter)  

Chla_Fig<-ggplot(Chla, aes(x = Chla_ug_per_Liter)) +  

  geom_histogram(binwidth = 0.05, color = "black", fill = "skyblue") +  

  geom_vline(aes(xintercept = mean_Chla), color = "red3", linetype = "dashed", linewidth = 1) +  

  labs(  

    title = "Distribution of Epilimnion Chlorophyll a Values", x = "Chlorophyll a (ug/L)", y = "Frequency")  

  theme_bw()  

Chla_Fig  

###  

#7#

```

```

####
DOC<-read.csv("Revised2_DOC_2024.csv")
DOC_no_outlier <- DOC[DOC$DOC != -0.8245, ]

DOC_Plot<-ggplot(DOC_no_outlier, aes(x = depth, y = DOC, fill = depth)) +
  geom_boxplot()+
  labs(title = "DOC Levels in Epilimnion vs Hypolimnion", x="Depth", y="Dissolved Organic Carbon (mg/L)")
scale_fill_manual(values = c("coral3", "cornflowerblue")) +theme_bw()
DOC_Plot

df <- read.csv("Phytoplankton.csv")
total_row <- df %>% filter(Slide == "TOTAL:")
df <- df %>% filter(Slide != "TOTAL:")
shannon_diversity <- function(counts) {
  proportions <- counts / sum(counts)
  proportions <- proportions[propportions > 0]
  -sum(proportions * log(proportions))
}
simpsons_index <- function(counts) {
  proportions <- counts / sum(counts)
  1 - sum(proportions^2)
}
results <- df %>%
  rowwise() %>%
  mutate(
    Shannon_Index = shannon_diversity(c_across(Diatoms:Unidentified.Phytoplankton)),
    Simpsons_Index = simpsons_index(c_across(Diatoms:Unidentified.Phytoplankton))
  ) %>%
  ungroup()
total_indices <- total_row %>%
  rowwise() %>%
  mutate(
    Shannon_Index = shannon_diversity(c_across(Diatoms:Unidentified.Phytoplankton)),
    Simpsons_Index = simpsons_index(c_across(Diatoms:Unidentified.Phytoplankton))
  )
combined_results <- bind_rows(results, total_indices)
plot_data <- combined_results %>%
  select(Slide, Shannon_Index, Simpsons_Index) %>%
  pivot_longer(cols = c(Shannon_Index, Simpsons_Index), names_to = "Index", values_to = "Value")

plot_data$Index <- recode(plot_data$Index,
                           "Shannon_Index" = "Shannon Index",
                           "Simpsons_Index" = "Simpson's Index")

ggplot(plot_data, aes(x = Slide, y = Value, fill = Index)) +
  geom_bar(stat = "identity", position = "dodge") +
  theme_minimal() +
  labs(
    title = "Phytoplankton Diversity Indices",
    x = "Slide",

```

```

y = "Index Value",
  fill = "Index Type") +
theme(axis.text.x = element_text(angle = 45, hjust = 1))

###  

#9#  

###  

secchi<-read.csv("HorsetoothSampling_SecchiDepth_2024.csv")
mean_depth<-mean(secchi$depth_m)
secchi$group_number <- str_replace(secchi$group_number, "Group_|group_|Group ", "")  

secchi_fig<-ggplot(secchi, aes(x = "", y = depth_m)) +
  geom_boxplot(fill = "cadetblue3", color = "black") +
  geom_hline(aes(yintercept = mean_depth), color = "red2", linetype = "dashed", linewidth = 1) +
  scale_y_reverse() +
  labs(title = "Distribution of Secchi Depth", x = NULL,y = "Depth Below Surface (m)") +
  theme_bw() +
  theme(axis.ticks.x = element_blank(), axis.text.x = element_blank())

secchi_fig

```