

Assignment 5: Data Visualization

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OVERVIEW

This exercise accompanies the lessons in Environmental Data Analytics on Data Visualization

Directions

1. Change “Student Name” on line 3 (above) with your name.
2. Work through the steps, **creating code and output** that fulfill each instruction.
3. Be sure to **answer the questions** in this assignment document.
4. When you have completed the assignment, **Knit** the text and code into a single PDF file.
5. After Knitting, submit the completed exercise (PDF file) to the dropbox in Sakai. Add your last name into the file name (e.g., “Salk_A05_DataVisualization.Rmd”) prior to submission.

The completed exercise is due on Tuesday, February 11 at 1:00 pm.

Set up your session

1. Set up your session. Verify your working directory and load the tidyverse and cowplot packages. Upload the NTL-LTER processed data files for nutrients and chemistry/physics for Peter and Paul Lakes (tidy and gathered) and the processed data file for the Niwot Ridge litter dataset.
2. Make sure R is reading dates as date format; if not change the format to date.

```
#1
getwd()

## [1] "/Users/emilymcnamara/Desktop/Env Data Analytics/Environmental_Data_Analytics_2020"

library(tidyverse)

## -- Attaching packages -----
## v ggplot2 3.2.1      v purrr   0.3.3
## v tibble  2.1.3      v dplyr  0.8.3
## v tidyr   1.0.0      v stringr 1.4.0
## v readr   1.3.1      v forcats 0.4.0

## -- Conflicts -----
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

library(cowplot)

##
## *****
## Note: As of version 1.0.0, cowplot does not change the
## default ggplot2 theme anymore. To recover the previous
```

```

## behavior, execute:
## theme_set(theme_cowplot())

## *****

library(viridis)

## Loading required package: viridisLite

library(RColorBrewer)
library(colormap)

PeterPaul.chem.nutrients <-
  read.csv("./Data/Processed/NTL-LTER_Lake_Chemistry_Nutrients_PeterPaul_Processed.csv")

PeterPaul.chem.nutrients.gathered <-
  read.csv("./Data/Processed/NTL-LTER_Lake_Nutrients_PeterPaulGathered_Processed.csv")

NIWO.Litter <-
  read.csv("./Data/Processed/NEON_NIWO_Litter_mass_trap_Processed.csv")

#2
class(PeterPaul.chem.nutrients$sampleddate)

## [1] "factor"

PeterPaul.chem.nutrients$sampleddate <-
  as.Date(PeterPaul.chem.nutrients$sampleddate, format = "%Y-%m-%d")
class(PeterPaul.chem.nutrients$sampleddate)

## [1] "Date"

class(PeterPaul.chem.nutrients.gathered$sampleddate)

## [1] "factor"

PeterPaul.chem.nutrients.gathered$sampleddate <-
  as.Date(PeterPaul.chem.nutrients.gathered$sampleddate, format = "%Y-%m-%d")
class(PeterPaul.chem.nutrients.gathered$sampleddate)

## [1] "Date"

class(NIWO.Litter$collectDate)

## [1] "factor"

NIWO.Litter$collectDate <-
  as.Date(NIWO.Litter$collectDate, format = "%Y-%m-%d")
class(NIWO.Litter$collectDate)

## [1] "Date"

```

Define your theme

3. Build a theme and set it as your default theme.

```

mytheme <- theme_classic(base_size = 14) +
  theme(axis.text = element_text(color = "black"),
        legend.position = "top")

```

```
theme_set(mytheme)
```

Create graphs

For numbers 4-7, create ggplot graphs and adjust aesthetics to follow best practices for data visualization. Ensure your theme, color palettes, axes, and additional aesthetics are edited accordingly.

4. [NTL-LTER] Plot total phosphorus by phosphate, with separate aesthetics for Peter and Paul lakes. Add a line of best fit and color it black. Adjust your axes to hide extreme values.

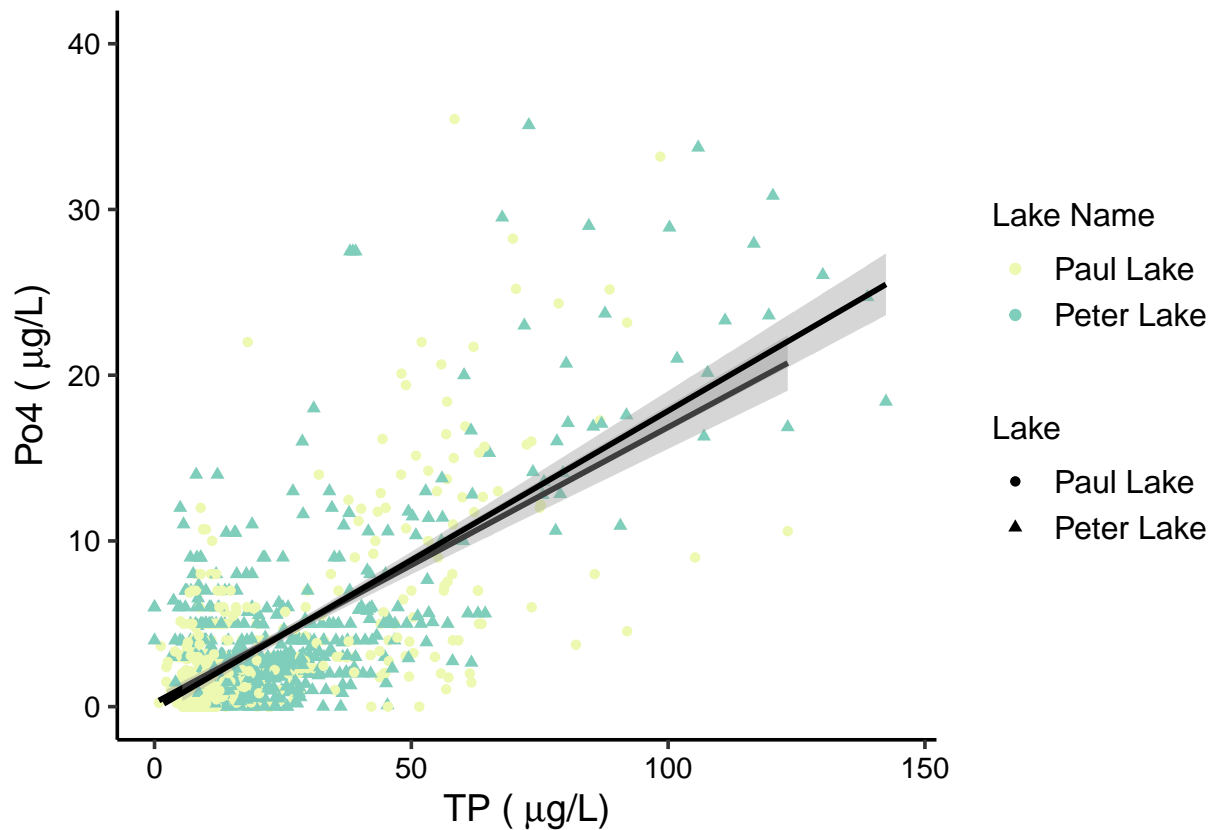
```
# Graph of Total Phosphorus by Phosphate for Peter and Paul Lakes
```

```
NTL.TP.PO4 <-  
ggplot(PeterPaul.chem.nutrients, aes(x = tp_ug, y = po4, color = lakename, shape = lakename)) +  
  geom_point() +  
  labs(x = expression(paste("TP ( ", mu, "g/L)")),  
       y = expression(paste("Po4 ( ", mu, "g/L)")),  
       color = "Lake Name", shape = "Lake") +  
  scale_color_brewer(palette = "YlGnBu") +  
  scale_y_continuous(limits = c(0,40)) +  
  scale_x_continuous(limits = c(0, 145)) +  
  geom_smooth(method='lm', formula= y~x, color = "black") +  
  theme(legend.position = "right",  
        legend.text = element_text(size = 12), legend.title = element_text(size = 12))  
print(NTL.TP.PO4)
```

```
## Warning: Removed 21950 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 21950 rows containing missing values (geom_point).
```

```
## Warning: Removed 1 rows containing missing values (geom_smooth).
```

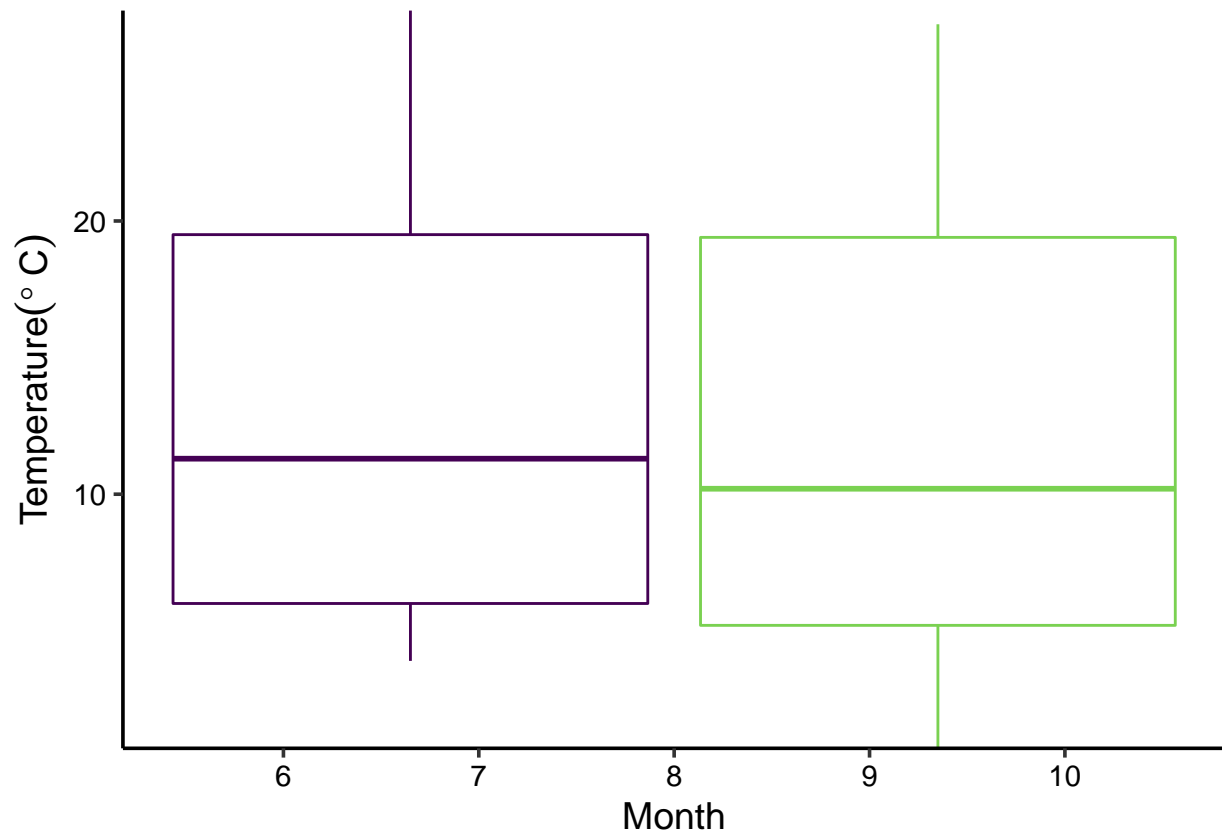


5. [NTL-LTER] Make three separate boxplots of (a) temperature, (b) TP, and (c) TN, with month as the x axis and lake as a color aesthetic. Then, create a cowplot that combines the three graphs. Make sure that only one legend is present and that graph axes are aligned.

```
# Temperature Boxplot

Temp.Boxplot <-
  ggplot(PeterPaul.chem.nutrients, aes(x = month, y = temperature_C, color = lakename)) +
  geom_boxplot() +
  labs(x = expression(paste("Month")),
       y = expression(paste("Temperature" (degree-C))), color = "Lake") +
  scale_y_continuous(expand = c(0,0)) +
  scale_color_viridis(discrete = TRUE, option = "viridis", end = 0.8) +
  theme(legend.position = "none")
print(Temp.Boxplot)
```

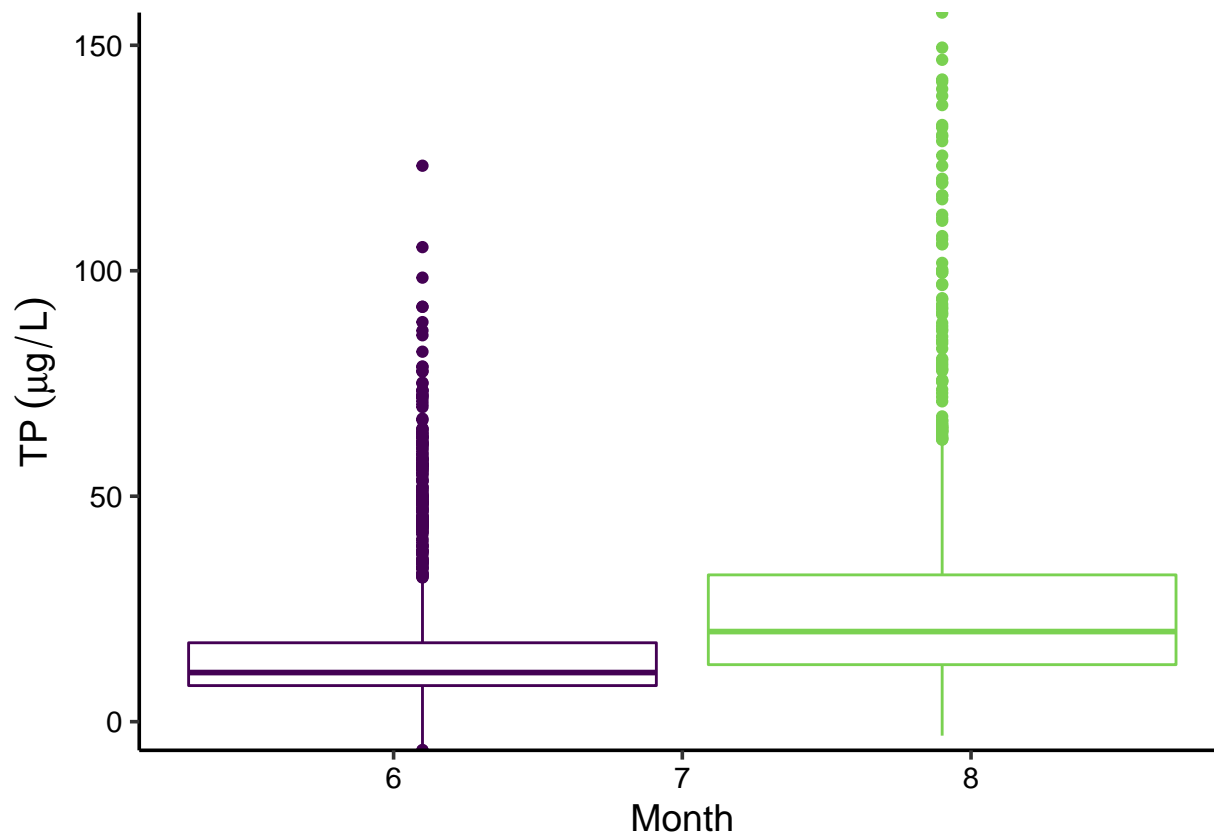
```
## Warning: Removed 3566 rows containing non-finite values (stat_boxplot).
```



```
# TP Boxplot
```

```
TP.Boxplot <-
  ggplot(PeterPaul.chem.nutrients, aes(x = month, y = tp_ug, color = lakename)) +
  geom_boxplot() +
  labs(x = expression(paste("Month")),
       y = expression(paste("TP" ~ (mu*g / L))), color = "Lake") +
  scale_y_continuous(expand = c(0,0)) +
  scale_color_viridis(discrete = TRUE, option = "viridis", end = 0.8) +
  theme(legend.position = "none")
print(TP.Boxplot)
```

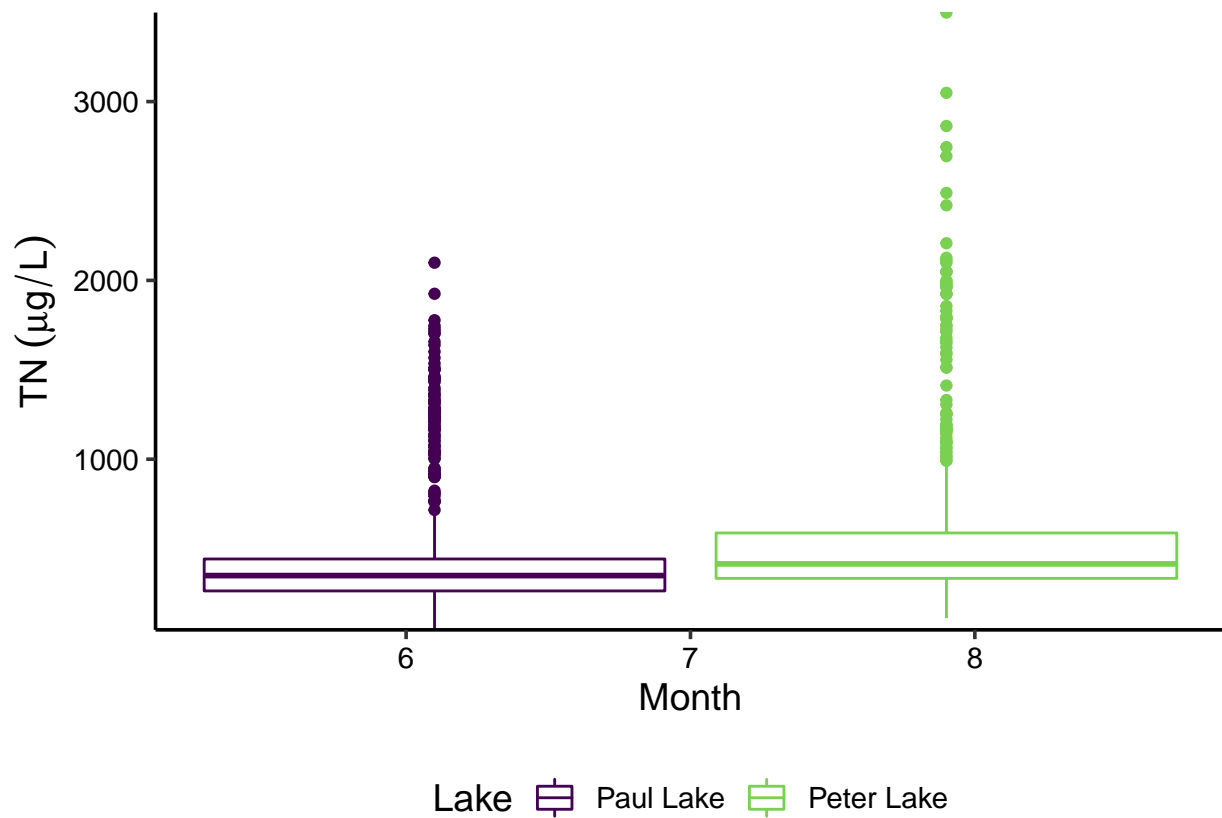
```
## Warning: Removed 20729 rows containing non-finite values (stat_boxplot).
```



```
# TN Boxplot
```

```
TN.Boxplot <-  
  ggplot(PeterPaul.chem.nutrients, aes(x = month, y = tn_ug, color = lakename)) +  
  geom_boxplot() +  
  labs(x = expression(paste("Month")),  
       y = expression(paste("TN" ~ (mu*g / L))), color = "Lake") +  
  scale_y_continuous(expand = c(0,0)) +  
  scale_color_viridis(discrete = TRUE, option = "viridis", end = 0.8) +  
  theme(legend.position = "bottom")  
print(TN.Boxplot)
```

```
## Warning: Removed 21583 rows containing non-finite values (stat_boxplot).
```



3 Graphs Combined

```
three.plots <- plot_grid(Temp.Boxplot, TP.Boxplot, TN.Boxplot, labels = c('Temp', 'TP', 'TN'),
                          label_size = 10, align = "vh", ncol = 1)
```

```
## Warning: Removed 3566 rows containing non-finite values (stat_boxplot).
```

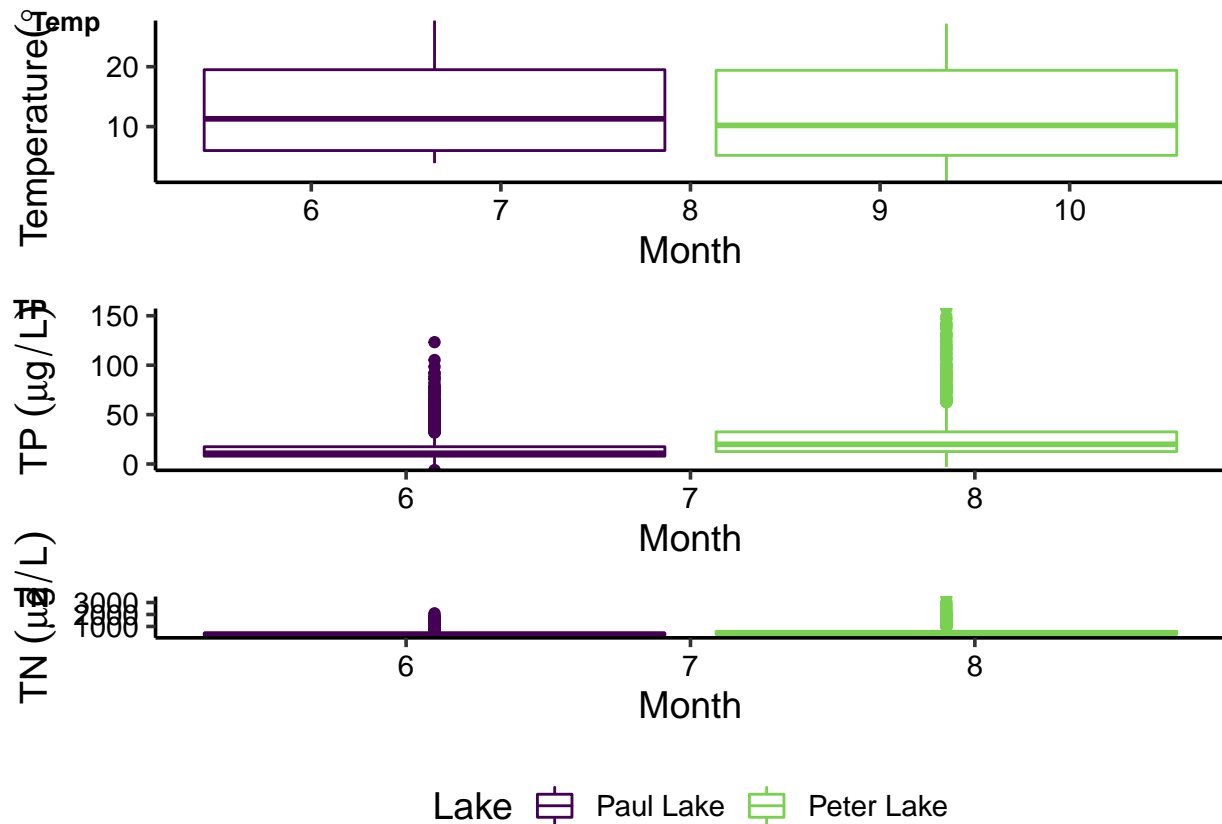
```
## Warning: Removed 20729 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 21583 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Graphs cannot be horizontally aligned unless the axis parameter is set.
```

```
## Placing graphs unaligned.
```

```
print(three.plots)
```



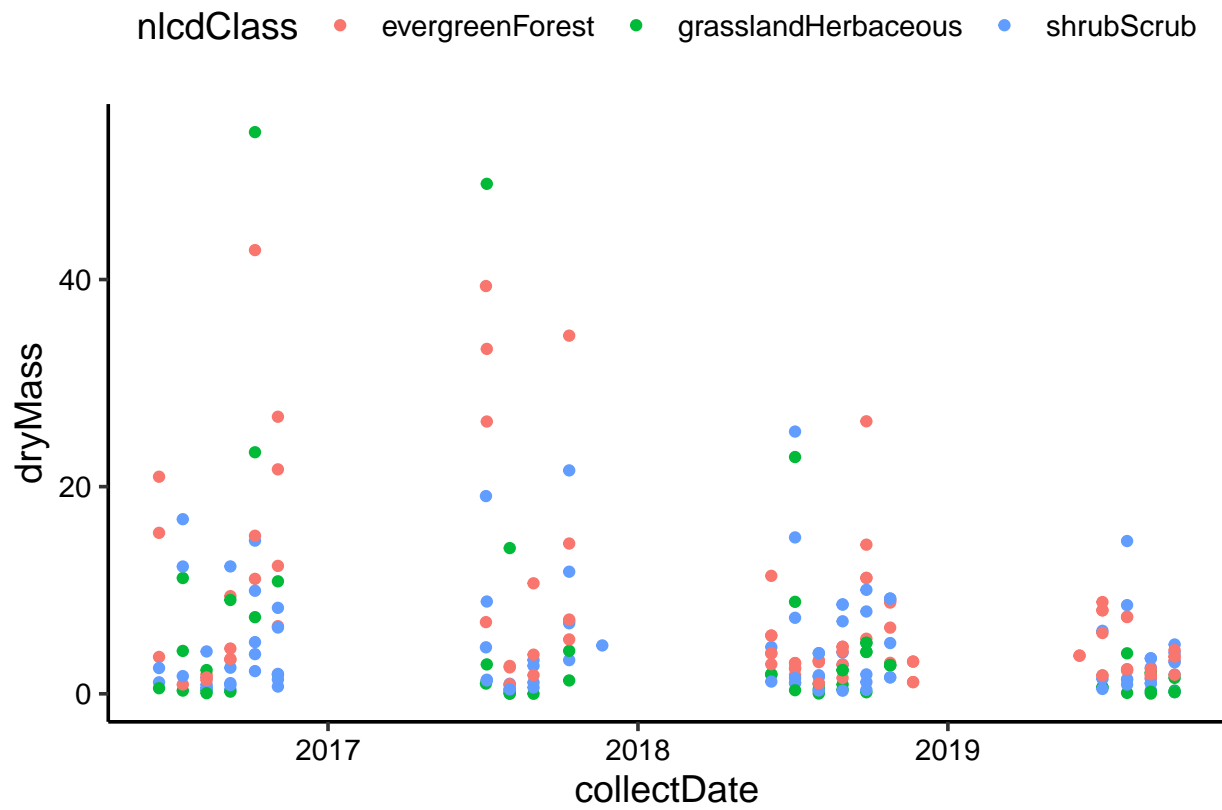
Question: What do you observe about the variables of interest over seasons and between lakes?

Answer: In the summer, Paul Lake has slightly higher temperatures, but lower TP and TN concentrations. The lower TP and TN concentrations in Paul Lake could be due to the fact that samples from Paul Lake were taken in between May and June when the temperature in the lake was higher whereas samples from Peter Lake were taken in July and August when the average temperature was lower than Paul Lake.

6. [Niwot Ridge] Plot a subset of the litter dataset by displaying only the “Needles” functional group. Plot the dry mass of needle litter by date and separate by NLCD class with a color aesthetic. (no need to adjust the name of each land use)
7. [Niwot Ridge] Now, plot the same plot but with NLCD classes separated into three facets rather than separated by color.

```
# 6
NIWO.needles <-
  ggplot(subset(NIWO.Litter, functionalGroup == "Needles"),
    aes(x = collectDate, y = dryMass, color = nlcdClass)) +
  geom_point()

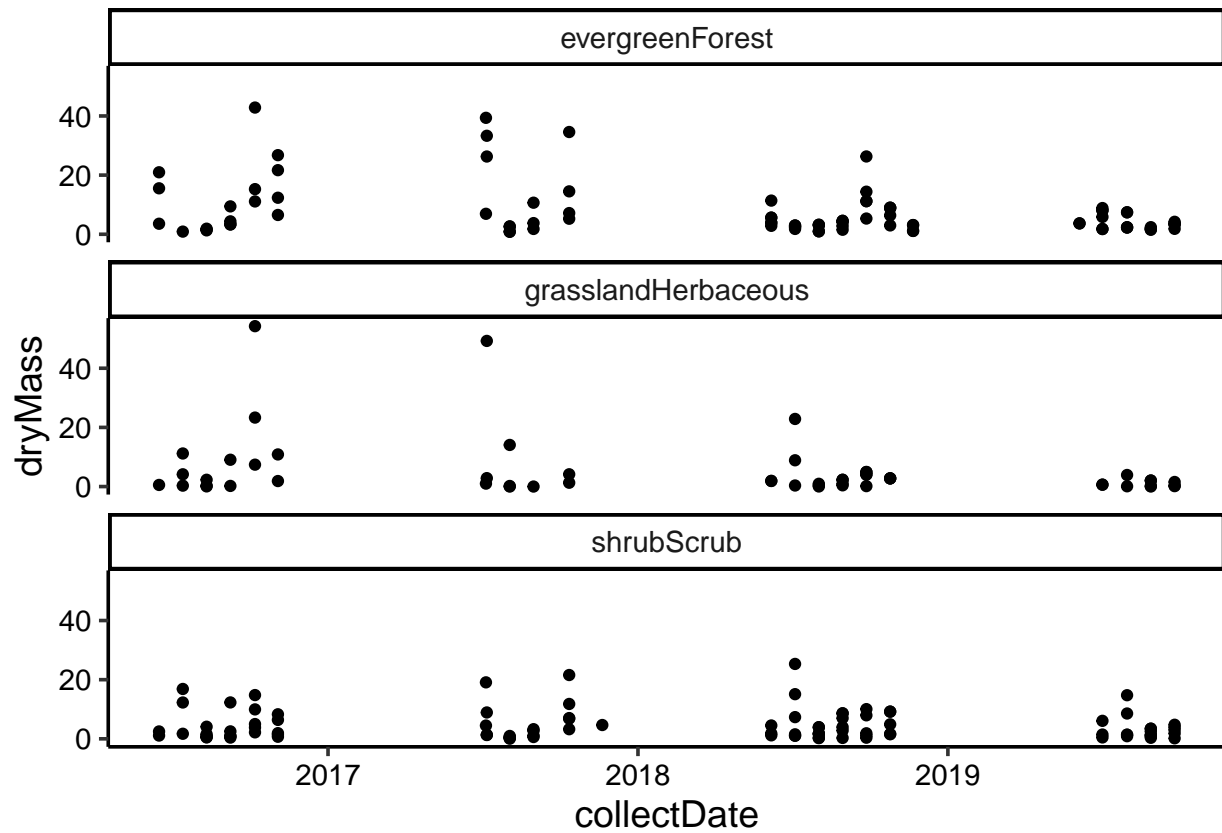
print(NIWO.needles)
```

7

```
NIWO.needles.facet <-
  ggplot(subset(NIWO.Litter, functionalGroup == "Needles"),
    aes(x = collectDate, y = dryMass)) +
  geom_point() +
  facet_wrap(vars(nlcdClass), nrow = 3)

print(NIWO.needles.facet)
```



Question: Which of these plots (6 vs. 7) do you think is more effective, and why?

Answer: Plot 7 is more effective because you are able to easily differentiate the NLCD classes whereas plot 6 displayed all the NLCD classes within each collection year so it was difficult to distinguish the dry mass and collection date of each NLCD class.