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., "Fay_A05_DataVisualization.Rmd") prior to submission.

The completed exercise is due on Tuesday, February 23 at 11:59 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 (both the tidy [`NTL-LTER_Lake_Chemistry_Nutrients_PeterPaul_Processed.csv`] and the gathered [`NTL-LTER_Lake_Nutrients_PeterPaulGathered_Processed.csv`] versions) 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.

Define your theme

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

```
mytheme <-
  theme_classic(base_size = 12) +
  theme(axis.title = element_text(color = "black"), legend.position = "bottom", legend.background = ele

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 (`tp_ug`) by phosphate (`po4`), 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.

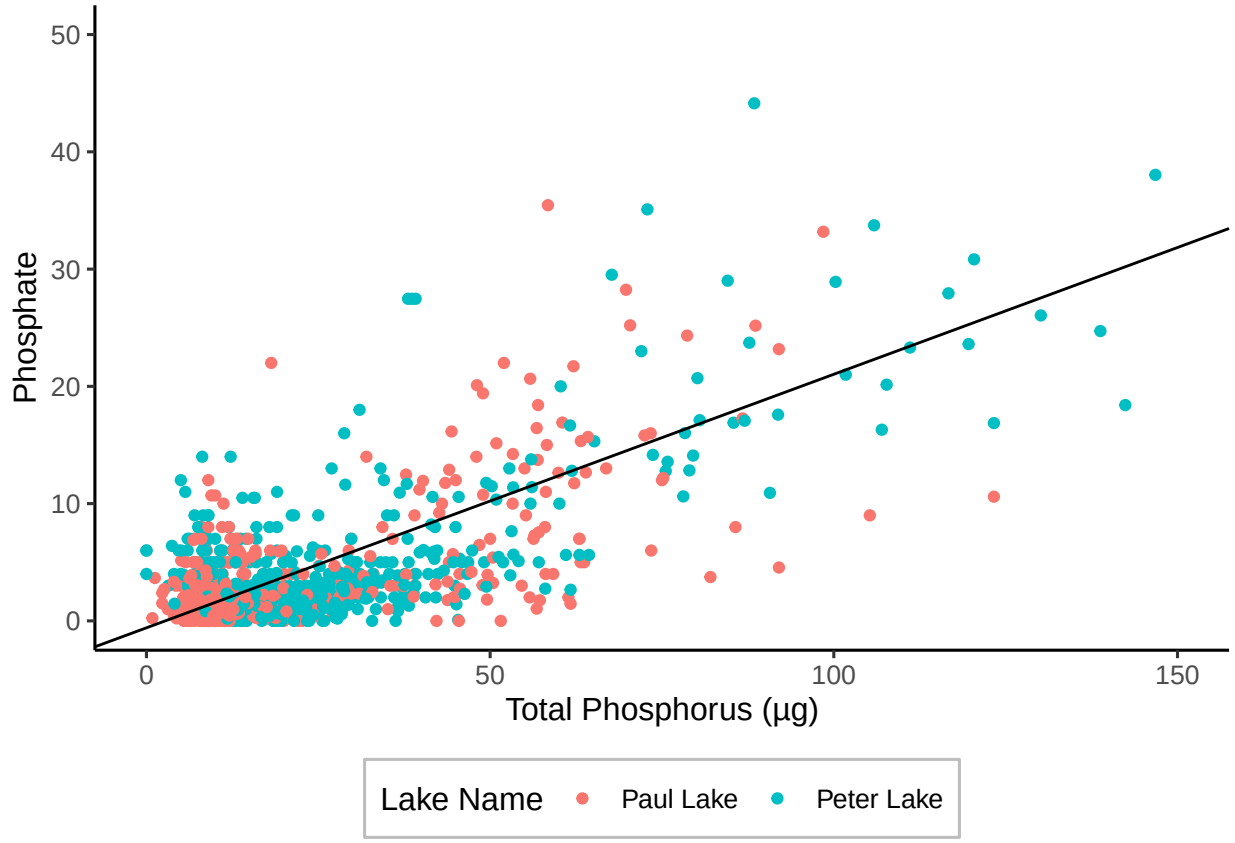
```
#get slope and intercept for linear regression
lm(formula = chemnutrients_PeterPaul_processed$po4 ~ chemnutrients_PeterPaul_processed$tp_ug)
```

```
##
```

```
## Call:
## lm(formula = chemnutrients_PeterPaul_processed$po4 ~ chemnutrients_PeterPaul_processed$tp_ug)
##
## Coefficients:
##                                  (Intercept)
##                                      -0.5894
## chemnutrients_PeterPaul_processed$tp_ug
##                                       0.2162
```

```
phos_plot <- ggplot(chemnutrients_PeterPaul_processed, aes(x = tp_ug, y = po4, color = lakename)) +
  geom_point() +
  geom_abline(slope = 0.2162, intercept = -0.5894) + #using geom_smooth(method = lm) gives 2 lines, but
  xlim(0, 150) +
  ylim(0, 50) +
  xlab("Total Phosphorus (µg)") +
  ylab("Phosphate") +
  labs(color = "Lake Name")
print(phos_plot)
```

```
## Warning: Removed 21948 rows containing missing values (geom_point).
```



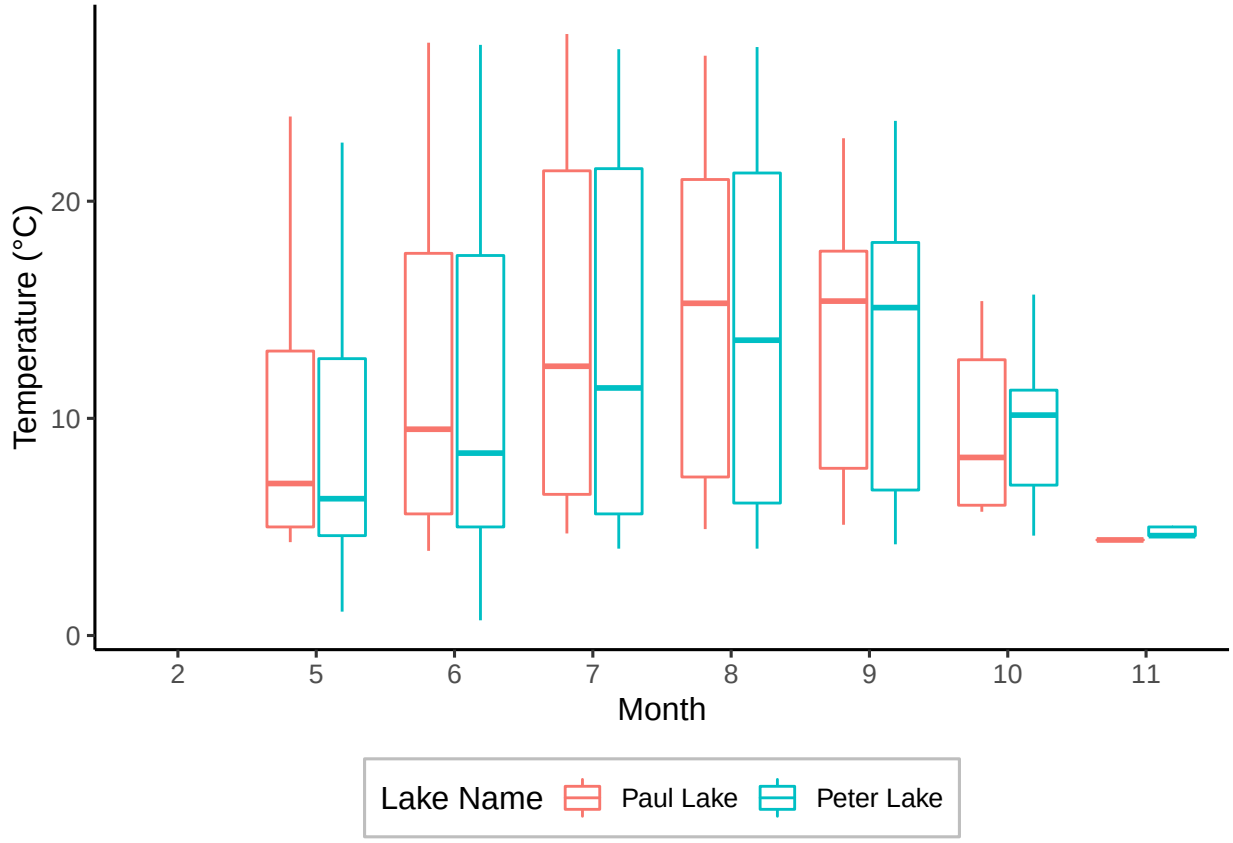
5. [NTL-LTER] Make three separate boxplots of (a) temperature, (b) TP, and (c) TN, with month as the x axis and lake as a color aesthetic. Then, create a cowplot that combines the three graphs. Make sure that only one legend is present and that graph axes are aligned.

```
#5a

box_temp <- ggplot(chemnutrients_PeterPaul_processed, aes(x = as.factor(month), y = temperature_C, colo
```

```
  geom_boxplot() +
  labs(color = "Lake Name") +
  xlab("Month") +
  ylab("Temperature (°C)")
print(box_temp)
```

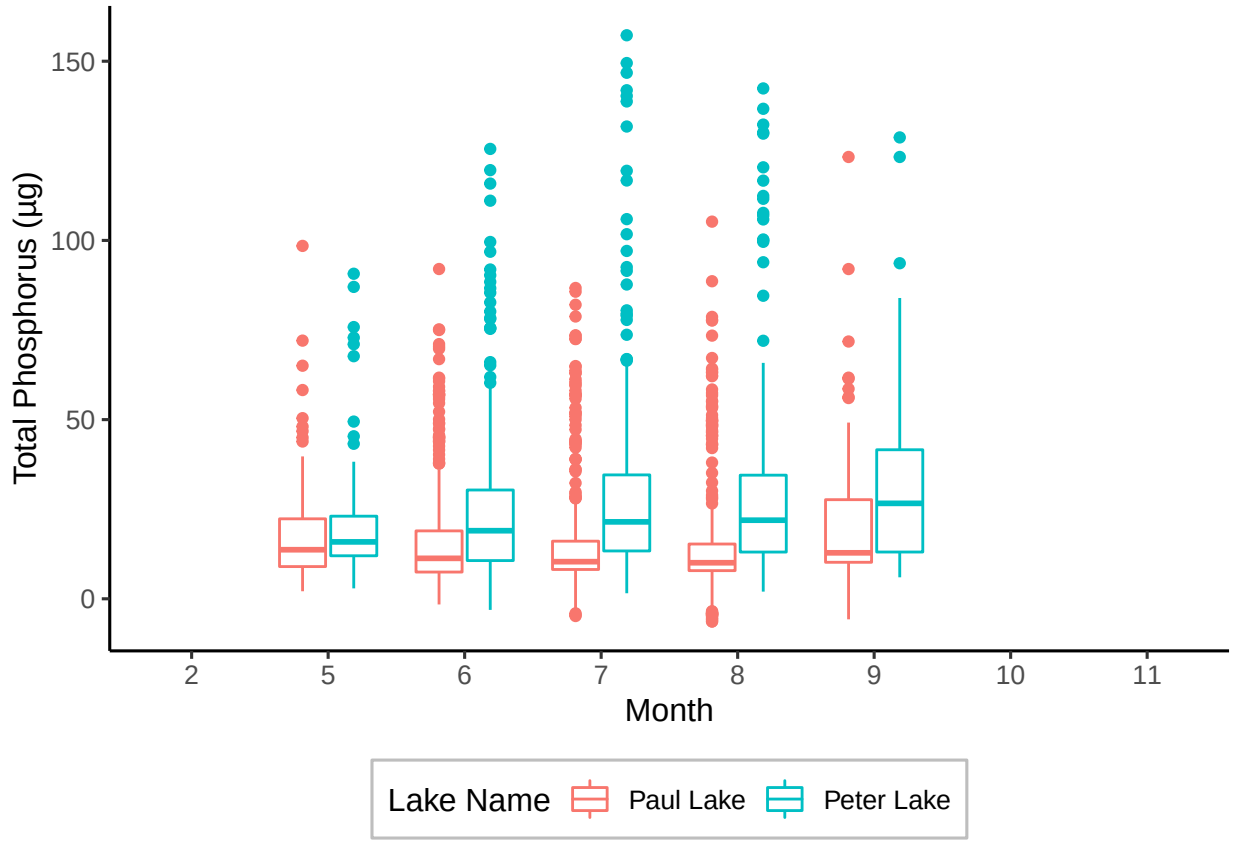
```
## Warning: Removed 3566 rows containing non-finite values (stat_boxplot).
```




```
#5b

box_tp <- ggplot(chemnutrients_PeterPaul_processed, aes(x = as.factor(month), y = tp_ug, color = lakenar
  geom_boxplot() +
  labs(color = "Lake Name") +
  xlab("Month") +
  ylab("Total Phosphorus (µg)")
print(box_tp)
```

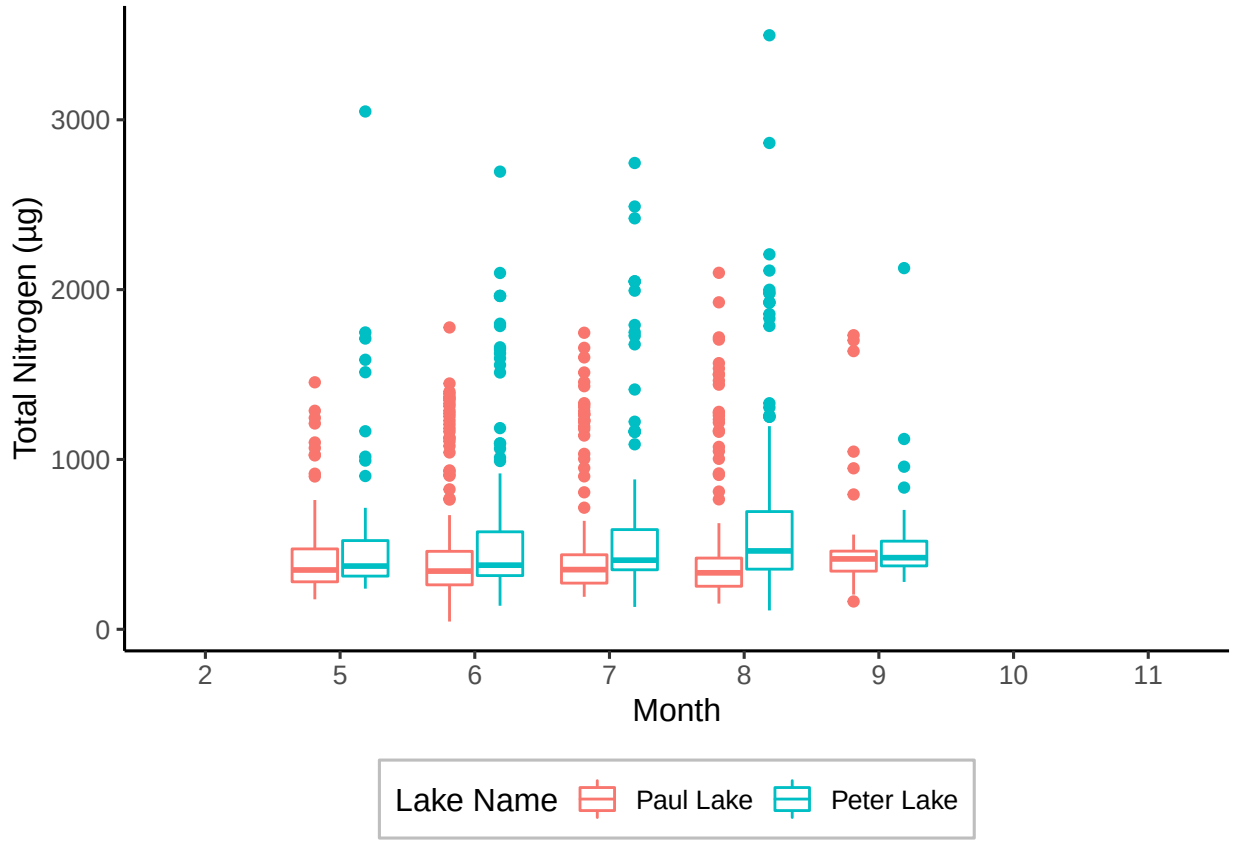
```
## Warning: Removed 20729 rows containing non-finite values (stat_boxplot).
```




```
#5c

box_tn <- ggplot(chemnutrients_PeterPaul_processed, aes(x = as.factor(month), y = tn_ug, color = lakenar
  geom_boxplot() +
  labs(color = "Lake Name") +
  xlab("Month") +
  ylab("Total Nitrogen (µg)")
print(box_tn)
```

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

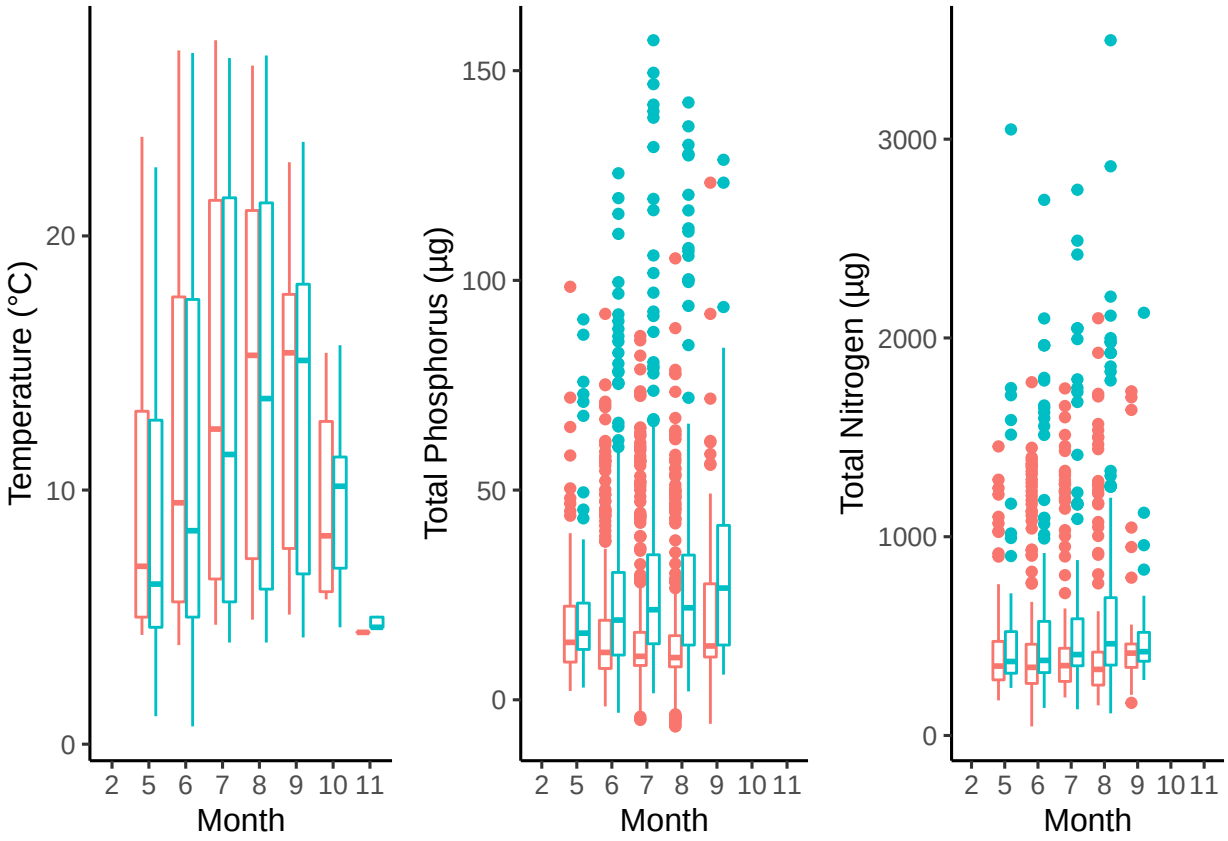



```
#5d

box_combo_nl <-
  plot_grid(box_temp + theme(legend.position="none"),
  box_tp + theme(legend.position="none"),
  box_tn + theme(legend.position="none"),
  nrow = 1,
  axis = "b",
  rel_heights = c(1.25, 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).
```

```
print(box_combo_nl)
```

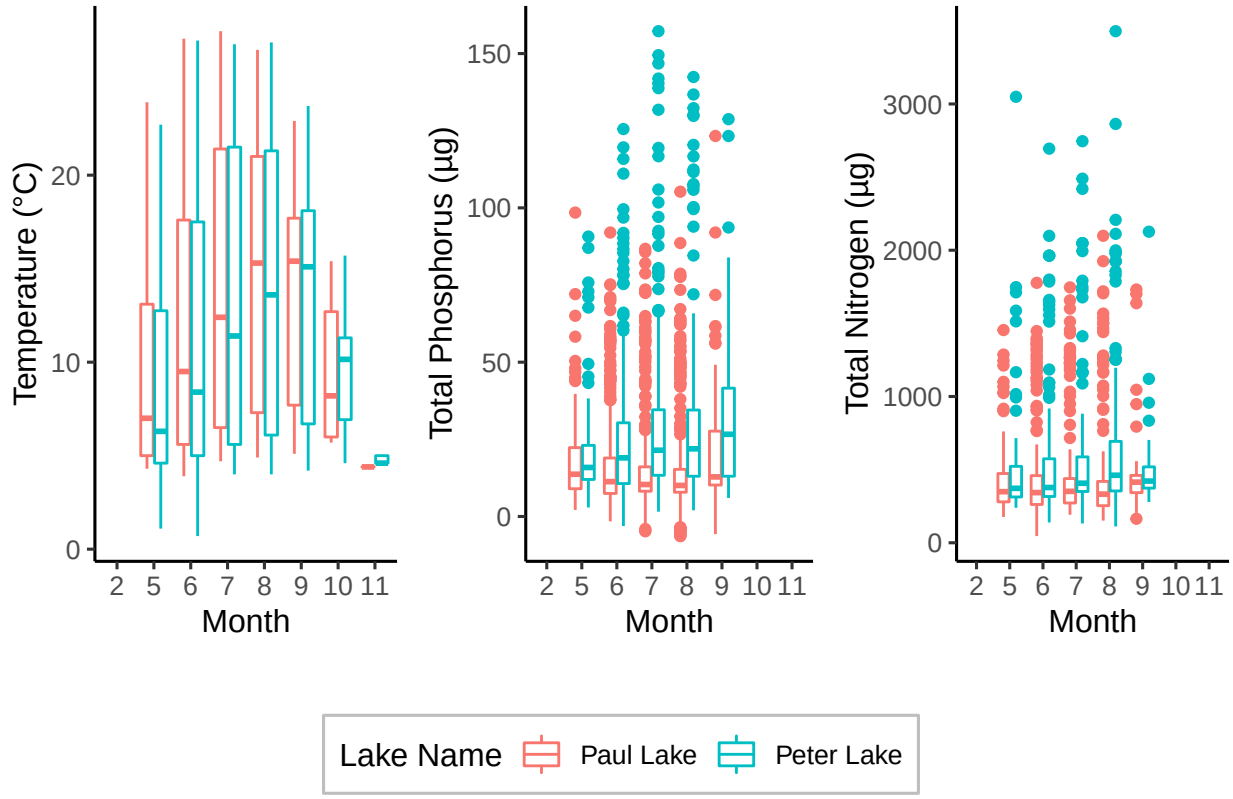



```
legend <- get_legend(box_temp +
                       guides(color = guide_legend(nrow = 1)) +
                        theme(legend.position = "bottom"))
```

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

```
box_combo <-
  plot_grid(box_combo_nl,
            legend,
            ncol = 1,
            align = "v",
            axis = "bt",
            rel_heights = c(1, .3))

print(box_combo)
```



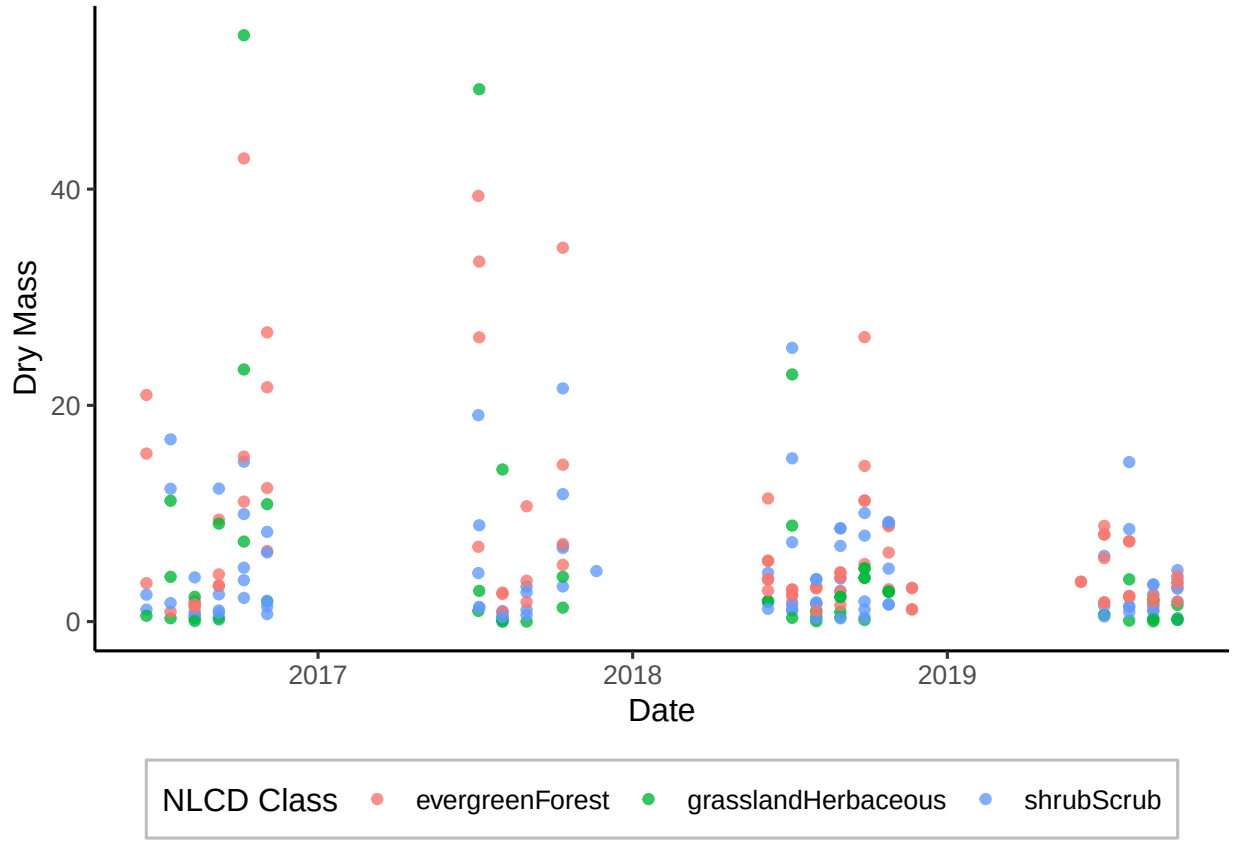
Question: What do you observe about the variables of interest over seasons and between lakes?

> Answer: Temperatures have very large ranges at the start of the calendar year, but htey shrink over time as we enter the fall. We also don't have any outliers in our temperature plot. Total phosphorus measurements seem to peak in the summer months. The total phosphorus measurements for Peter Lake become more dispersed over the months, whereas the measurements for Paul Lake become less dispersed, with the exception of the final month. Our total nitrogen measurements also have a substantial number of outliers. The range of data seems relatively limited (short-ish whiskers) and the data from Peter Lake is generally more dispersed than the data from Paul Lake (longer boxes).

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)

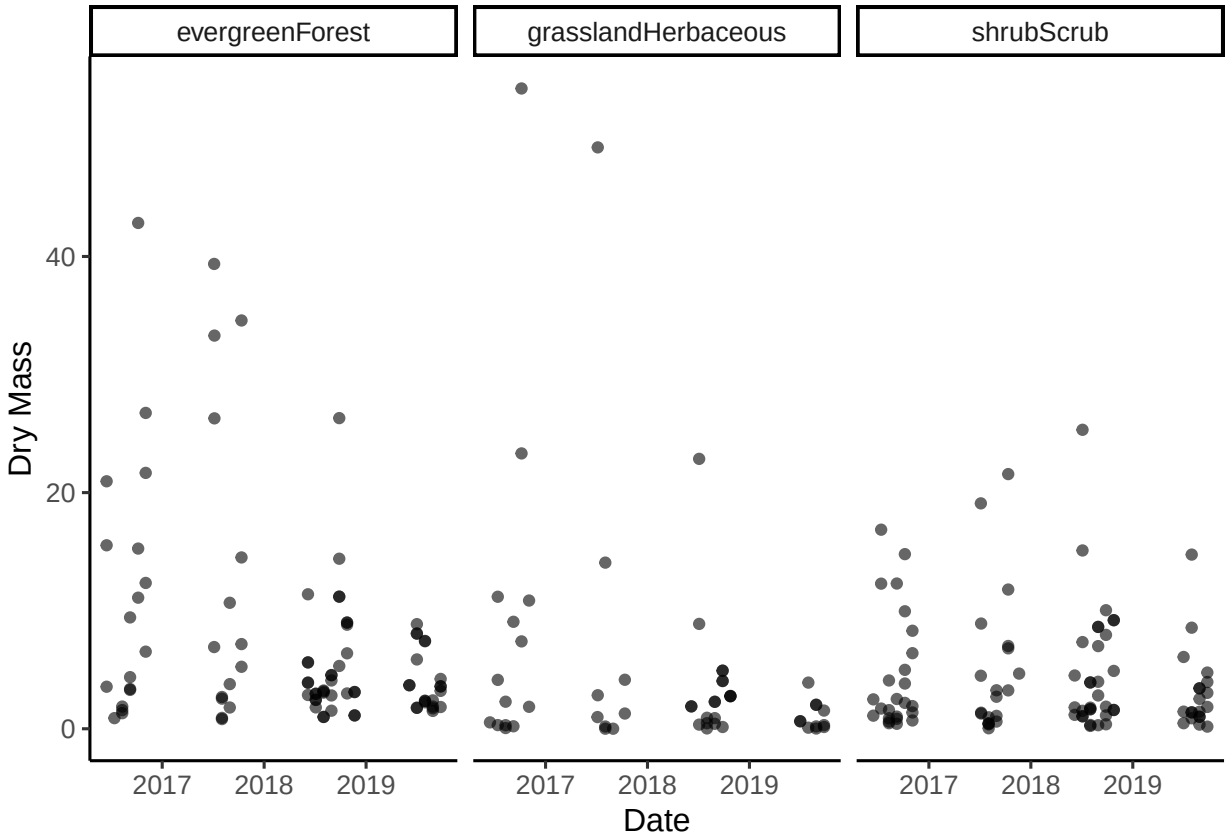
7. [Niwot Ridge] Now, plot the same plot but with NLCD classes separated into three facets rather than separated by color.

```
#6
needles_plot <-
  ggplot(filter(Litter, functionalGroup == "Needles"),
         aes(x = collectDate, y = dryMass, color = nlcdClass)) +
  geom_point(alpha = 0.8) +
  xlab("Date") +
  ylab("Dry Mass") +
  labs(color='NLCD Class')
print(needles_plot)
```




```
#7

needles_facet <-
  ggplot(filter(Litter, functionalGroup == "Needles"),
         aes(x = collectDate, y = dryMass)) +
  geom_point(alpha = 0.6) +
  xlab("Date") +
  ylab("Dry Mass") +
  facet_wrap(vars(nlcdClass))
print(needles_facet)
```



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

Answer: I think plot 7 is much more effective. In plot 6, the clustering on the x-axis makes it confusing to interpret the data. It's much easier to see the NLCD classes side by side in plot 7 with the same y-axis. You can still compare dry masses measured by year pretty easily, and I think it's also easier to spot trends in amount of dry mass measured over time for the 3 NLCD classes.