5: Part 1 - Data Visualization Basics

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List of Figures

Objectives

1. Perform simple data visualizations in the R package `ggplot`
2. Develop skills to adjust aesthetics and layers in graphs
3. Apply a decision tree framework for appropriate graphing methods

Opening discussion

Effective data visualization depends on purposeful choices about graph types. The ideal graph type depends on the type of data and the message the visualizer desires to communicate. The best visualizations are clear and simple. A good resource for data visualization is Data to Viz, which includes both a decision tree for visualization types and explanation pages for each type of data, including links to R resources to create them. Take a few minutes to explore this website.

Set Up

```
library(tidyverse);library(lubridate);library(here)
library(ggridges)

here()
```

```
## [1] "/home/guest/EDE_Fall2024"
```

```
PeterPaul.chem.nutrients <-
  read.csv(here("Data/Processed_KEY/NTL-LTER_Lake_Chemistry_Nutrients_PeterPaul_Processed.csv"), string
PeterPaul.chem.nutrients.gathered <-
  read.csv(here("Data/Processed_KEY/NTL-LTER_Lake_Nutrients_PeterPaulGathered_Processed.csv"), stringsA
EPAair <- read.csv(here("Data/Processed_KEY/EPAair_O3_PM25_NC1819_Processed.csv"), stringsAsFactors = T

EPAair$Date <- ymd(EPAair$Date)
PeterPaul.chem.nutrients$sampledate <- ymd(PeterPaul.chem.nutrients$sampledate)
PeterPaul.chem.nutrients.gathered$sampledate <- ymd(PeterPaul.chem.nutrients.gathered$sampledate)
```

ggplot

ggplot, called from the package `ggplot2`, is a graphing and image generation tool in R. This package is part of tidyverse. While base R has graphing capabilities, ggplot has the capacity for a wider range and more sophisticated options for graphing. ggplot has only a few rules:

- The first line of ggplot code always starts with `ggplot()`
- A data frame must be specified within the `ggplot()` function. Additional datasets can be specified in subsequent layers.
- Aesthetics must be specified, most commonly x and y variables but including others. Aesthetics can be specified in the `ggplot()` function or in subsequent layers.
- Additional layers must be specified to fill the plot.

Geoms

Here are some commonly used layers for plotting in ggplot:

- geom_bar
- geom_histogram
- geom_freqpoly
- geom_boxplot
- geom_violin
- geom_dotplot
- geom_density_ridges
- geom_point
- geom_errorbar
- geom_smooth
- geom_line
- geom_area
- geom_abline (plus geom_hline and geom_vline)
- geom_text

Aesthetics

Here are some commonly used aesthetic types that can be manipulated in ggplot:

- color
- fill
- shape
- size
- transparency

Plotting continuous variables over time: Scatterplot and Line Plot

```
# Scatterplot
ggplot(EPAair, aes(x = Date, y = Ozone)) +
  geom_point()
```

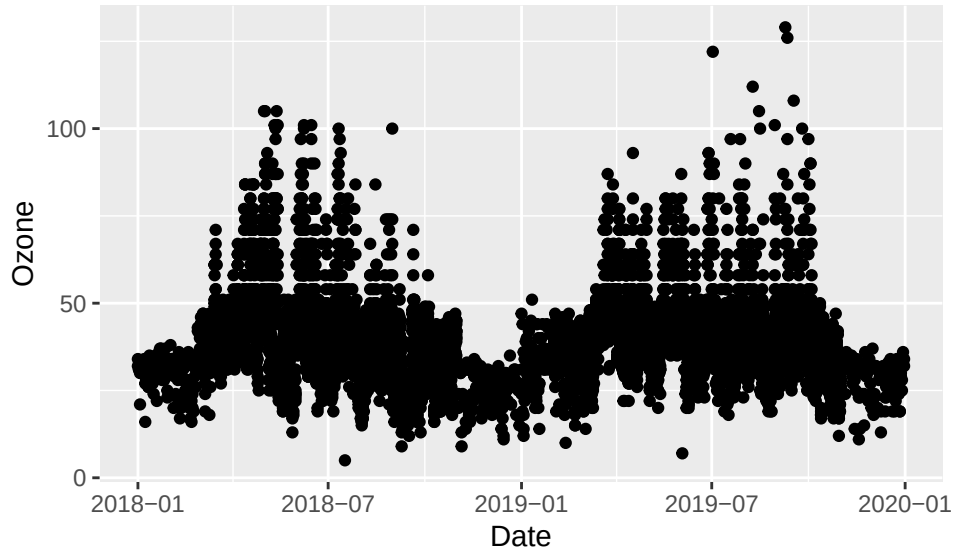


Figure 1: Scatterplot

```
O3plot <- ggplot(EPAair) + #storing plot as an object
  geom_point(aes(x = Date, y = Ozone))
print(O3plot) #printing that object
```

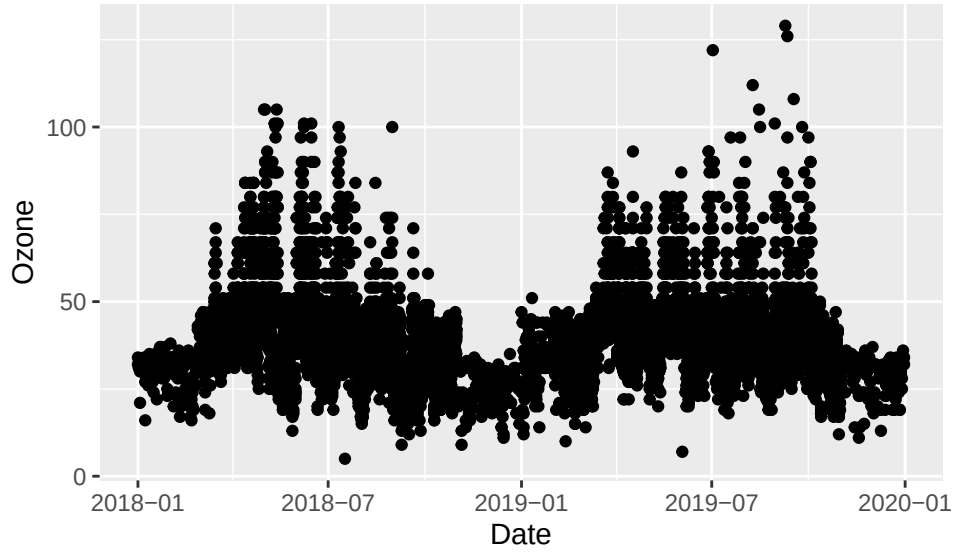


Figure 2: Scatterplot

```r
# Fix this code
O3plot2 <- ggplot(EPAair) +
  geom_point(aes(x = Date, y = Ozone), color = "blue")
print(O3plot2) #cannot have the color be another layer ...
```

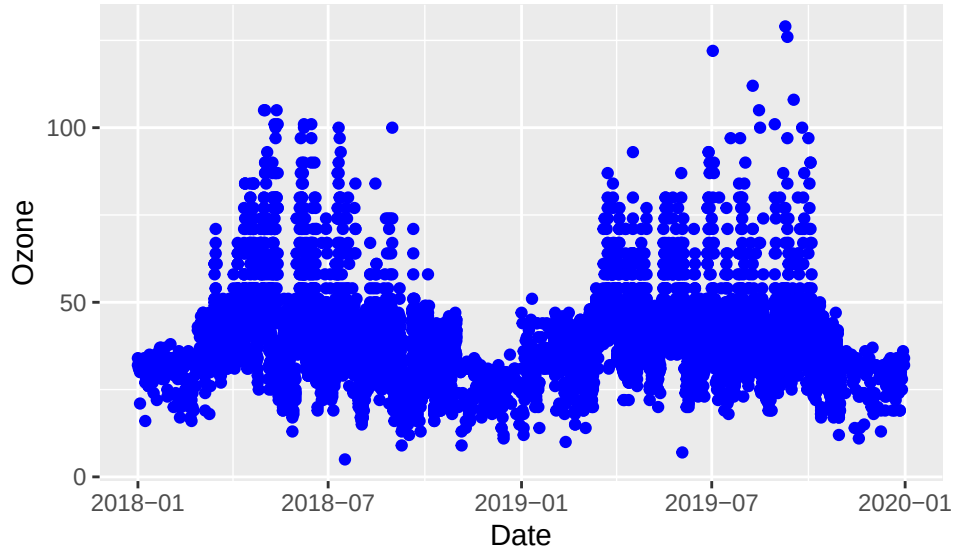


Figure 3: Scatterplot

```r
#do the way listed above


# Add additional variables
# How could you automatically assign a marker color to a variable?
PMplot <-
  ggplot(EPAair, aes(x = Month, y = PM2.5, shape = as.factor(Year),
  color = Site.Name)) + #changing shape by year, color by site name
  geom_point()
print(PMplot)
```

```r
# Separate plot with facets
PMplot.faceted <-
  ggplot(EPAair, aes(x = Month, y = PM2.5, shape = as.factor(Year))) +
  geom_point() +
  facet_wrap(vars(Site.Name), nrow = 3) #create different plots for each site
print(PMplot.faceted)
```

```r
# Filter dataset within plot building and facet by multiple variables
PMplot.faceted2 <-
  ggplot(subset(EPAair, Site.Name == "Clemmons Middle" | Site.Name == "Leggett" |
                  Site.Name == "Bryson City"), #subset of sites
         aes(x = Month, y = PM2.5)) +
  geom_point() +
```

Figure 4: Scatterplot

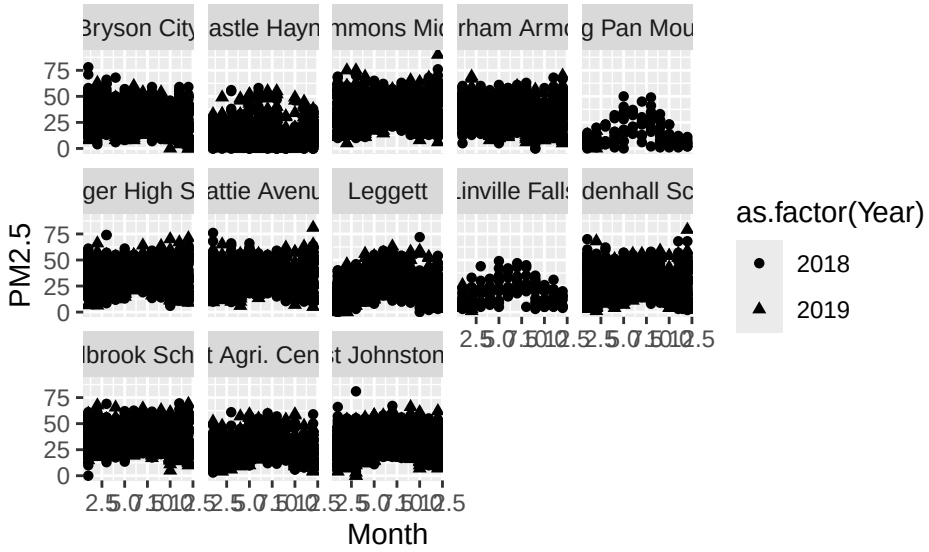


Figure 5: Scatterplot

```
  facet_grid(Site.Name ~ Year) #column representing year,
#rows selcting three sites
print(PMplot.faceted2)
```

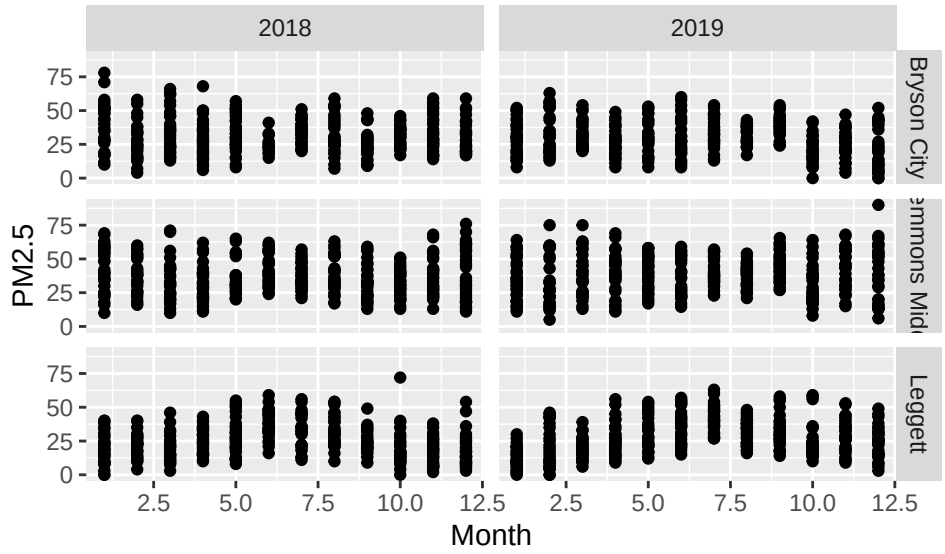


Figure 6: Scatterplot

```
# Plot true time series with geom_line
PMplot.line <-
  ggplot(subset(EPAair, Site.Name == "Leggett"),
         aes(x = Date, y = PM2.5)) +
  geom_line() #geom_line connects points by line
print(PMplot.line)
```

Plotting the relationship between two continuous variables: Scatterplot

```
# Scatterplot
lightvsDO <-
  ggplot(PeterPaul.chem.nutrients, aes(x = irradianceWater, y = dissolvedOxygen)) +
  geom_point()
print(lightvsDO) #two outlier, adjust axes
```

```
# Adjust axes
lightvsDOfixed <-
  ggplot(PeterPaul.chem.nutrients, aes(x = irradianceWater, y = dissolvedOxygen)) +
  geom_point() +
  xlim(0, 250) +
  ylim(0, 20)
print(lightvsDOfixed)
```

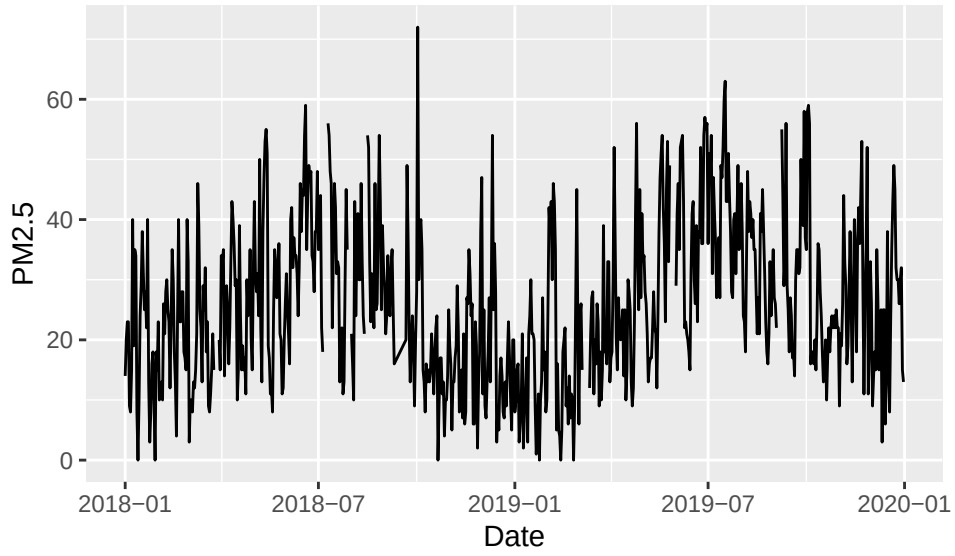


Figure 7: Scatterplot

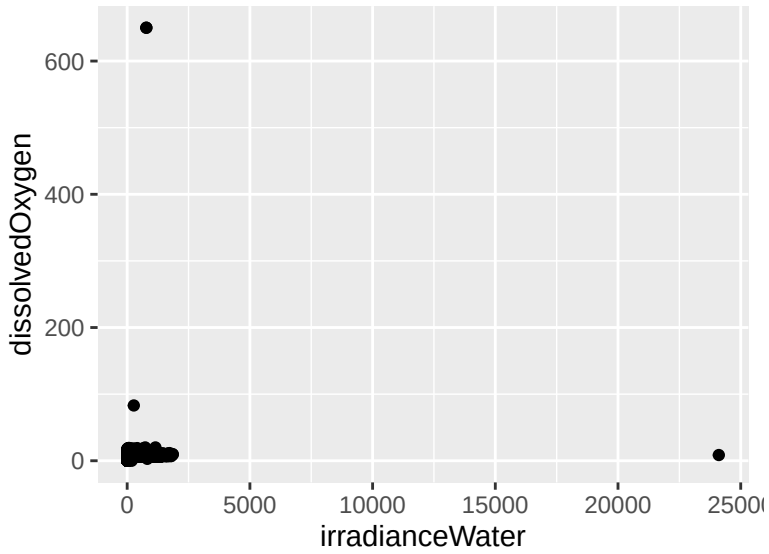


Figure 8: Another Scatterplot

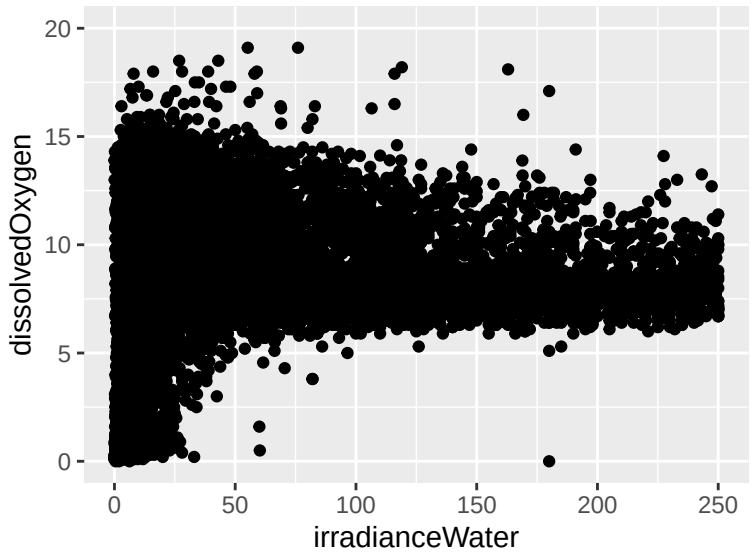


Figure 9: Another Scatterplot

```
# Depth in the fields of limnology and oceanography is on a reverse scale
tempvsdepth <-
  ggplot(PeterPaul.chem.nutrients, aes(x = temperature_C, y = depth)) +
  #ggplot(PeterPaul.chem.nutrients, aes(x = temperature_C, y = depth, color = daynum)) +
  geom_point() +
  scale_y_reverse() #otherwise, values will be plotted 0 to max
print(tempvsdepth)
```

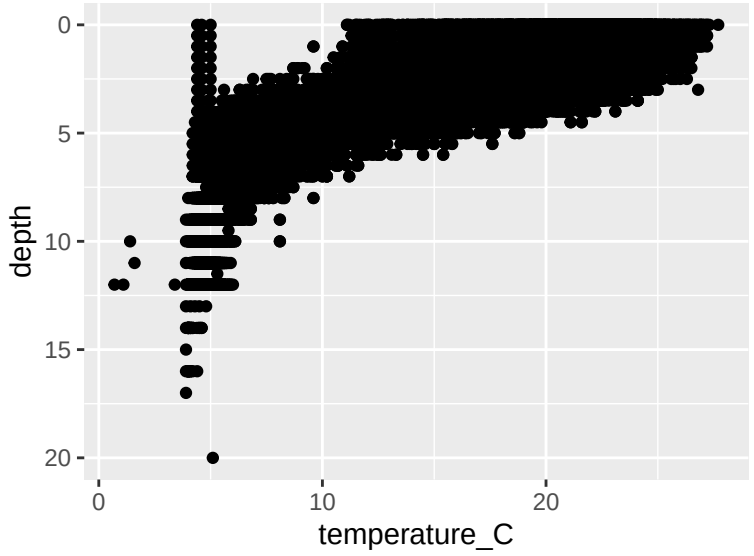


Figure 10: Another Scatterplot

```
NvsP <-
  ggplot(PeterPaul.chem.nutrients, aes(x = tp_ug, y = tn_ug, color = depth)) +
  geom_point() + #colored by depth
  geom_smooth(method = lm) + #lm = linear model trendline
  geom_abline(aes(slope = 16, intercept = 0))
print(NvsP)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

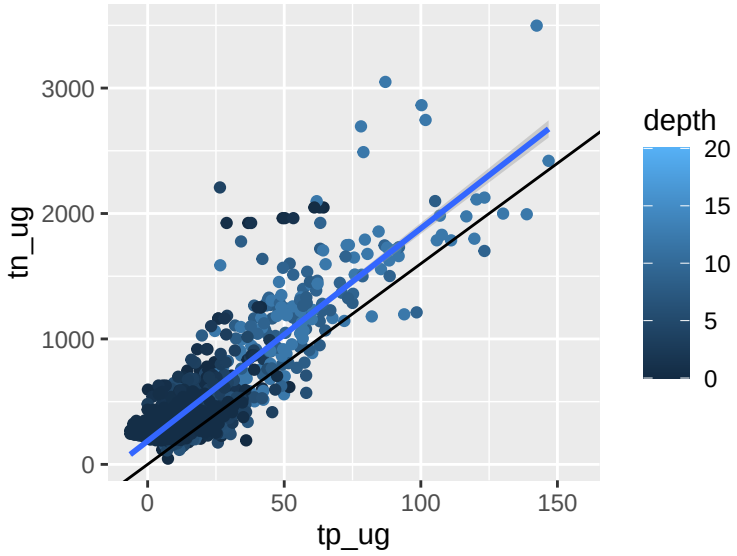


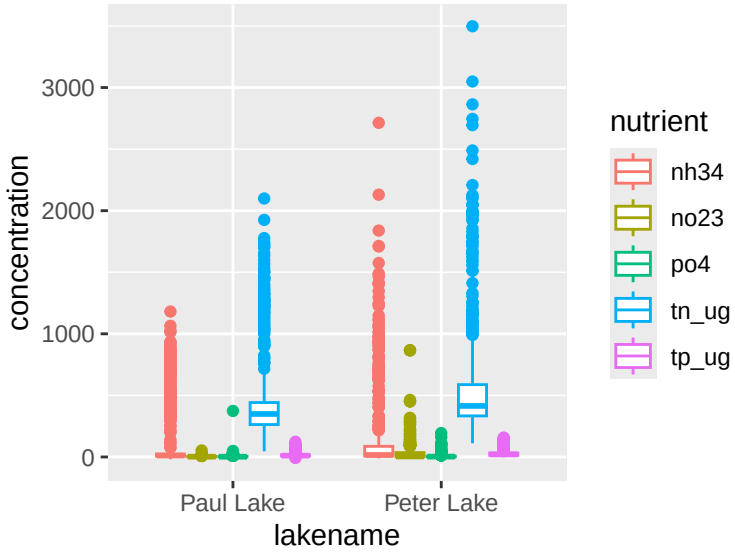
Figure 11: Another Scatterplot

Plotting continuous vs. categorical variables

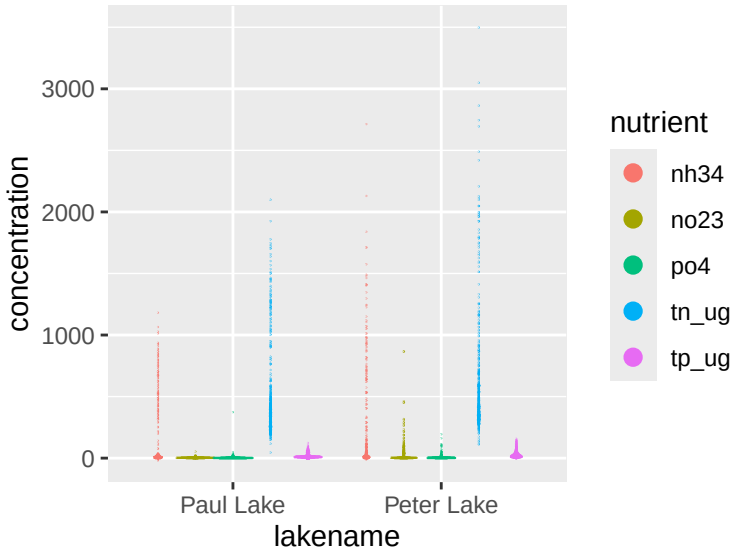
A traditional way to display summary statistics of continuous variables is a bar plot with error bars. Let's explore why this might not be the most effective way to display this type of data. Navigate to the Caveats page on Data to Viz (https://www.data-to-viz.com/caveats.html) and find the page that explores barplots and error bars.

What might be more effective ways to display the information? Navigate to the boxplots page in the Caveats section to explore further.

```
# Box and whiskers plot
Nutrientplot3 <-
  ggplot(PeterPaul.chem.nutrients.gathered, aes(x = lakename, y = concentration)) +
  geom_boxplot(aes(color = nutrient)) # Why didn't we use "fill"?
print(Nutrientplot3) #fill = filling of shape, not data points
```

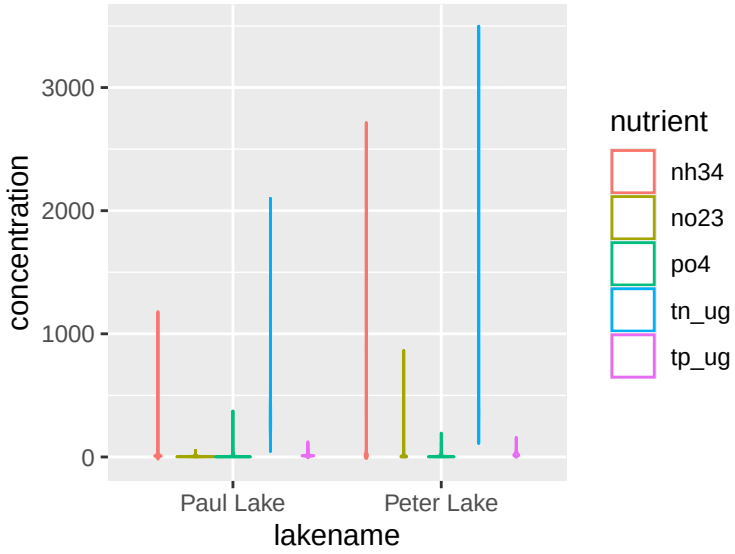



```
# Dot plot
Nutrientplot4 <-
  ggplot(PeterPaul.chem.nutrients.gathered, aes(x = lakename, y = concentration)) +
  geom_dotplot(aes(color = nutrient, fill = nutrient), binaxis = "y", binwidth = 1,
               stackdir = "center", position = "dodge", dotsize = 2) #
print(Nutrientplot4) #dot plot is good if you can't see the IQ range
```




```
#for some of your box plots

# Violin plot
Nutrientplot5 <-
  ggplot(PeterPaul.chem.nutrients.gathered, aes(x = lakename, y = concentration)) +
  geom_violin(aes(color = nutrient)) #
print(Nutrientplot5) #difference in densities
```




```
# Frequency polygons
# Using a tidy dataset
Nutrientplot6 <-
  ggplot(PeterPaul.chem.nutrients) +
  geom_freqpoly(aes(x = tn_ug), color = "darkred") +
  geom_freqpoly(aes(x = tp_ug), color = "darkblue") +
  geom_freqpoly(aes(x = nh34), color = "blue") +
  geom_freqpoly(aes(x = no23), color = "royalblue") +
  geom_freqpoly(aes(x = po4), color = "red")
print(Nutrientplot6) #not a good way of generating freq plots
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
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## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
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## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```
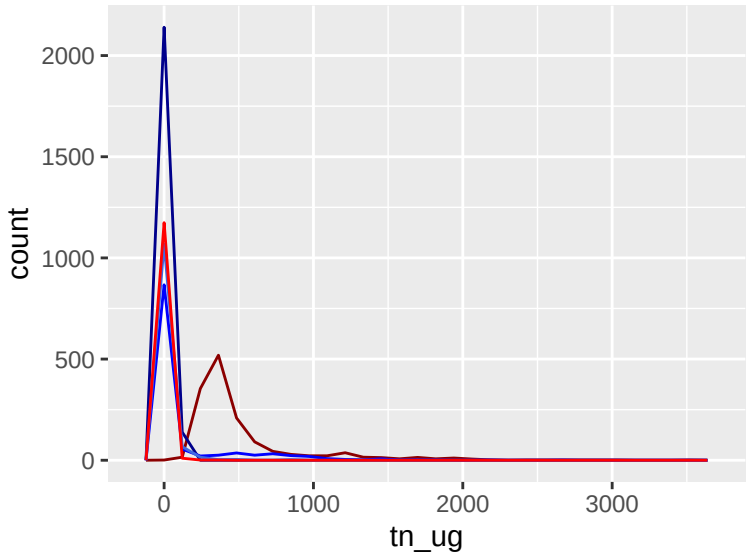
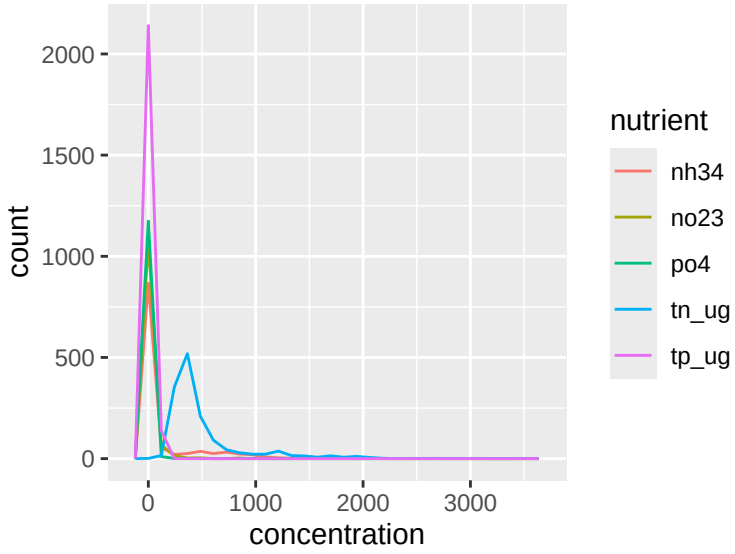



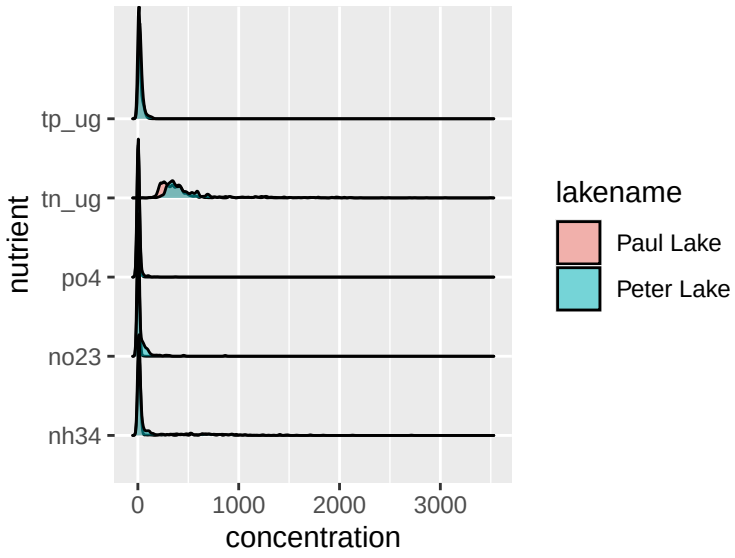
```
# Using a gathered dataset
Nutrientplot7 <-
  ggplot(PeterPaul.chem.nutrients.gathered) +
  geom_freqpoly(aes(x = concentration, color = nutrient))
print(Nutrientplot7) #important to have gathered dataset!
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
# Frequency polygons have the risk of becoming spaghetti plots.
# See <https://www.data-to-viz.com/caveat/spaghetti.html> for more info.

# Ridgeline plot
Nutrientplot6 <-
  ggplot(PeterPaul.chem.nutrients.gathered, aes(y = nutrient, x = concentration)) +
  geom_density_ridges(aes(fill = lakename), alpha = 0.5) #
print(Nutrientplot6) #used fill because wanted to color the inside of curves
```

```
## Picking joint bandwidth of 10.9
```


tp_ug
tn_ug
po4
no23
nh34
nutrient
0
1000
2000
3000
concentration
lakename
Paul Lake
Peter Lake