9: Data Visualization Advanced

Environmental Data Analytics | Kateri Salk

Spring 2020

LESSON OBJECTIVES

1. Perform advanced edits on ggplot objects to follow best practices for data visualization
2. Troubleshoot visualization challenges

SET UP YOUR DATA ANALYSIS SESSION

```
getwd()
```

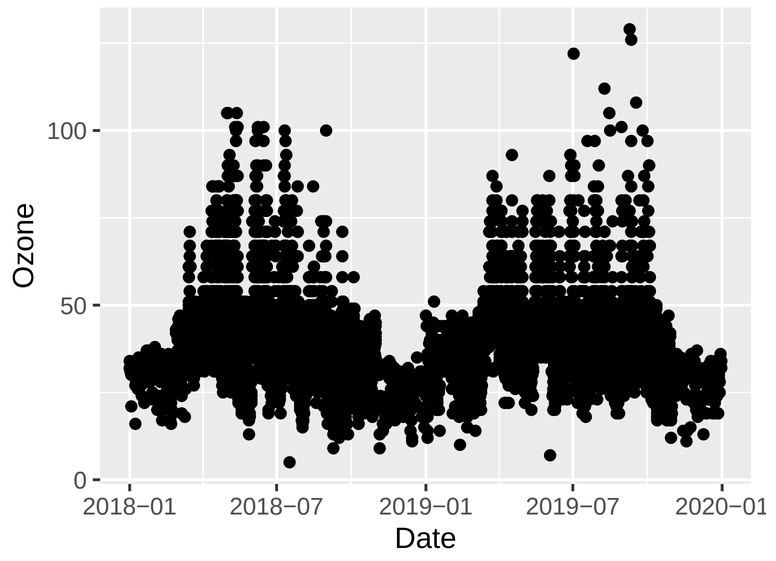
```
## [1] "/Users/Victoria/Environmental_Data_Analytics_2020/Lessons"
```

```
library(tidyverse)

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")
EPAair <- read.csv("../Data/Processed/EPAair_O3_PM25_NC1819_Processed.csv")

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

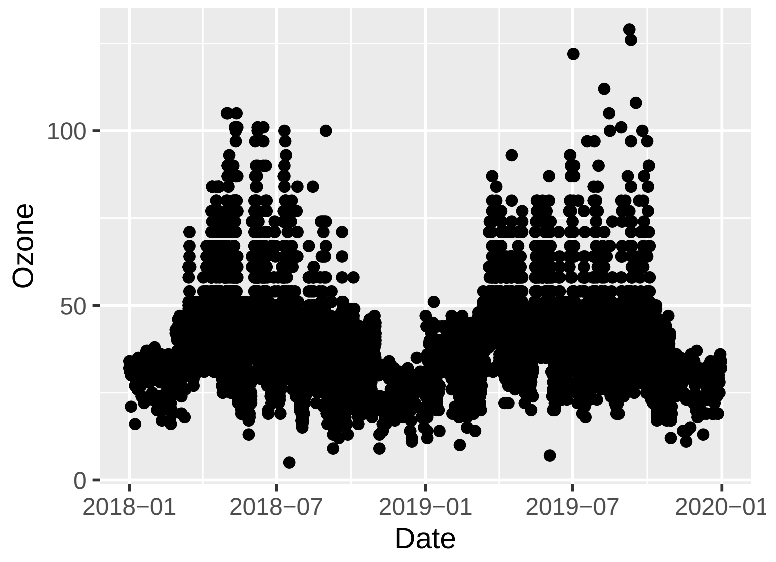
Themes

Often, we will want to change multiple visual aspects of a plot. Ggplot comes with pre-built themes that will adjust components of plots if you call that theme.

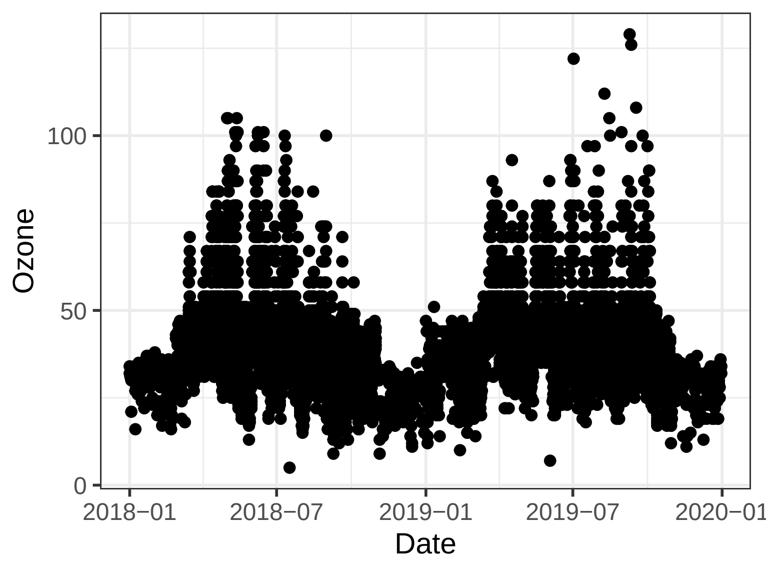
```
O3plot <- ggplot(EPAair) +
  geom_point(aes(x = Date, y = Ozone))
print(O3plot)
```



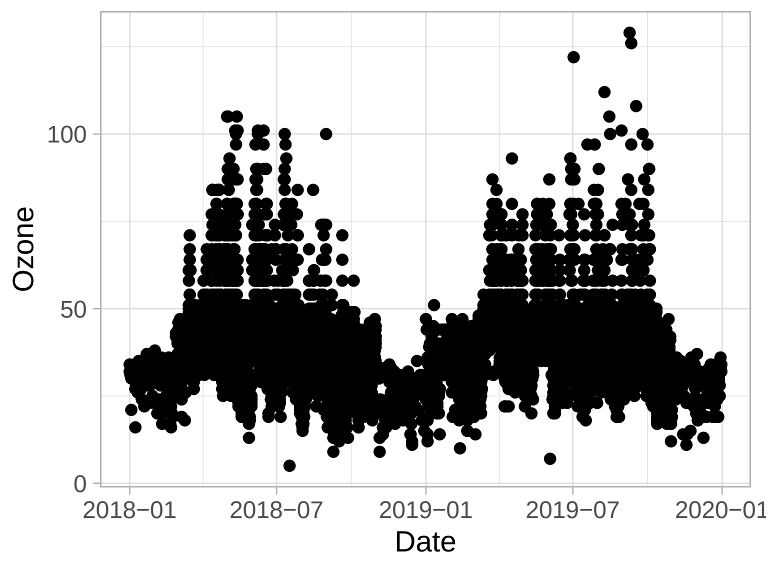
```
O3plot1 <- ggplot(EPAair) +
  geom_point(aes(x = Date, y = Ozone)) +
  theme_gray()
print(O3plot1)
```



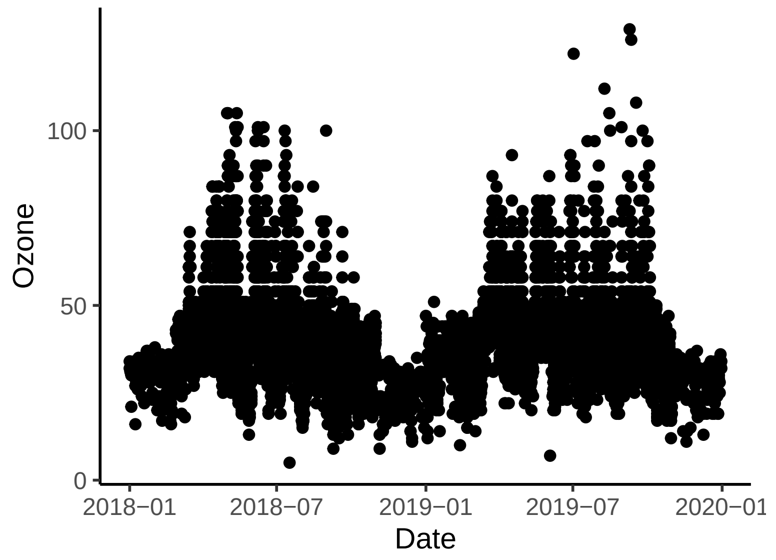
```
O3plot2 <- ggplot(EPAair) +
  geom_point(aes(x = Date, y = Ozone)) +
  theme_bw()
print(O3plot2)
```



```
O3plot3 <- ggplot(EPAair) +
  geom_point(aes(x = Date, y = Ozone)) +
  theme_light()
print(O3plot3)
```



```
O3plot4 <- ggplot(EPAair) +
  geom_point(aes(x = Date, y = Ozone)) +
  theme_classic()
print(O3plot4)
```

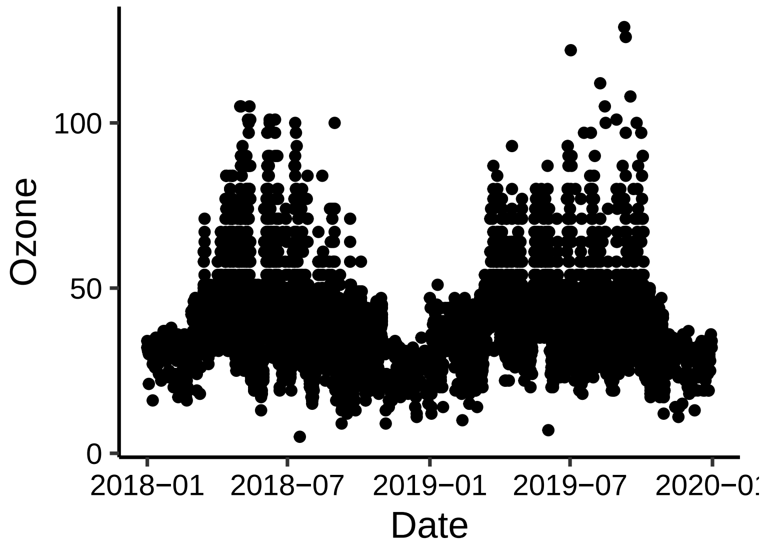


Notice that some aspects of your graph have not been adjusted, including:

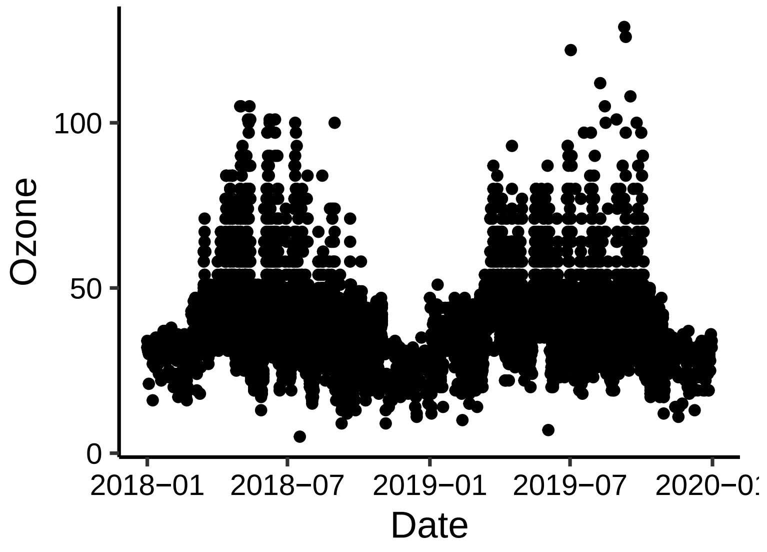
- text size
- axis label colors
- legend position and justification

If you would like to set a common theme across all plots in your analysis session, you may define a theme and call up that theme for each graph. This eliminates the need to add multiple lines of code in each plot.

```r
mytheme <- theme_classic(base_size = 14) +
  theme(axis.text = element_text(color = "black"),
        legend.position = "top") #alternative: legend.position + legend.justification

# options: call the theme in each plot or set the theme at the start.

O3plot5 <- ggplot(EPAair) +
  geom_point(aes(x = Date, y = Ozone)) +
  mytheme
print(O3plot5)
```



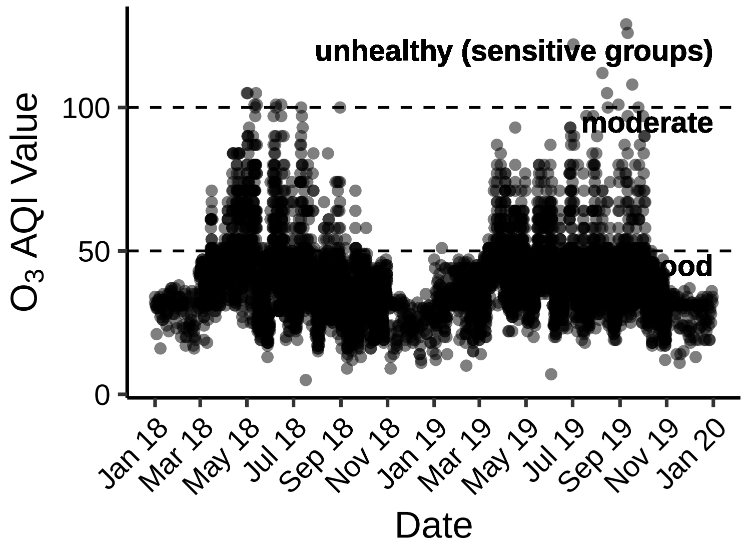
```r
theme_set(mytheme)

O3plot6 <- ggplot(EPAair) +
  geom_point(aes(x = Date, y = Ozone))
print(O3plot6)
```



Adjusting multiple components of your plots

While the theme allows us to set multiple aspects of plots, ggplot allows us to adjust other parts of plots outside of the theme.

```r
O3plot7 <- ggplot(EPAair, aes(x = Date, y = Ozone)) +
  geom_hline(yintercept = 50, lty = 2) +
  geom_hline(yintercept = 100, lty = 2) +
  geom_point(alpha = 0.5, size = 1.5) +
  geom_text(x = as.Date("2020-01-01"), y = 45, label = "good", hjust = 1, fontface = "bold") +
  geom_text(x = as.Date("2020-01-01"), y = 95, label = "moderate", hjust = 1, fontface = "bold") +
  geom_text(x = as.Date("2020-01-01"), y = 120, label = "unhealthy (sensitive groups)", hjust = 1, font
  scale_x_date(limits = as.Date(c("2018-01-01", "2019-12-31")),
    date_breaks = "2 months", date_labels = "%b %y") +
  ylab(expression("O"[3]* " AQI Value")) +
  theme(axis.text.x = element_text(angle = 45,  hjust = 1))
print(O3plot7)
```



Color palettes

Color palettes are an effective way to communicate additional aspects of our data, often illustrating a third categorical or continuous variable in addition to the variables on the x and y axes. A few rules for choosing colors:

- Consider if your plot needs to be viewed in black and white. If so, choose a sequential palette with varying color intensity.
- Choose a palette that is color-blind friendly
- Maximize contrast (e.g., no pale colors on a white background)
- Diverging color palettes should be used for diverging values (e.g., warm-to-cool works well for values on a scale encompassing negative and positive values)

Does your color palette communicate additional and necessary information? If the answer is no, then you might consider removing it and going with a single color. Common instances of superfluous or redundant color palettes include:

- Color that duplicates an axis
- Color that distinguishes categories when labels already exist (exception: if category colors repeat throughout a series of interrelated visualizations and help the reader build a frame of reference across a report)
- Color that reduces the conciseness of a plot

Perception is key! Choose palettes that are visually pleasing and will communicate what you are hoping your audience to perceive.

RColorBrewer (package)

- http://colorbrewer2.org
- https://moderndata.plot.ly/create-colorful-graphs-in-r-with-rcolorbrewer-and-plotly/

viridis and viridisLite (packages)

- https://cran.r-project.org/web/packages/viridis/vignettes/intro-to-viridis.html
- https://ggplot2.tidyverse.org/reference/scale_viridis.html

colorRamp (function; comes with base R as part of the grDevices package)

- https://bookdown.org/rdpeng/exdata/plotting-and-color-in-r.html#colorramp

LaCroixColoR (package)

- https://github.com/johannesbjork/LaCroixColoR

wesanderson (package)

- https://github.com/karthik/wesanderson

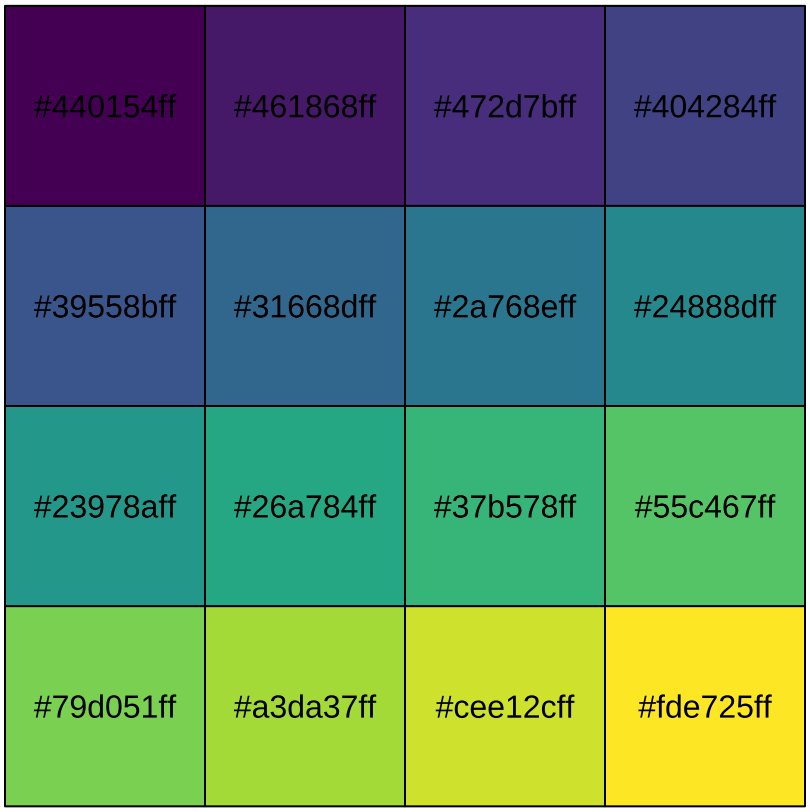
nationalparkcolors (package)

- https://github.com/katiejolly/nationalparkcolors

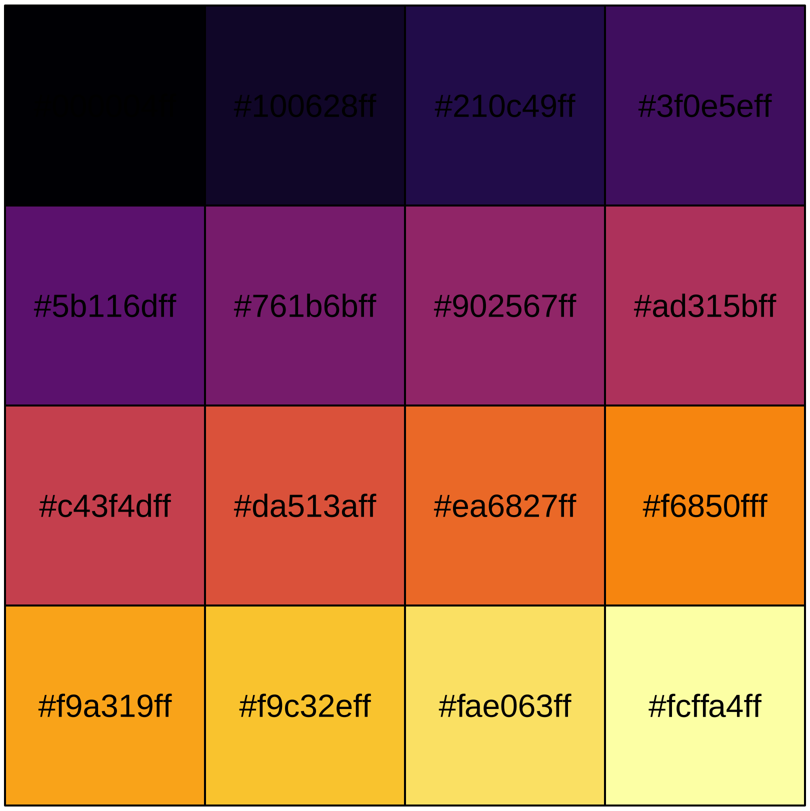
```
# install.packages("viridis")
# install.packages("RColorBrewer")
# install.packages("colormap")
library(viridis)
```

```
## Loading required package: viridisLite
```

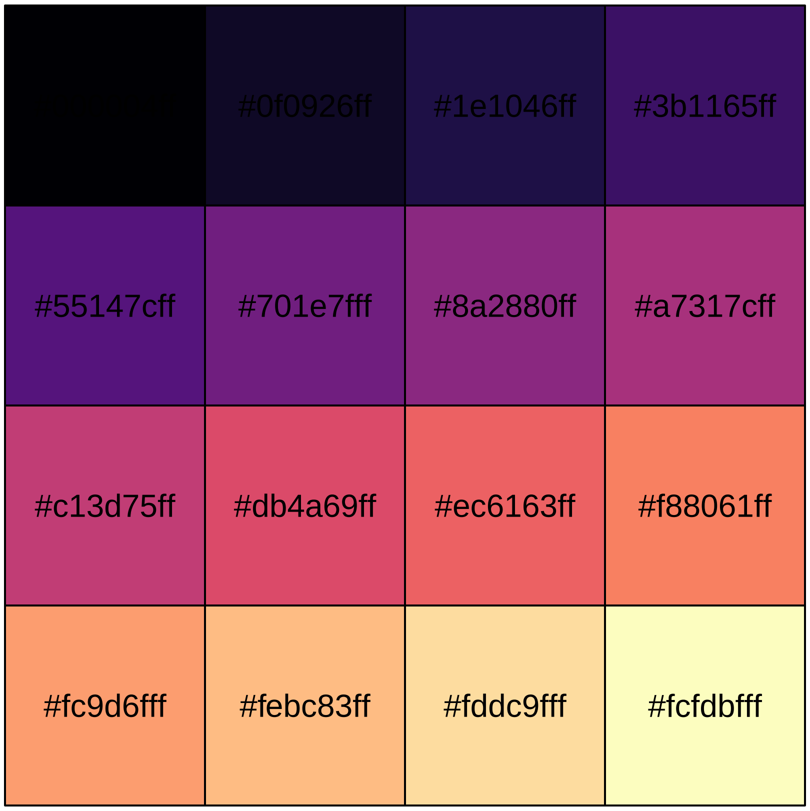
```
library(RColorBrewer)
library(colormap)

scales::show_col(colormap(colormap = colormaps$viridis, nshades = 16))
```



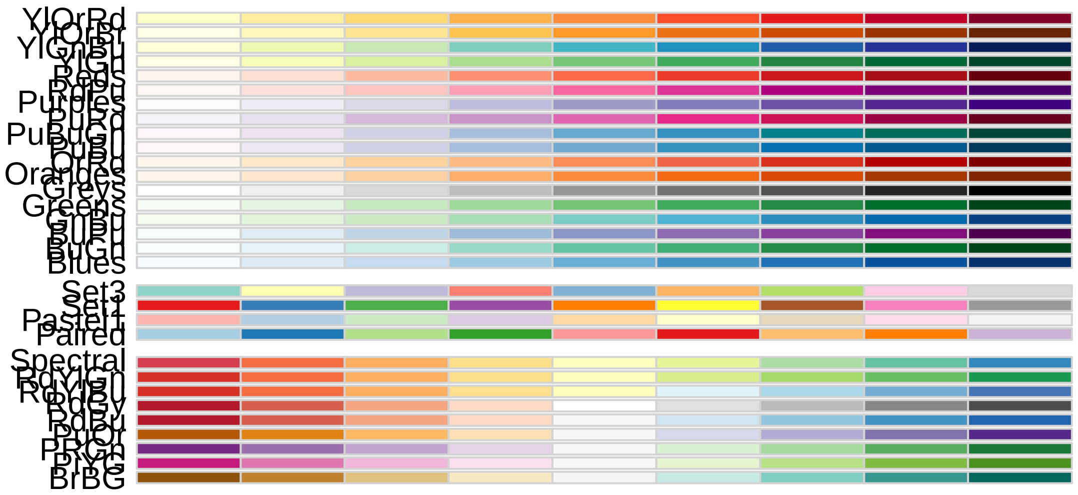
```r
scales::show_col(colormap(colormap = colormaps$inferno, nshades = 16))
```



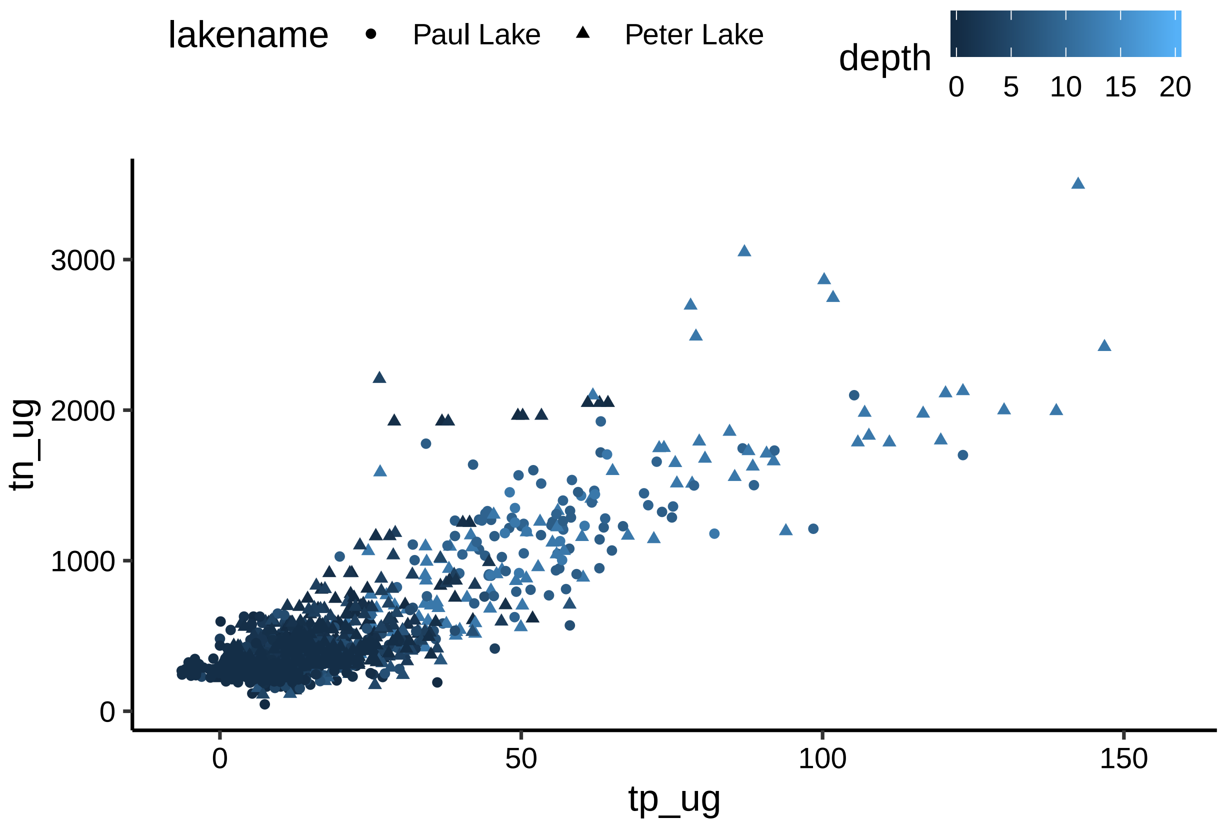
```r
scales::show_col(colormap(colormap = colormaps$magma, nshades = 16))
```



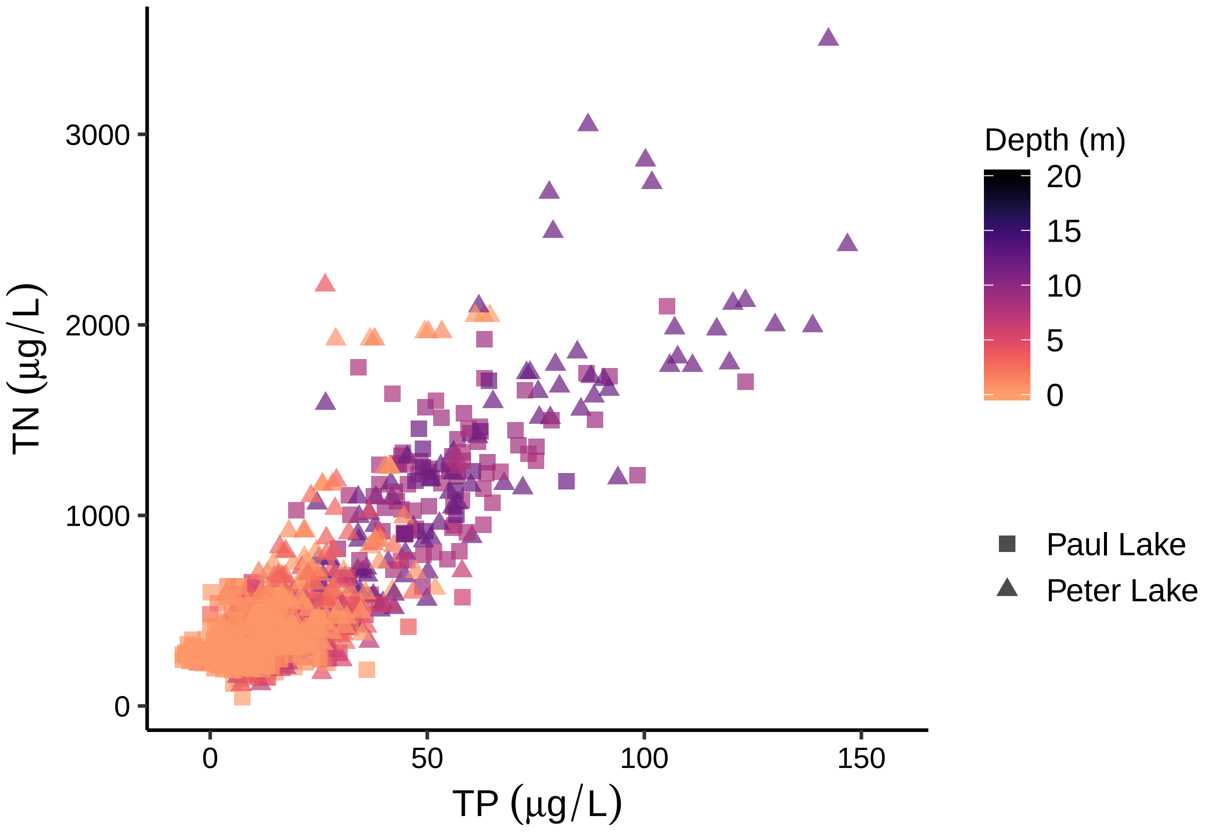
```r
display.brewer.all(n = 9)
```



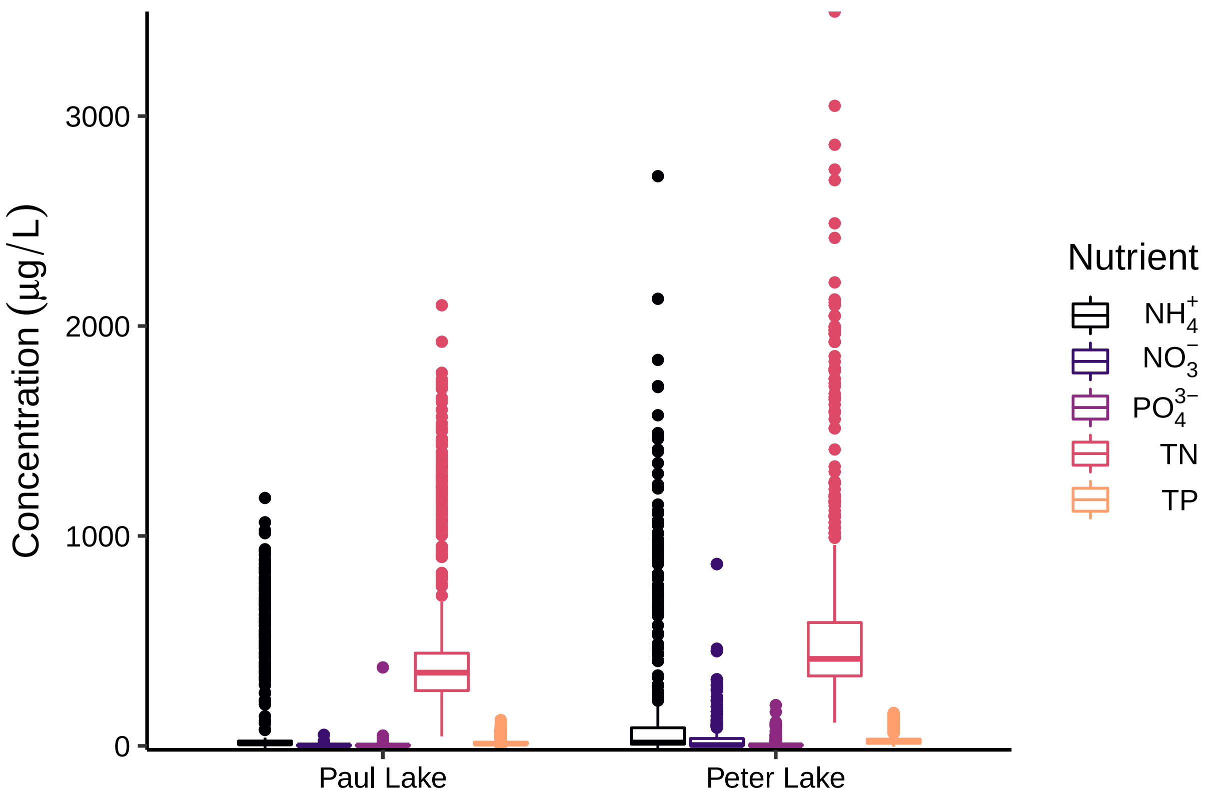
```r
NvsP <-
  ggplot(PeterPaul.chem.nutrients, aes(x = tp_ug, y = tn_ug, color = depth, shape = lakename)) +
  geom_point()
print(NvsP)
```



```
# let's first make the plot look better.
# change your axis labels to reflect TN and TP in micrograms per liter.
# change your legend labels
NvsP2 <-
  ggplot(PeterPaul.chem.nutrients, aes(x = tp_ug, y = tn_ug, color = depth, shape = lakename)) +
  geom_point(alpha = 0.7, size = 2.5) +
  # note: the labs function allows you to relabel anything specified as an aesthetic in the first line
  labs(x = expression(TP ~ (mu*g / L)), y = expression(TN ~ (mu*g / L)),
       color = "Depth (m)", shape = "") +
  scale_shape_manual(values = c(15, 17)) +
  #scale_color_distiller(palette = "Blues", direction = 1) + # use scale_color_brewer for discrete vari
  scale_color_viridis(option = "magma", direction = -1, end = 0.8) +
  theme(legend.position = "right",
        legend.text = element_text(size = 12), legend.title = element_text(size = 12))
print(NvsP2)
```



```r
# change your y axis label to list concentration in micrograms per liter
# remove your x axis label
# change labels for nutrients in the legend
# try out the different color palette options and choose one (or edit)
Nutrientplot <-
  ggplot(PeterPaul.chem.nutrients.gathered, aes(x = lakename, y = concentration, color = nutrient)) +
  geom_boxplot() +
# place your additional edits here
  labs(x = "", y = expression(Concentration ~ (mu*g / L)), color = "Nutrient") +
  scale_y_continuous(expand = c(0, 0)) +
  # scale_color_brewer(palette = "YlGnBu", values = (n = 9)[4:9],
  #                     labels = c(expression(NH[4]^{"+"}), expression(NO[3]^{"-"}),
  #                                expression(PO[4]^{"3-"}), "TN", "TP")) +
  # scale_color_manual(values = c("#7fcdbb", "#41b6c4", "#1d91c0", "#225ea8", "#0c2c84"),
  #                     labels = c(expression(NH[4]^{"+"}), expression(NO[3]^{"-"}),
  #                                expression(PO[4]^{"3-"}), "TN", "TP")) +
  scale_color_viridis(discrete = TRUE, option = "magma", end = 0.8,
                    labels = c(expression(NH[4]^{"+"}), expression(NO[3]^{"-"}),
                               expression(PO[4]^{"3-"}), "TN", "TP")) +
  theme(legend.position = "right")
print(Nutrientplot)
```



Multiple plots on a page

In situations where facets don't fill our needs to place multiple plots on a page, we can use the package `cowplot` to arrange plots. The `plot_grid` function is extremely flexible in its ability to arrange plots in specific configurations. A useful guide can be found here: https://cran.r-project.org/web/packages/cowplot/vignettes/introduction.html.

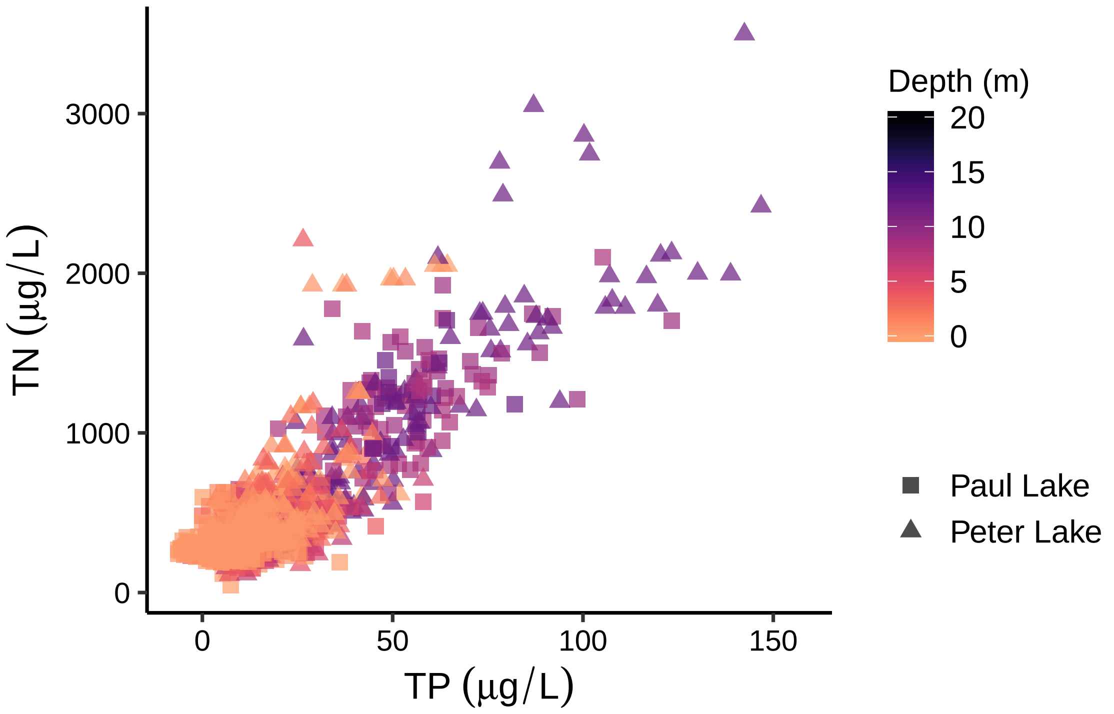
A useful guide for aligning plots by axis can be found here: https://wilkelab.org/cowplot/articles/aligning_plots.html

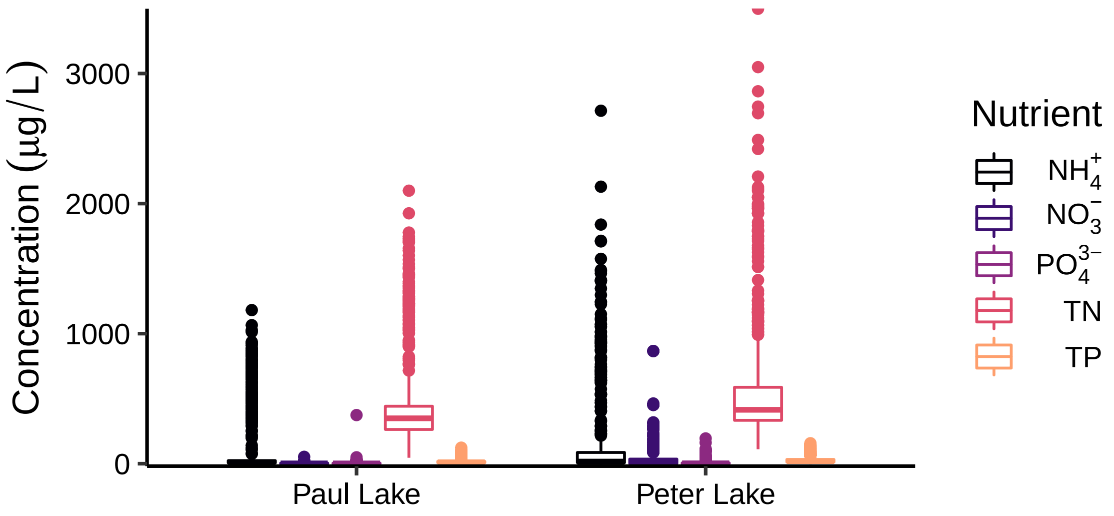
```
#install.packages("cowplot")
library(cowplot)
```

```
##
## ********************************************************

## 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())

## ********************************************************
```

```
plot_grid(NvsP2, Nutrientplot, nrow = 2, align = 'h', rel_heights = c(1.25, 1))
```

```
## Warning: Removed 21587 rows containing missing values (geom_point).
```





Saving plots

The `ggsave` function allows you to save plots in jpg, png, eps, pdf, tiff, and other formats. The following information can be supplied:

- filename and relative path, with file extension and in quotes (required)
- plot object (required)
- width, height, units
- resolution (dpi)

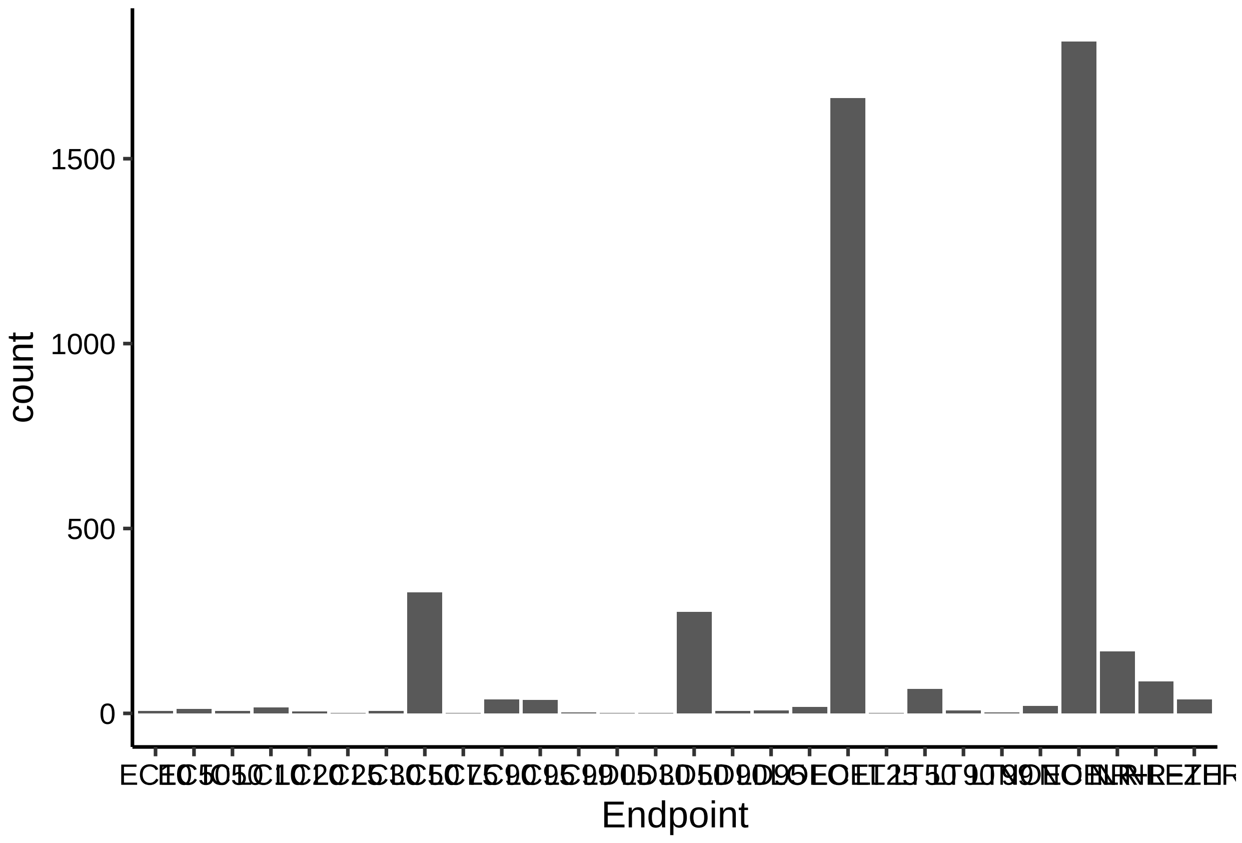
For example: `ggsave("./Output/PMplot.jpg", PMplot.faceted, height = 4, width = 6, units = "in", dpi = 300)`

Visualization challenge

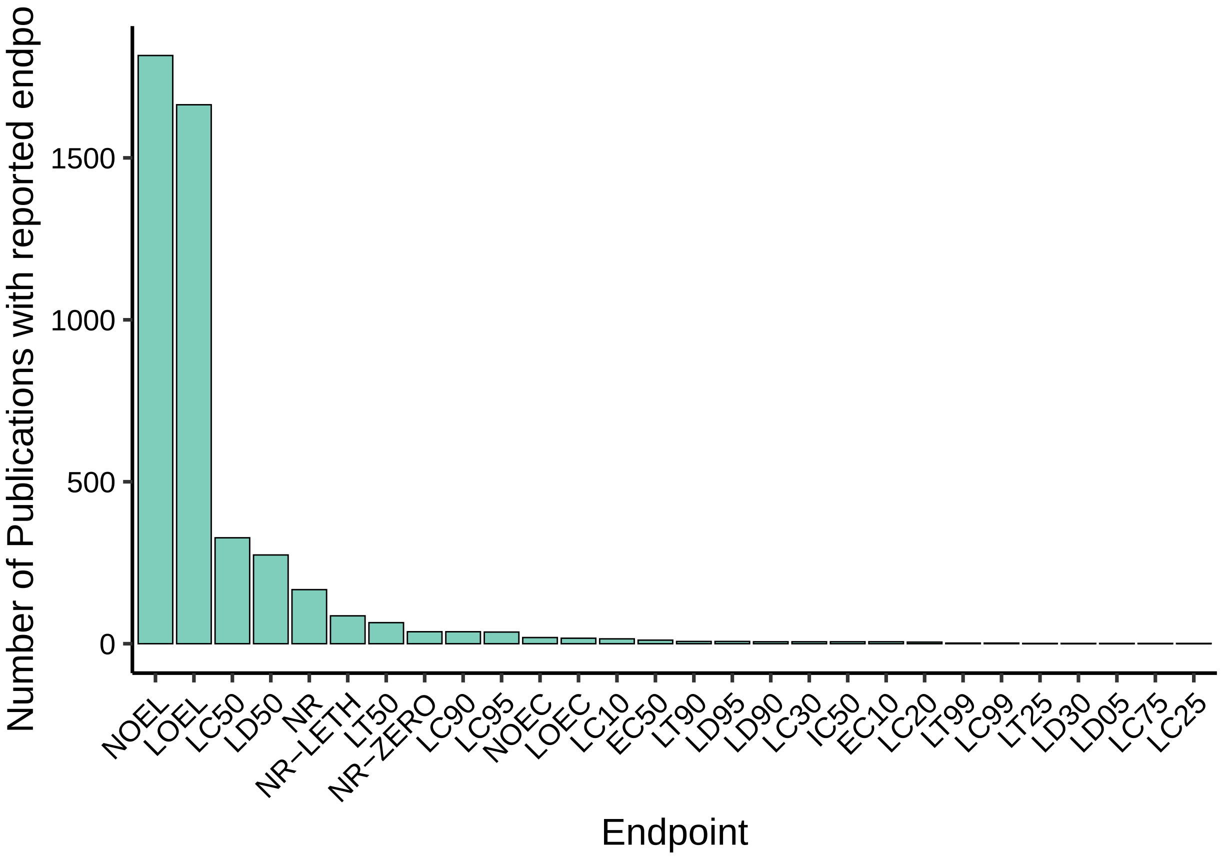
The following graph displays the counts of specific endpoints measured in neonicotinoid ecotoxicology studies. The way it is visualized, however, is not effective. Make the following coding changes to improve the graph:

1. Change the ordering of the "Endpoint" factor (function: `reorder`) so that the highest counts are listed first (hint: FUN = length)
2. Plot the barplot with the reordered factor levels. Add this line of code to make the bars show up left to right: scale_x_discrete(limits = rev(levels(Neonics$Endpoint)))
3. Adjust the x axis labels so they appear at a 45 degree angle.
4. Change the color and/or border on the bars. Should you have a consistent color across all bars, or a different color for each bar?

```
Neonics <- read.csv("../Data/Raw/ECOTOX_Neonicotinoids_Insects_raw.csv")
ggplot(Neonics) +
  geom_bar(aes(x = Endpoint))
```



```
Neonics$Endpoint <- reorder(Neonics$Endpoint, Neonics$Endpoint, FUN = length)

Neonics.plot <- ggplot(Neonics, aes(x = Endpoint)) +
  geom_bar(fill = "#7fcdbb", color = "black", size = 0.25) +
  scale_x_discrete(limits = rev(levels(Neonics$Endpoint))) +
  labs(y = "Number of Publications with reported endpoint") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
print(Neonics.plot)
```


Number of Publications with reported endpo
1500
1000
500
0
NOEL
LOEL
LC50
LD50
NR
NR−LETH
LT50
NR−ZERO
LC90
LC95
NOEC
LOEC
LC10
EC50
LT90
LD95
LD90
LC30
IC50
EC10
LC20
LT99
LC99
LT25
LD30
LD05
LC75
LC25
Endpoint