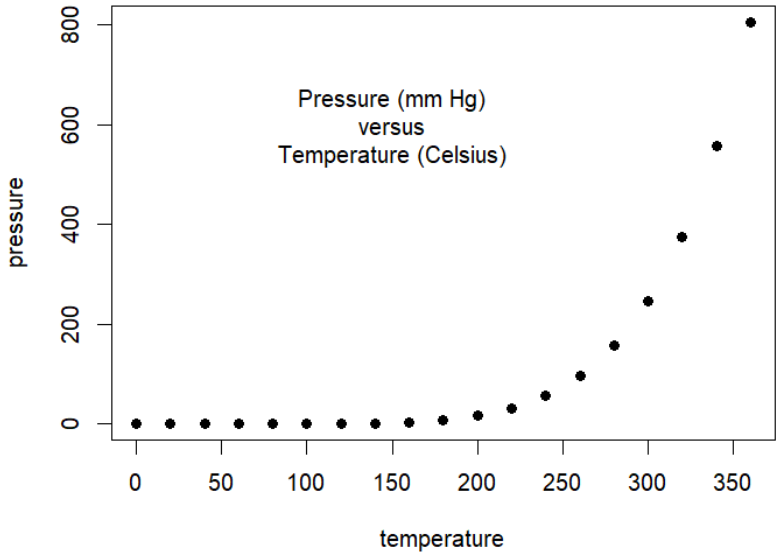
EPPS6356: Data Visualization **James S. Norcross**
Assignment 2 24 September 2024

Paul Murrell's R examples

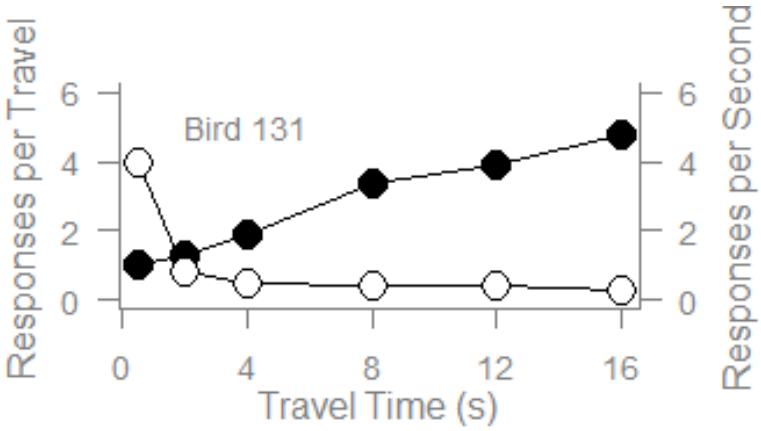
```
## Start plotting from basics
# Note the order
plot(pressure, pch=16)  # Can you change pch?
text(150, 600,
     "Pressure (mm Hg)\nversus\nTemperature (Celsius)")
```

Question: Can you change the pch? **Yes you can change it, and it will change the shapes and fill of the plots in the graph**




```
#  Examples of standard high-level plots
#  In each case, extra output is also added using low-level
#  plotting functions.
#

# Setting the parameter (3 rows by 2 cols)
par(mfrow=c(3, 2))

# Scatterplot
# Note the incremental additions

x <- c(0.5, 2, 4, 8, 12, 16)
y1 <- c(1, 1.3, 1.9, 3.4, 3.9, 4.8)
y2 <- c(4, .8, .5, .45, .4, .3)

# Setting label orientation, margins c(bottom, left, top, right) & text size
par(las=1, mar=c(4, 4, 2, 4), cex=.7)
plot.new()
plot.window(range(x), c(0, 6))
lines(x, y1)
lines(x, y2)
points(x, y1, pch=16, cex=2) # Try different cex value?
points(x, y2, pch=21, bg="white", cex=2)  # Different background color
par(col="gray50", fg="gray50", col.axis="gray50")
```

```
axis(1, at=seq(0, 16, 4)) # What is the first number standing for?
axis(2, at=seq(0, 6, 2))
axis(4, at=seq(0, 6, 2))
box(bty="u")
mtext("Travel Time (s)", side=1, line=2, cex=0.8)
mtext("Responses per Travel", side=2, line=2, las=0, cex=0.8)
mtext("Responses per Second", side=4, line=2, las=0, cex=0.8)
text(4, 5, "Bird 131")
par(mar=c(5.1, 4.1, 4.1, 2.1), col="black", fg="black", col.axis="black")
```



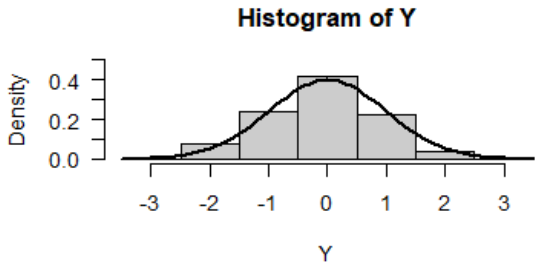
QUESTIONS:

Try different CEX value? **The CEX parameter in points() controls the size of the plotting symbols. Changing CEX, affects how large or small the symbols appear on the plot.**

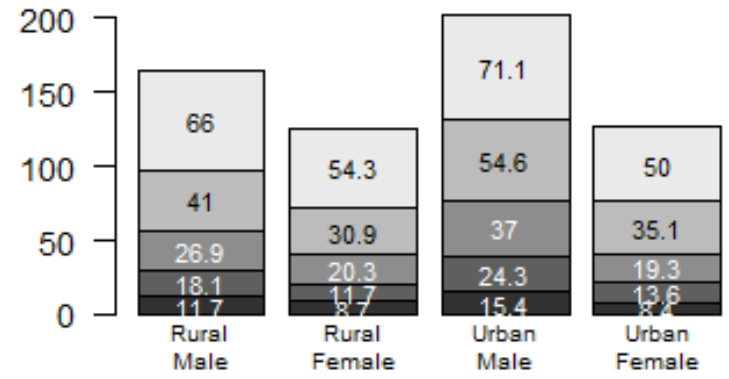
What is the first number standing for? **In the axis() function, the first argument represents the side of the plot where the axis is to be drawn. For example:**

1 stands for the bottom side
2 stands for the left side
3 stands for the top side
4 stands for the right side

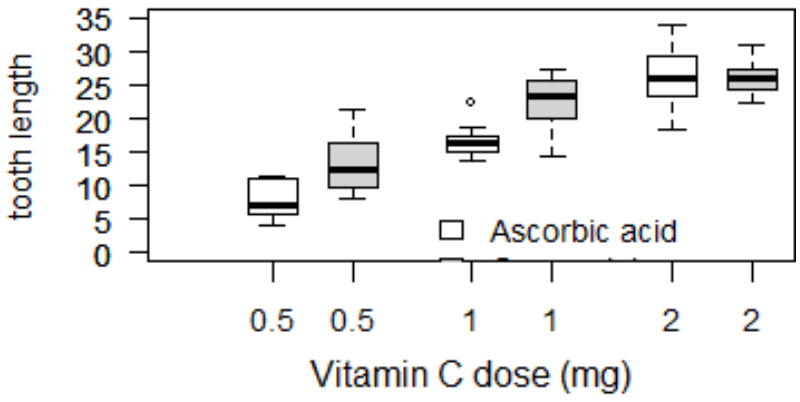
```
# Histogram
# Random data
Y <- rnorm(50)
# Make sure no Y exceed [-3.5, 3.5]
Y[Y < -3.5 | Y > 3.5] <- NA # Selection/set range
x <- seq(-3.5, 3.5, .1)
dn <- dnorm(x)
par(mar=c(4.5, 4.1, 3.1, 0))
hist(Y, breaks=seq(-3.5, 3.5), ylim=c(0, 0.5),
     col="gray80", freq=FALSE
lines(x, dnorm(x), lwd=2)
par(mar=c(5.1, 4.1, 4.1, 2.1))
```



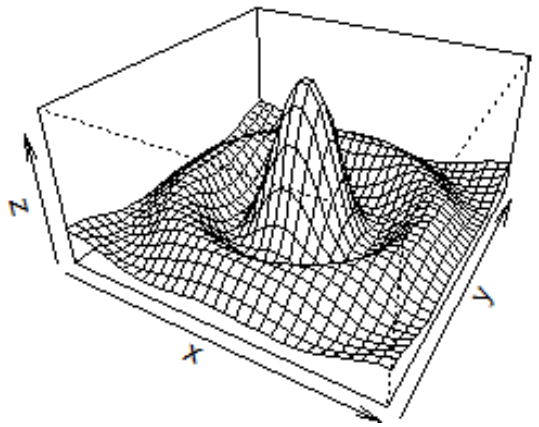
```
# Barplot
par(mar=c(2, 3.1, 2, 2.1))
midpts <- barplot(VADeaths,
                  col=gray(0.1 + seq(1, 9, 2)/11),
                  names=rep("", 4))
mtext(sub(" ", "\n", colnames(VADeaths)),
      at=midpts, side=1, line=0.5, cex=0.5)
text(rep(midpts, each=5), apply(VADeaths, 2, cumsum) - VADeaths/2,
     VADeaths,
     col=rep(c("white", "black"), times=3:2),
     cex=0.8)
par(mar=c(5.1, 4.1, 4.1, 2.1))
```



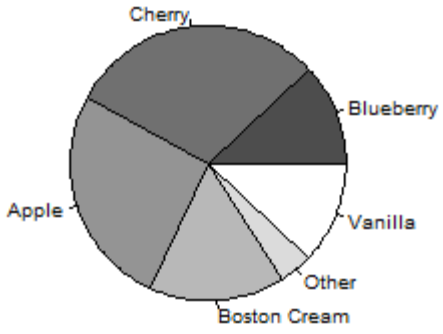

```
# Boxplot
par(mar=c(3, 4.1, 2, 0))
boxplot(len ~ dose, data = ToothGrowth,
        boxwex = 0.25, at = 1:3 - 0.2,
        subset= supp == "VC", col="white",
        xlab="",
        ylab="tooth length", ylim=c(0,35))
mtext("Vitamin C dose (mg)", side=1, line=2.5, cex=0.8)
boxplot(len ~ dose, data = ToothGrowth, add = TRUE,
        boxwex = 0.25, at = 1:3 + 0.2,

        subset= supp == "OJ")
legend(1.5, 9, c("Ascorbic acid", "Orange juice"),
       fill = c("white", "gray"),
       bty="n")
par(mar=c(5.1, 4.1, 4.1, 2.1))
```

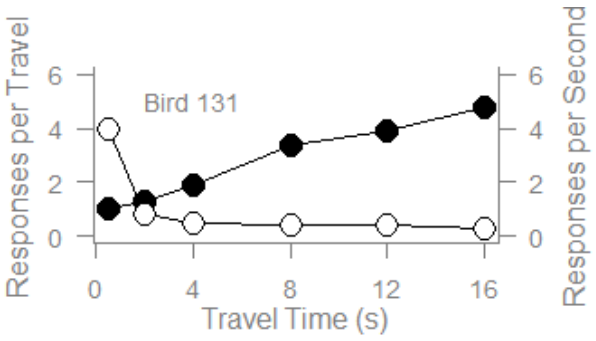


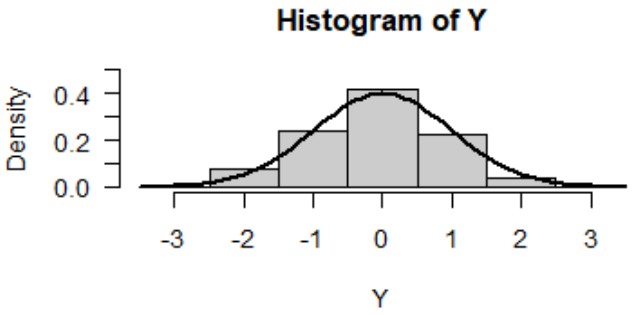
```
# Persp
x <- seq(-10, 10, length= 30)
y <- x
f <- function(x,y) { r <- sqrt(x^2+y^2); 10 * sin(r)/r }
z <- outer(x, y, f)
z[is.na(z)] <- 1
# 0.5 to include z axis label
par(mar=c(0, 0.5, 0, 0), lwd=0.5)
persp(x, y, z, theta = 30, phi = 30,
      expand = 0.5)
par(mar=c(5.1, 4.1, 4.1, 2.1), lwd=1)
```

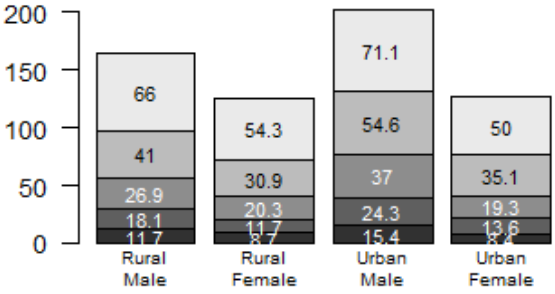


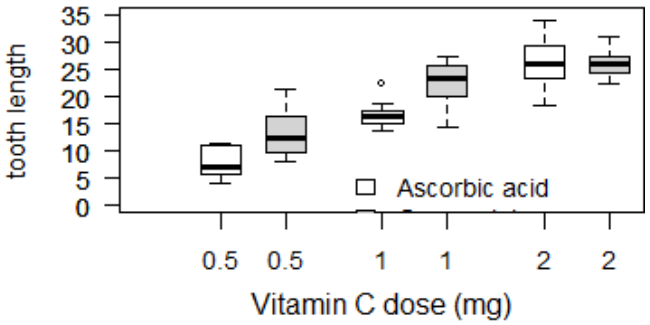

```
# Piechart
par(mar=c(0, 2, 1, 2), xpd=FALSE, cex=0.5)
pie.sales <- c(0.12, 0.3, 0.26, 0.16, 0.04, 0.12)
names(pie.sales) <- c("Blueberry", "Cherry",
                      "Apple", "Boston Cream", "Other", "Vanilla")
pie(pie.sales, col = gray(seq(0.3,1.0,length=6)))
```

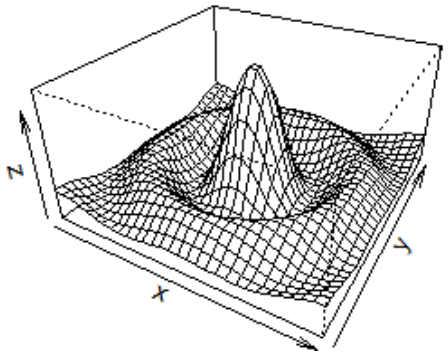


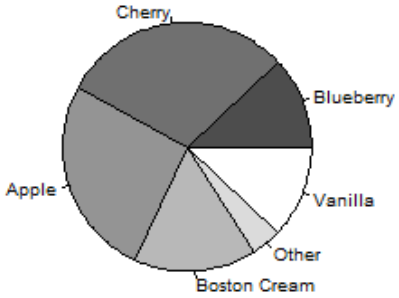












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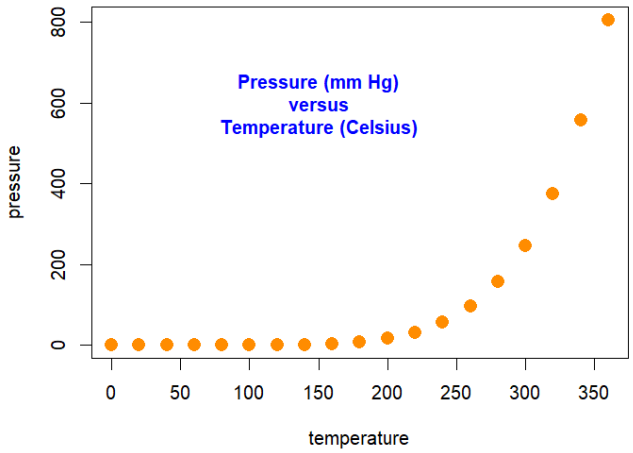
 # Exercise: Can you generate these charts individually?

First I will plot these charts individually and with different color schemes.

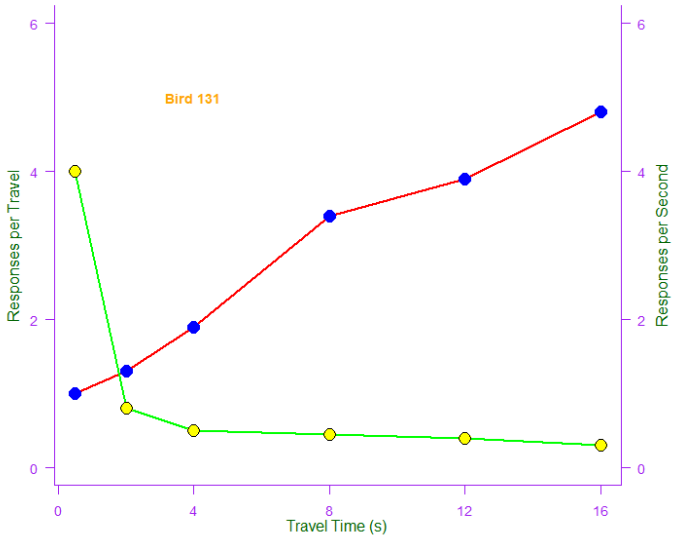
INITIAL PLOT OF PRESSURE VS. TEMPERATURE

```
plot(pressure, pch=16, col="darkorange", cex=1.5)
text(150, 600,
     "Pressure (mm Hg)\nversus\nTemperature (Celsius)", col="blue", font=2)
```



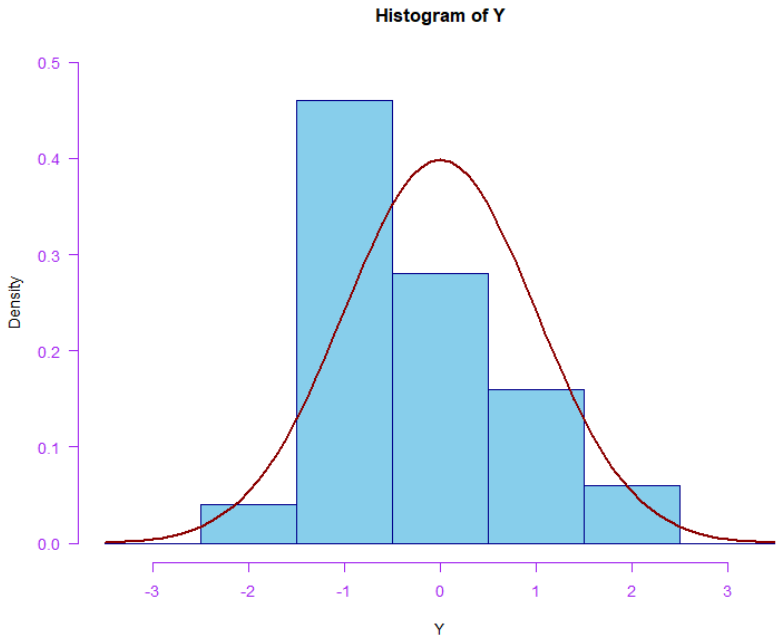
SCATTERPLOT

```
x <- c(0.5, 2, 4, 8, 12, 16)
y1 <- c(1, 1.3, 1.9, 3.4, 3.9, 4.8)
y2 <- c(4, .8, .5, .45, .4, .3)
par(las=1, mar=c(4, 4, 2, 4), cex=.7)
plot.new()
plot.window(range(x), c(0, 6))
lines(x, y1, col="red", lwd=2)  # Bright red line for y1
lines(x, y2, col="green", lwd=2)  # Bright green line for y2
points(x, y1, pch=16, col="blue", cex=2)  # Blue points for y1
points(x, y2, pch=21, bg="yellow", cex=2)  # Yellow-filled points for y2
par(col="purple", fg="purple", col.axis="purple")  # Purple axis colors
axis(1, at=seq(0, 16, 4))
axis(2, at=seq(0, 6, 2))
axis(4, at=seq(0, 6, 2))
box(bty="u", col="purple")
mtext("Travel Time (s)", side=1, line=2, cex=0.8, col="darkgreen")
mtext("Responses per Travel", side=2, line=2, las=0, cex=0.8, col="darkgreen")
mtext("Responses per Second", side=4, line=2, las=0, cex=0.8, col="darkgreen")
text(4, 5, "Bird 131", col="orange", font=2)
dev.new()  # Create a new plot window
```



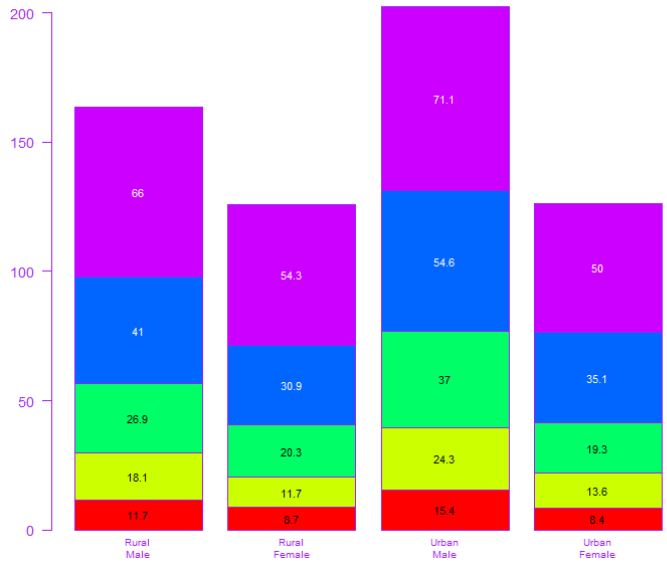
Histogram

```
Y <- rnorm(50)
Y[Y < -3.5 | Y > 3.5] <- NA
x <- seq(-3.5, 3.5, .1)
dn <- dnorm(x)
par(mar=c(4.5, 4.1, 3.1, 0))
hist(Y, breaks=seq(-3.5, 3.5), ylim=c(0, 0.5),
     col="skyblue", freq=FALSE, border="darkblue")  # Sky blue bars, dark blue border
lines(x, dnorm(x), lwd=2, col="darkred")  # Dark red line for the normal distribution
dev.new()  # Create a new plot window
```



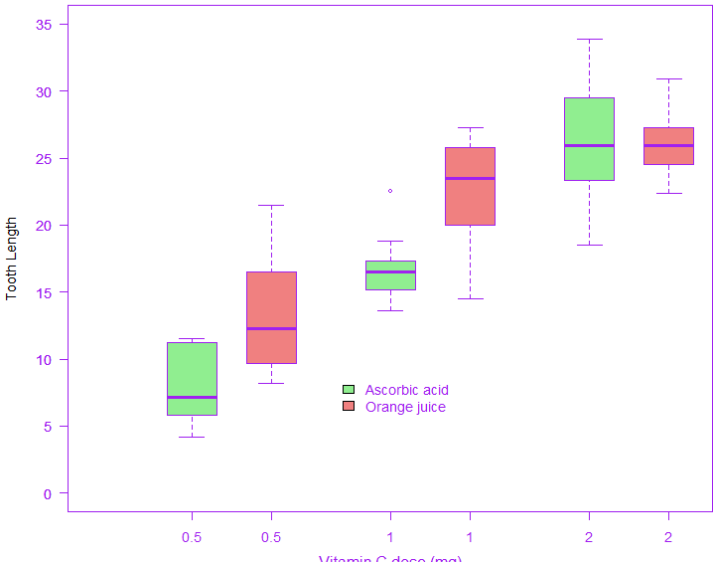
BAR PLOT

```
par(mar=c(2, 3.1, 2, 2.1))
midpts <- barplot(VADeaths,
                  col=rainbow(5),  # Rainbow colors for the bars
                  names=rep("", 4))
mtext(sub(" ", "\n", colnames(VADeaths)),
      at=midpts, side=1, line=0.5, cex=0.5)
text(rep(midpts, each=5), apply(VADeaths, 2, cumsum) - VADeaths/2,
     VADeaths,
     col=rep(c("black", "white"), times=3:2),
     cex=0.8)
dev.new()  # Create a new plot window
```



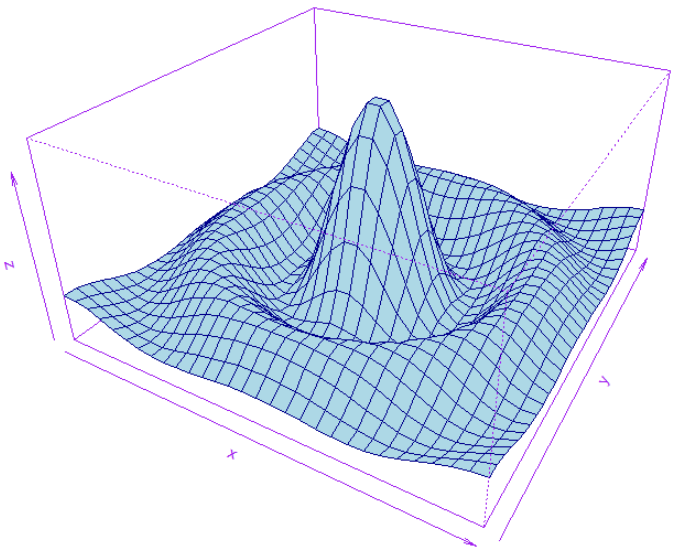
BOXPLOT

```
par(mar=c(3, 4.1, 2, 0))
boxplot(len ~ dose, data = ToothGrowth,
        boxwex = 0.25, at = 1:3 - 0.2,
        subset= supp == "VC", col="lightgreen",
        xlab="",
        ylab="Tooth Length", ylim=c(0,35))
mtext("Vitamin C dose (mg)", side=1, line=2.5, cex=0.8)
boxplot(len ~ dose, data = ToothGrowth, add = TRUE,
        boxwex = 0.25, at = 1:3 + 0.2,
        subset= supp == "OJ", col="lightcoral")  # Light coral for OJ group
legend(1.5, 9, c("Ascorbic acid", "Orange juice"),
       fill = c("lightgreen", "lightcoral"),
       bty="n")
dev.new()  # Create a new plot window
```



3D PERSPECTIVE PLOT

```
x <- seq(-10, 10, length=30)
y <- x
f <- function(x, y) { r <- sqrt(x^2 + y^2); 10 * sin(r)/r }
z <- outer(x, y, f)
z[is.na(z)] <- 1
persp(x, y, z, theta = 30, phi = 30,
      expand = 0.5, col="lightblue", border="darkblue")  # Light blue surface, dark blue
borders
dev.new()  # Create a new plot window
```



PIE CHART

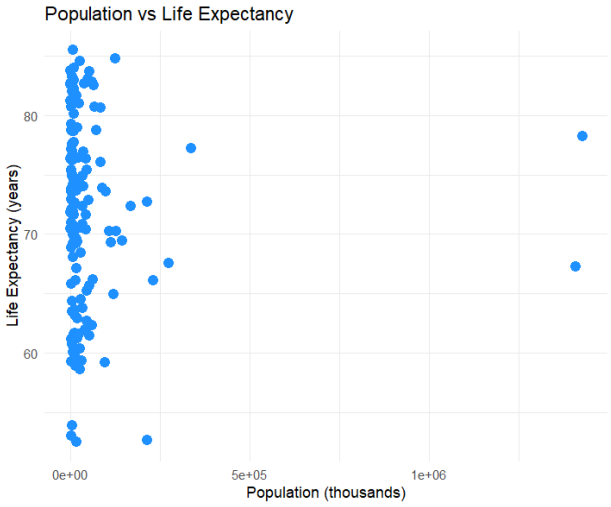
```
par(mar=c(0, 2, 1, 2), xpd=FALSE, cex=0.5)
pie.sales <- c(0.12, 0.3, 0.26, 0.16, 0.04, 0.12)
names(pie.sales) <- c("Blueberry", "Cherry",
                      "Apple", "Boston Cream", "Other", "Vanilla")
pie(pie.sales, col = rainbow(6))  # Use rainbow colors for the pie slices
```

#Try these functions using another dataset. Be sure to work on the layout and margins

Now I will plot these charts individually with different color schemes based on the data from the Happy Planet Index dataset.

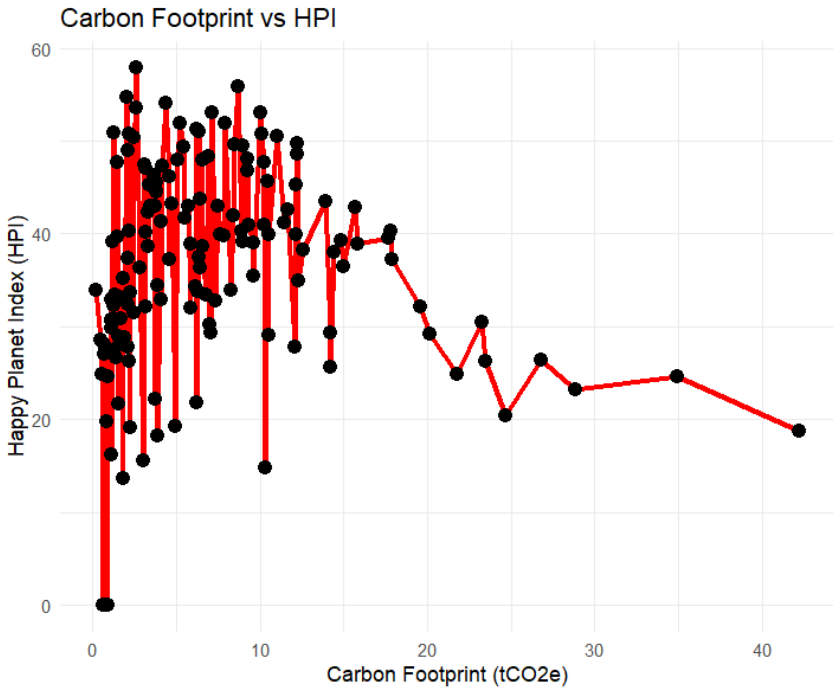
SCATTERPLOT

```
ggplot(mydata, aes(x = `Population (thousands)`, y = `Life Expectancy (years)`)) +
  geom_point(color = "dodgerblue", size = 3) +
  labs(x = "Population (thousands)", y = "Life Expectancy (years)",
       title = "Population vs Life Expectancy") +
  theme_minimal()
```



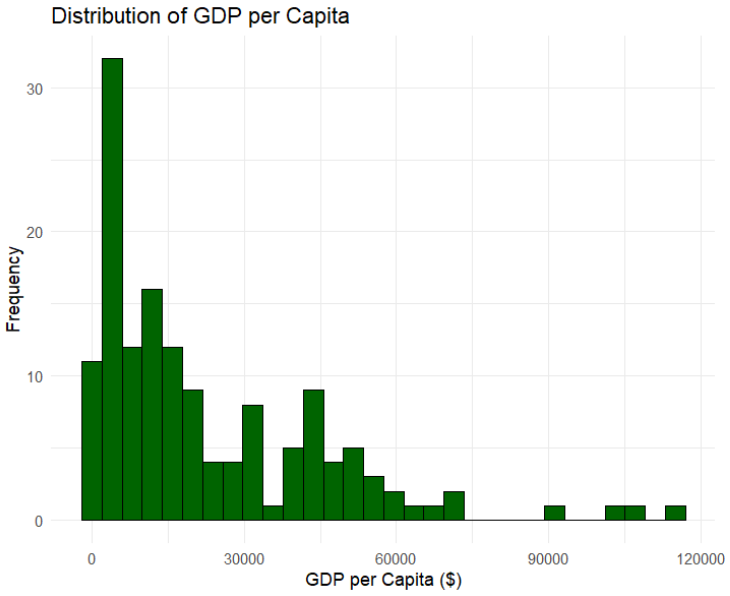
LINE PLOT

```
> ggplot(mydata, aes(x = `Carbon Footprint (tCO2e)`, y = HPI, group = 1)) +
+     geom_line(color = "red", linewidth = 1.2) +
+     geom_point(color = "black", size = 3) +
+     labs(x = "Carbon Footprint (tCO2e)", y = "Happy Planet Index (HPI)",
+          title = "Carbon Footprint vs HPI") +
+     theme_minimal()
```



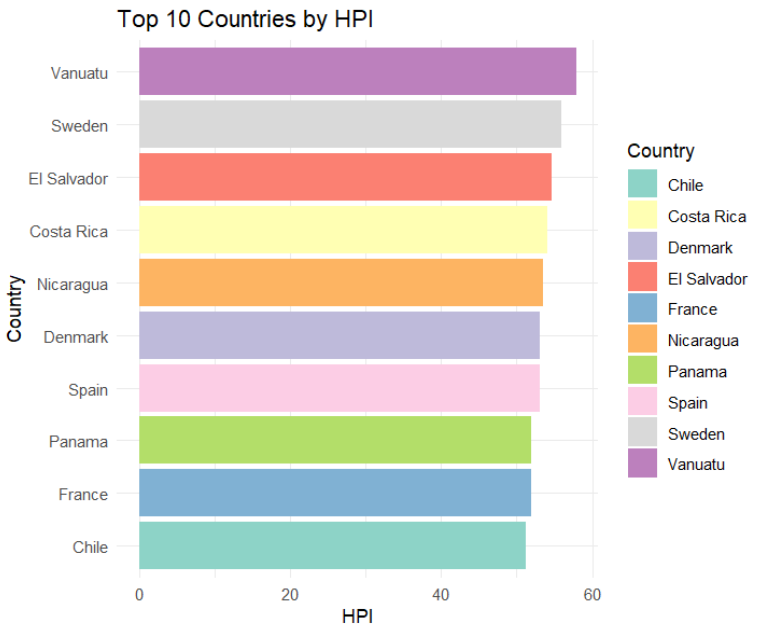
HISTOGRAM

```
ggplot(mydata, aes(x = `GDP per capita ($)`)) +
  geom_histogram(fill = "darkgreen", color = "black", bins = 30) +
  labs(x = "GDP per Capita ($)", y = "Frequency",
       title = "Distribution of GDP per Capita") +
  theme_minimal()
```



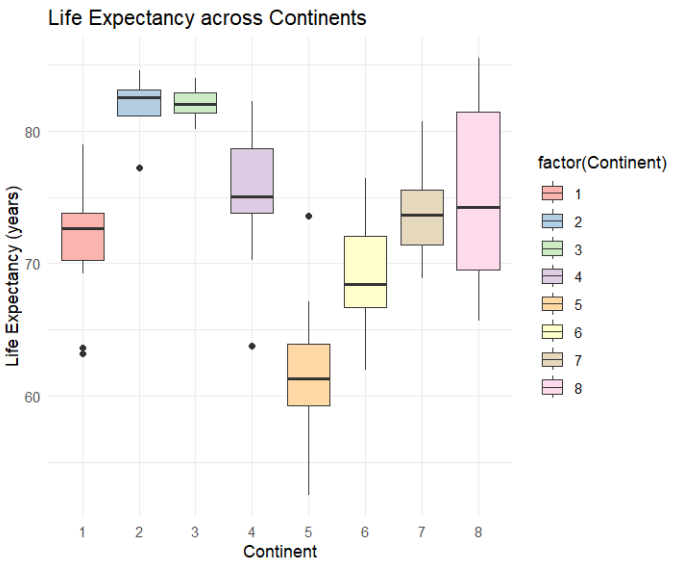
BAR PLOT

```
top10_hpi <- mydata[order(-mydata$HPI),][1:10,]
ggplot(top10_hpi, aes(x = reorder(Country, HPI), y = HPI, fill = Country)) +
  geom_bar(stat = "identity") +
  coord_flip() +
  scale_fill_brewer(palette = "Set3") +
  labs(x = "Country", y = "HPI", title = "Top 10 Countries by HPI") +
  theme_minimal()
```



BOX PLOT

```
ggplot(mydata, aes(x = factor(Continent), y = `Life Expectancy (years)`, fill =
factor(Continent))) +
  geom_boxplot() +
  scale_fill_brewer(palette = "Pastel1") +
  labs(x = "Continent", y = "Life Expectancy (years)",
       title = "Life Expectancy across Continents") +
  theme_minimal()
```



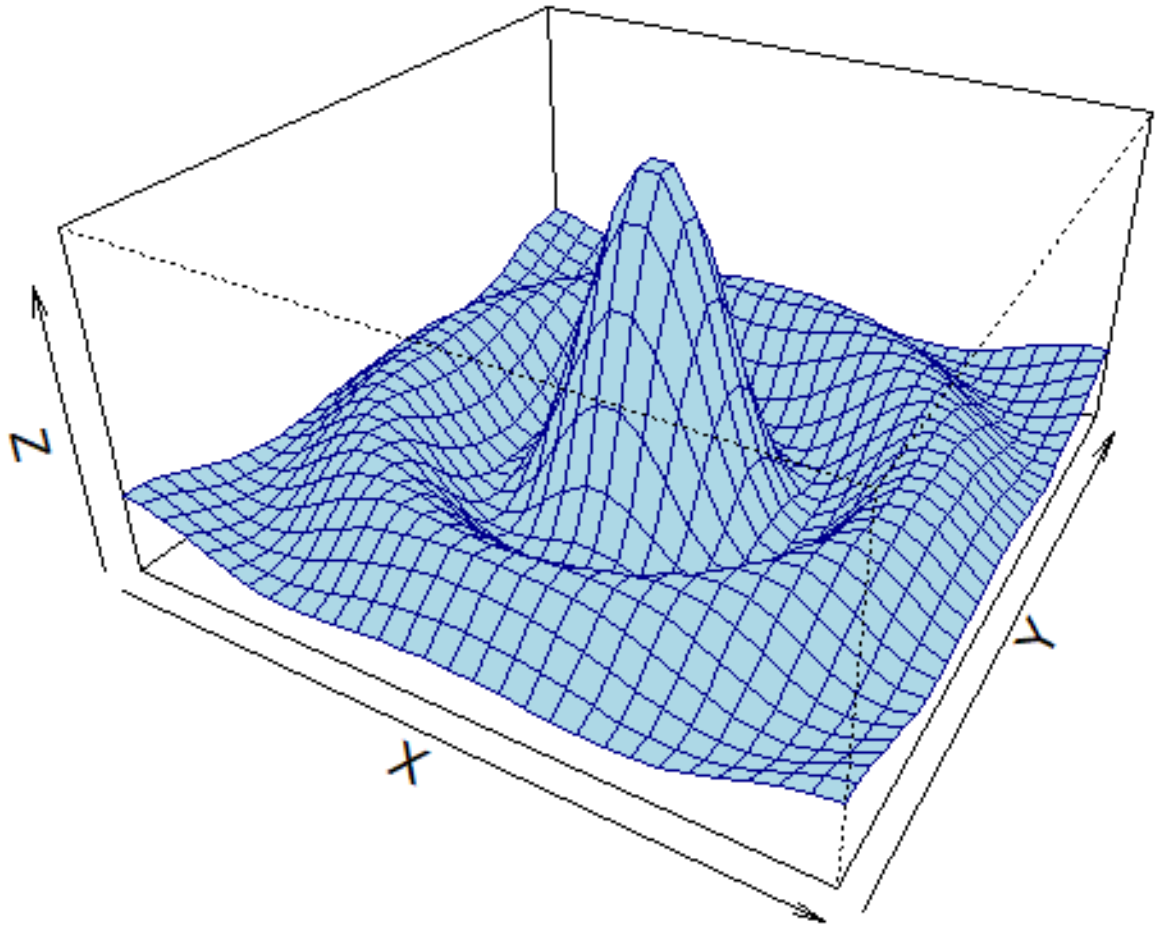
3D PERSPECTIVE PLOT

```
x <- seq(-10, 10, length=30)
y <- x

# Define the function for z values
f <- function(x, y) {
  r <- sqrt(x^2 + y^2)
  z <- sin(r) / r
  z[is.na(z)] <- 1  # Handle NaN values
  return(z)
}

# Create the z matrix
z <- outer(x, y, f)

# Create the 3D perspective plot
persp(x, y, z, theta = 30, phi = 30,
      expand = 0.5, col="lightblue", border="darkblue",
      xlab="X", ylab="Y", zlab="Z")
```



PIE CHART

```
continent_co2 <- aggregate(`CO2 threshold for year  (tCO2e)` ~ Continent, data = mydata,
sum)
pie(continent_co2$`CO2 threshold for year  (tCO2e)`,
    labels = continent_co2$Continent,
    col = rainbow(length(continent_co2$Continent)),
    main = "CO2 Thresholds by Continent")
```