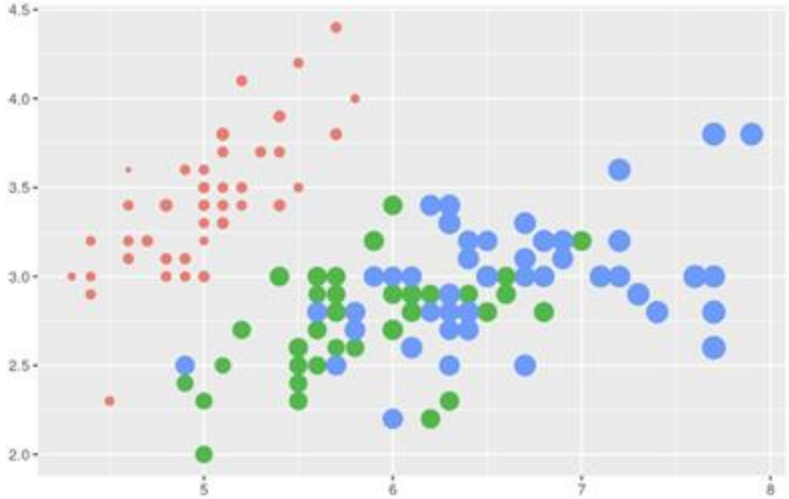
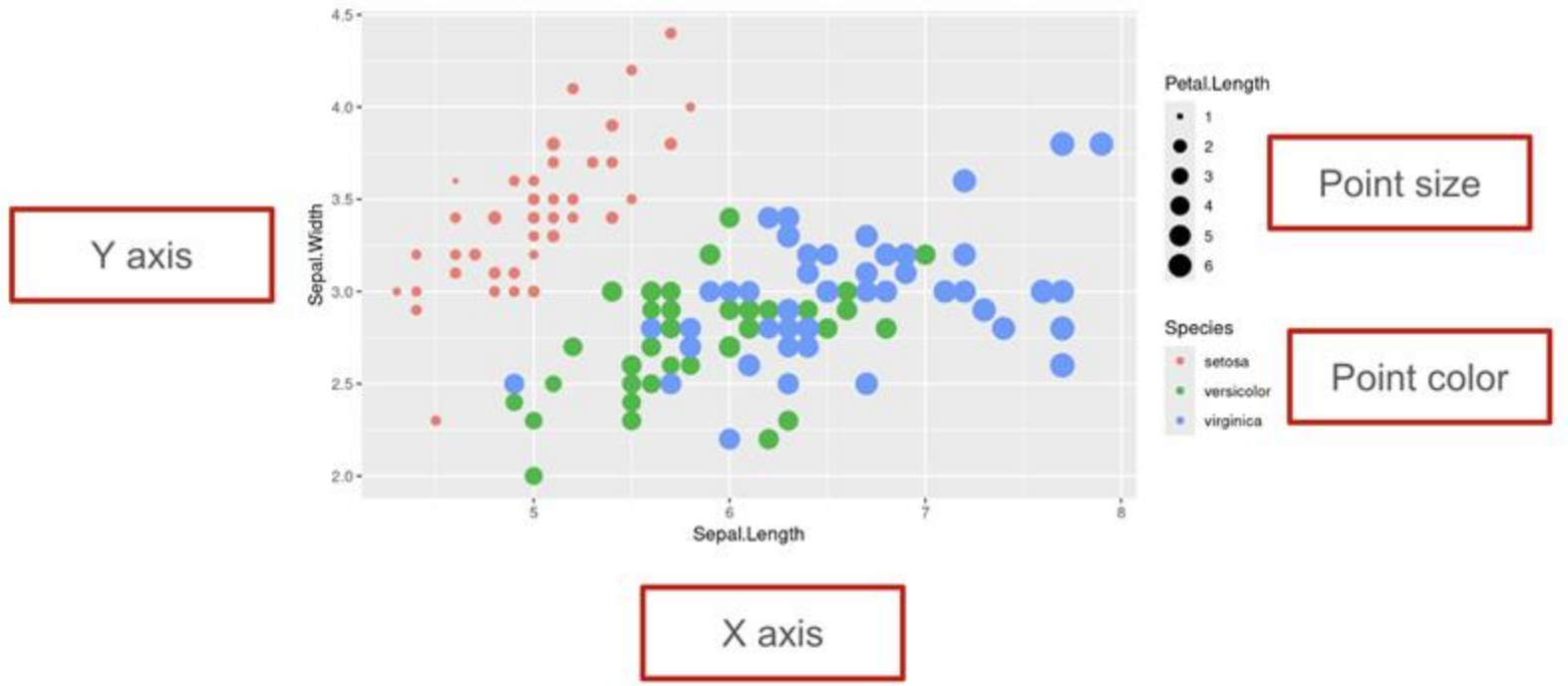
Introduction to plotting and statistics

- **Hands-on**: Plotting information from data structures for real-time analysis

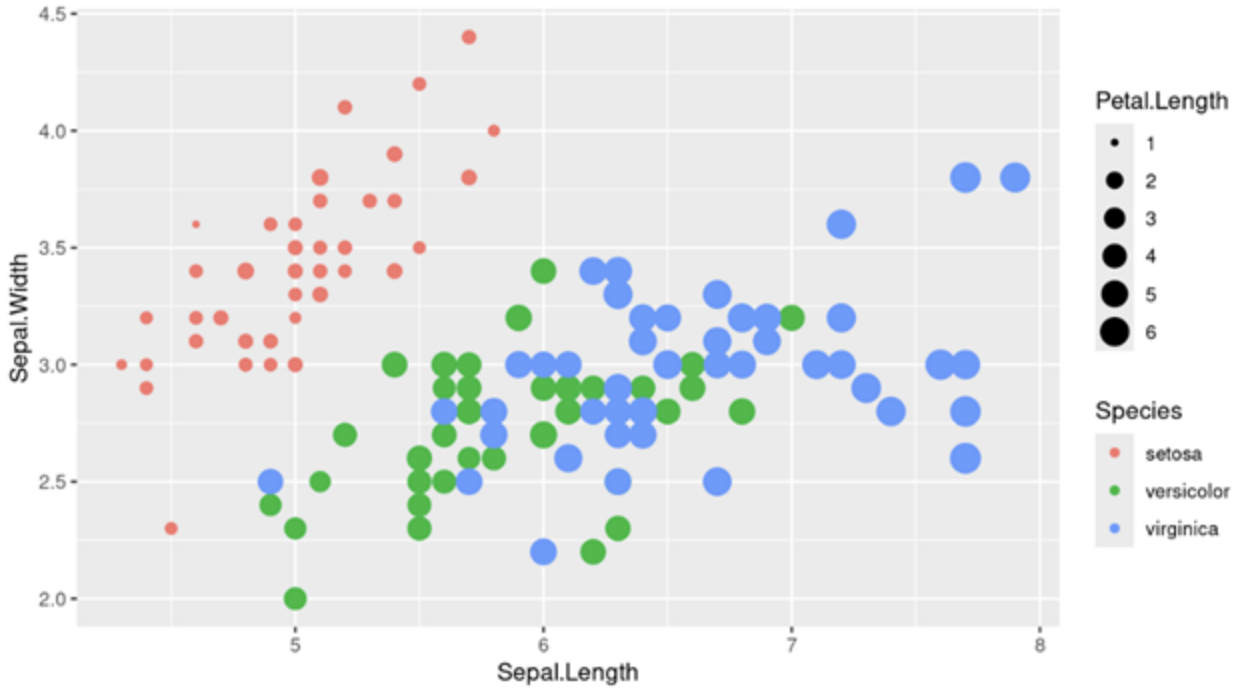
Student	Subject	Score
A	Math	99
A	Literature	45
A	PE	56
B	Math	73



Variables are individually represented in the dimensions of a plot



Plot dimensions motivate data interpretation and analysis



"The pink points are smaller and are higher/to the left of the bigger blue/green points."

"The **setosa** species has shorter petal lengths, and greater sepal width and sepal length, compared to the **versicolor** and **virginica** species.

To generate the plot, the data (oftentimes as a data frame) needs to include each variable as a column, with the data encoding each point within the row.

Data generally comes in “wide” format

Example of wide format:

Student	Math	Literature	PE
A	99	45	56
B	73	78	55
C	12	96	57

- Can be easier to understand
- More convenient for certain analyses or visualization
- No information is repeated in each line

https://rb.gy/e6uyis

Long data format is the “tidy” format

Example of long format:

Student	Subject	Score
A	Math	99
A	Literature	45
A	PE	56
B	Math	73
B	Literature	78
B	PE	55
C	Math	12

- Multiple rows correspond to a single observation and measurement
- One column for each variable
- Additional columns store metadata or grouping variables

Manipulating data frames: Long to wide data

```r
library(tidyr)

# Example long format data
long_data <- data.frame(
  Subject = c("A", "A", "B", "B"),
  Time = c(1, 2, 1, 2),
  Measurement = c(10, 15, 12, 18)
)

# Convert long format data to wide format
wide_data <- spread(long_data, key = Time, value = Measurement)

# View the wide format data
print(wide_data)
```

```
> head(long_data)
  Subject Time Measurement
1       A    1          10
2       A    2          15
3       B    1          12
4       B    2          18
```

```
> wide_data
  Subject  1  2
1       A 10 15
2       B 12 18
```

Now `1` and `2` can be directly compared

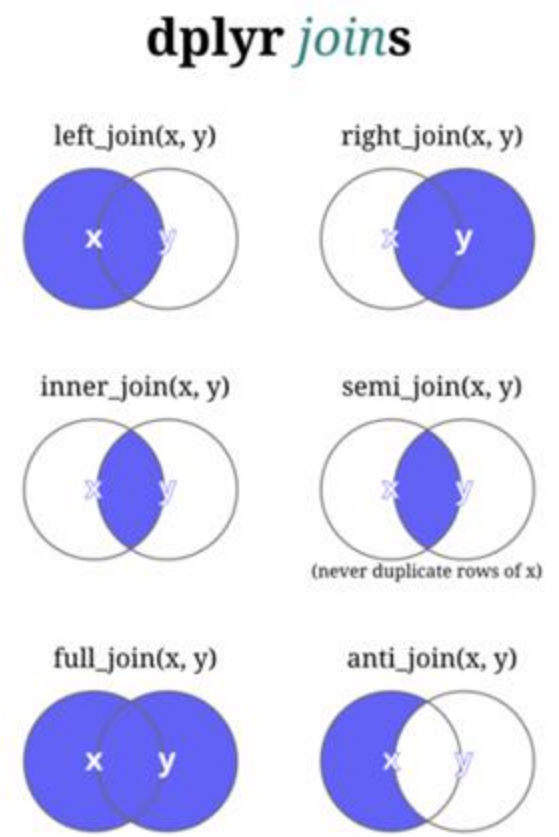
Manipulating data frames: Wide to long data

```r
library(tidyr)

# Example wide format data
wide_data <- data.frame(
  Subject = c("A", "B"),
  Time1 = c(10, 12),
  Time2 = c(15, 18)
)

# Convert wide format data to long format
long_data <- gather(wide_data, key = Time, value = Measurement, -Subject)

# View the long format data
print(long_data)
```

```
> wide_data
  Subject Time1 Time2
1       A    10    15
2       B    12    18
>
>
> long_data
  Subject Time Measurement
1       A    1          10
2       A    2          15
3       B    1          12
4       B    2          18
```

Now `Time` and `Measurement` can be directly compared

Merging data: What if you want to compare data from two different data frames?




```r
library(dplyr)

# Example datasets
df1 <- data.frame(ID = c(1, 2, 3), Name = c("Alice", "Bob", "Charlie"))
df2 <- data.frame(ID = c(2, 3, 4), Score = c(85, 90, 95))

# Inner join
inner_merged <- inner_join(df1, df2, by = "ID")

# Left join
left_merged <- left_join(df1, df2, by = "ID")

# Right join
right_merged <- right_join(df1, df2, by = "ID")

# Full join
full_merged <- full_join(df1, df2, by = "ID")

# Semi-join
semi_merged <- semi_join(df1, df2, by = "ID")

# Anti-join
anti_merged <- anti_join(df1, df2, by = "ID")
```

*_join() functions combine the information across two data frames

```
> full_merged
  ID    Name Score
1  1   Alice    NA
2  2     Bob    85
3  3 Charlie    90
4  4    <NA>    95
```

```r
library(dplyr)

# Example datasets
df1 <- data.frame(ID = c(1, 2, 3), Name = c("Alice", "Bob", "Charlie"))
df2 <- data.frame(ID = c(2, 3, 4), Score = c(85, 90, 95))

# Inner join
inner_merged <- inner_join(df1, df2, by = "ID")

# Left join
left_merged <- left_join(df1, df2, by = "ID")

# Right join
right_merged <- right_join(df1, df2, by = "ID")

# Full join
full_merged <- full_join(df1, df2, by = "ID")

# Semi-join
semi_merged <- semi_join(df1, df2, by = "ID")

# Anti-join
anti_merged <- anti_join(df1, df2, by = "ID")
```

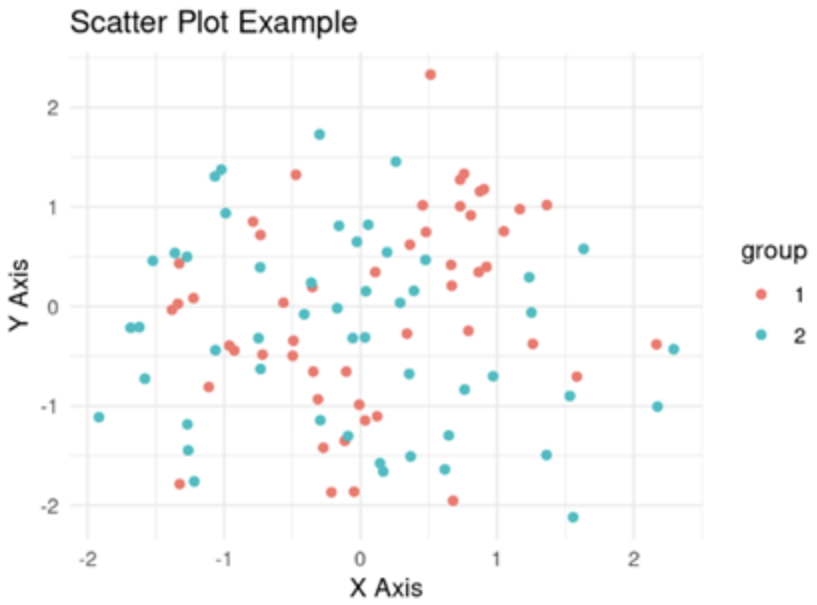
Using the ggplot2 package: Structuring a plot command

- Data
- Aesthetics (aes)
- Geometries (geom)
- Scales
- Coordinate systems
- Facets
- Themes

```r
library(ggplot2)

# Sample data
df <- data.frame(
  x = rnorm(100),
  y = rnorm(100),
  group = factor(rep(1:2, each = 50))
)

# Creating a scatter plot
ggplot(df, aes(x = x, y = y, color = group)) +
  geom_point() +
  theme_minimal() +
  labs(title = "Scatter Plot Example", x = "X Axis", y = "Y Axis")
```

https://ggplot2.tidyverse.org/reference/

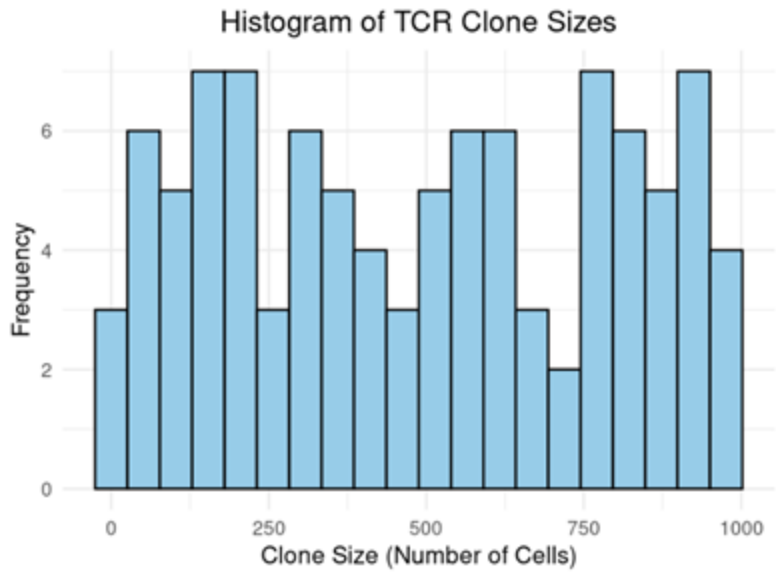
Using the ggplot2 package: Structuring a plot command




```r
library(ggplot2)

# Sample data
df <- data.frame(
  x = rnorm(100),
  y = rnorm(100),
  group = factor(rep(1:2, each = 50))
)

# Creating a scatter plot
ggplot(df, aes(x = x, y = y, color = group)) +
  geom_point() +
  theme_minimal() +
  labs(title = "Scatter Plot Example", x = "X Axis", y = "Y Axis")
```

Using the ggplot2 package: Structuring a plot command

```r
library(ggplot2)
library(dplyr)

# Step 1: Simulate data
set.seed(123)  # Set seed for reproducibility
num_clonotypes <- 100  # Specify the number of different clonotypes

# Create a data frame with random cell counts for each clonotype
tcr_data <- tibble(
  clonotype = paste("TCR", seq_len(num_clonotypes), sep=""),
  cell_count = sample(1:1000, num_clonotypes, replace=TRUE)  # Random cell
)

# Step 2: Create a histogram using ggplot2
ggplot(tcr_data, aes(x = cell_count)) +
  geom_histogram(bins = 20, fill = "skyblue", color = "black") +
  theme_minimal() +
  labs(
    title = "Histogram of TCR Clone Sizes",
    x = "Clone Size (Number of Cells)",
    y = "Frequency"
  ) +
  theme(
    plot.title = element_text(hjust = 0.5)  # Center the plot title
  )
```



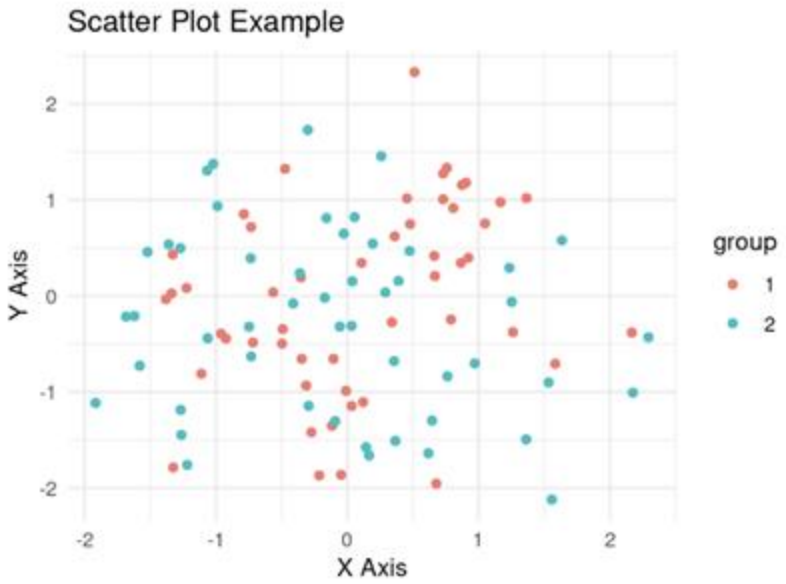
Performing statistics

```r
# Randomly generated sample data: Immune marker levels in two patient groups
group1 <- rnorm(30, mean = 5, sd = 1.5) # Patients with a mutation
group2 <- rnorm(30, mean = 4.5, sd = 1.2) # Patients without the mutation

# Perform a t-test
test <- t.test(group1, group2)

# Print the result
print(test)
```

```
> print(test)

        Welch Two Sample t-test

data:  group1 and group2
t = 1.2838, df = 57.999, p-value = 0.2043
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.2731337  1.2498937
sample estimates:
mean of x mean of y
  5.23333   4.74495
```

Most statistical test commands are just their names (e.g. wilcox)

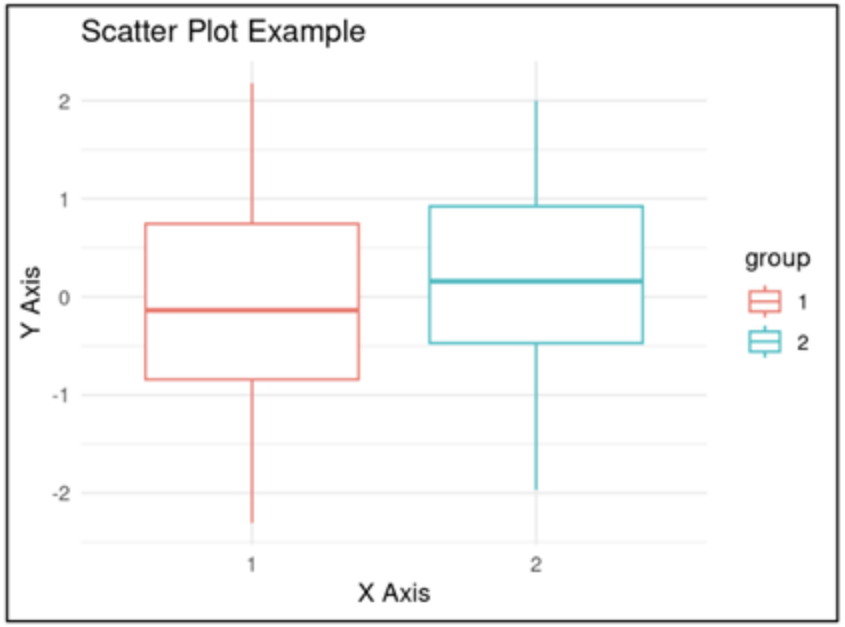
Adding statistics to your plot using ggpubr()




```r
library(ggplot2)

# Sample data
df <- data.frame(
  x = rnorm(100),
  y = rnorm(100),
  group = factor(rep(1:2, each = 50))
)

# Creating a scatter plot
ggplot(df, aes(x = x, y = y, color = group)) +
  geom_point() +
  theme_minimal() +
  labs(title = "Scatter Plot Example", x = "X Axis", y = "Y Axis")
```

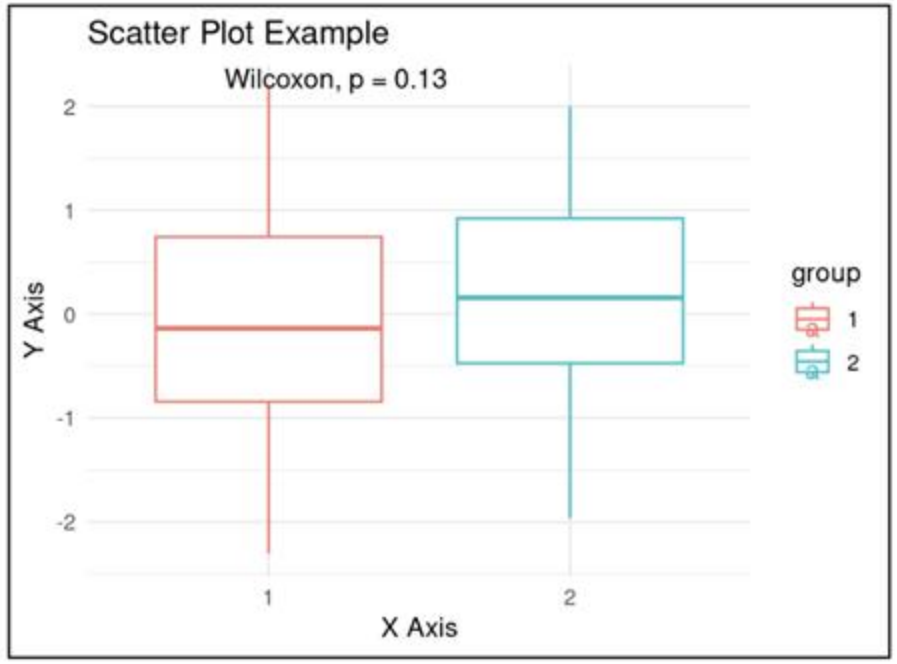
Is the visualization appropriate for the statistical test you're trying to use?

Consider different types of plots




```r
# Creating a box plot
ggplot(df, aes(x = group, y = y, color = group)) +
  geom_boxplot() +
  theme_minimal() +
  labs(title = "Scatter Plot Example", x = "X Axis", y = "Y Axis")
```

Adding a Wilcoxon test




```r
library(ggpubr)
# Creating a box plot
ggplot(df, aes(x = group, y = y, color = group)) +
  geom_boxplot() +
  stat_compare_means(method = 'wilcox') +
  theme_minimal() +
  labs(title = "Scatter Plot Example", x = "X Axis", y = "Y Axis")
```

Hands-on: Reading, writing, and interpreting data structures

1. Consider starting and saving a new RScript
2. Work through the blocks of code under the **Course: Basic plotting and statistics** page
   - Review the details on how the code works in the Lecture slides for assistance
   - Put a post-it on your laptop if you get stuck, indicating for a TA to come up to you
   - Work through the blocks of code on this page, practicing in both your Rscript and the console
3. Take the next step
   - There are a list of **Additional exercises** at the bottom of the page for you to try on your own

Goal: Design your first plot

How would you visualize one of your datasets?