MiA Case Study 2

Data Analysis in R

Image of grazer Oxyrrhis marina and phytoplankton Dunaliella tertiolecta in culture

Load packages and data

```
library(readxl)
library(ggplot2)
library(dplyr)

data <- read.csv("CaseStudy2_ROI_Data.csv")
```

Prepare the data for plotting and analysis

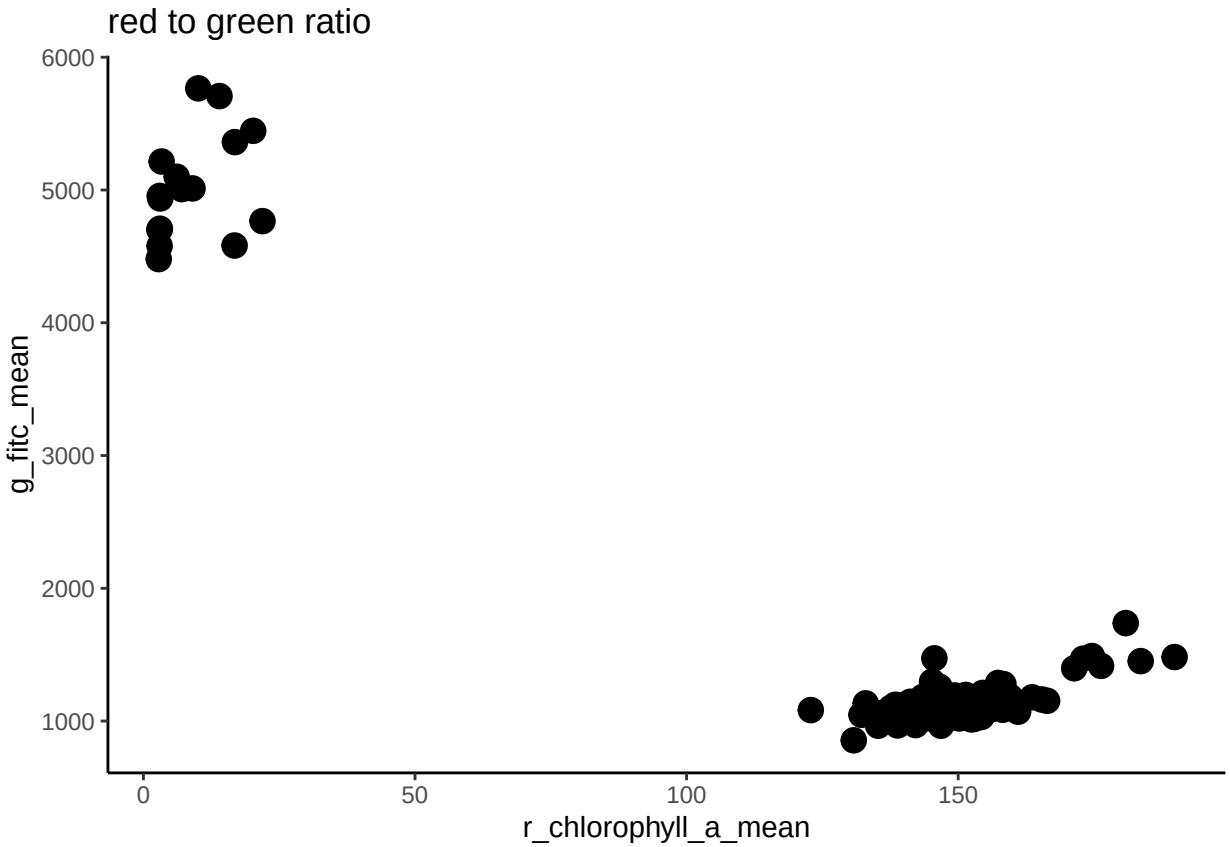
- Normalize by exposure times
- Convert pixels to micrometers for area and lengths
  - Set conversion factor (µm/pixel) for 20X
  - Remember to square for area since each pixel will equal length times width of the value.

```
data$g_fitc_mean_exp <- data$g_fitc_mean/data$g_fitc_exp
data$b_dapi_mean <- data$b_dapi_mean/data$b_dapi_exp
data$r_chlorophyll_a_mean <- data$r_chlorophyll_a_mean/data$r_chlorophyll_a_exp

X20 = 0.211

data$area <- data$area*(X20^2)
data$major_length <- data$major_length*(X20)
data$minor_length <- data$minor_length*(X20)
```

Separate cell populations by fluorescence signal

- Create a scatter plot of red to green fluorescent signal ratio

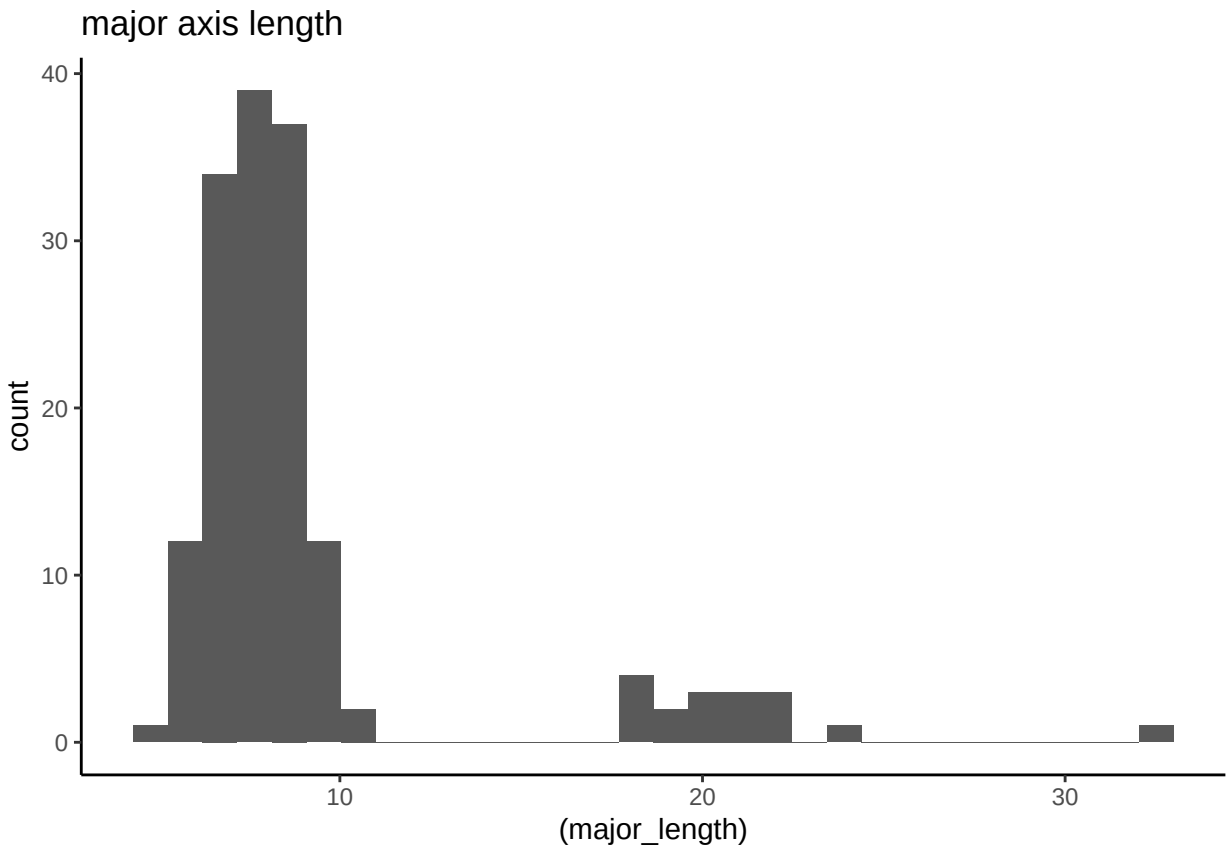
```
data %>%
    ggplot(aes(x = r_chlorophyll_a_mean,y = g_fitc_mean)) +
      geom_point(size =4) +
        theme_classic() +
          labs (title = "red to green ratio")
```



Separate cell populations by size

- Create a histogram of the major axis length

```
data %>%
    ggplot(aes(x = (major_length) )) +
      geom_histogram() +
        theme_classic() +
          labs (title = "major axis length")
```



Quantify cells in each size class using a cut-off value

- Based on the histogram above, use cutoff value of 15 for major length
- Assign labels based on that value
- Count the number of each cell type

```
data <- data %>%
                  mutate( id =
                            ifelse( major_length >= 15, "grazer",
                                ifelse( major_length < 15, "phytoplankton", "NA")))

table(data$id)
```

```
##
##        grazer phytoplankton
##            17           137
```