day 2 data visualization

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

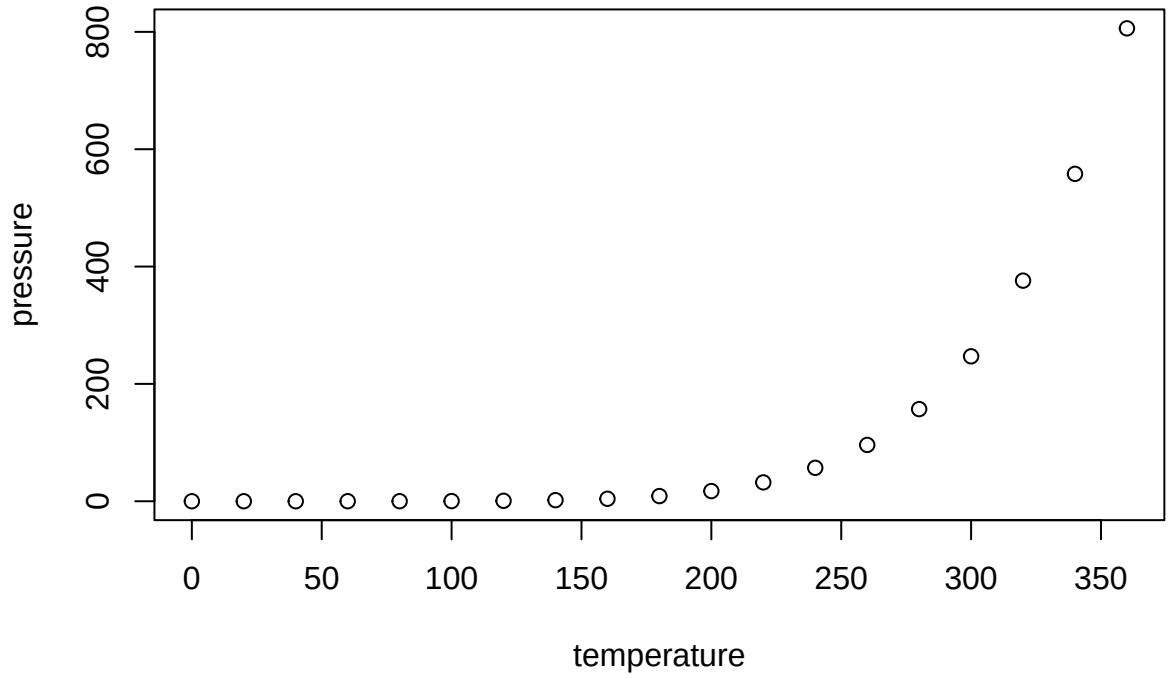
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed           dist       
##  Min.   : 4.0   Min.   :  2.00  
##  1st Qu.:12.0   1st Qu.: 26.00  
##  Median :15.0   Median : 36.00  
##  Mean   :15.4   Mean   : 42.98  
##  3rd Qu.:19.0   3rd Qu.: 56.00  
##  Max.   :25.0   Max.   :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

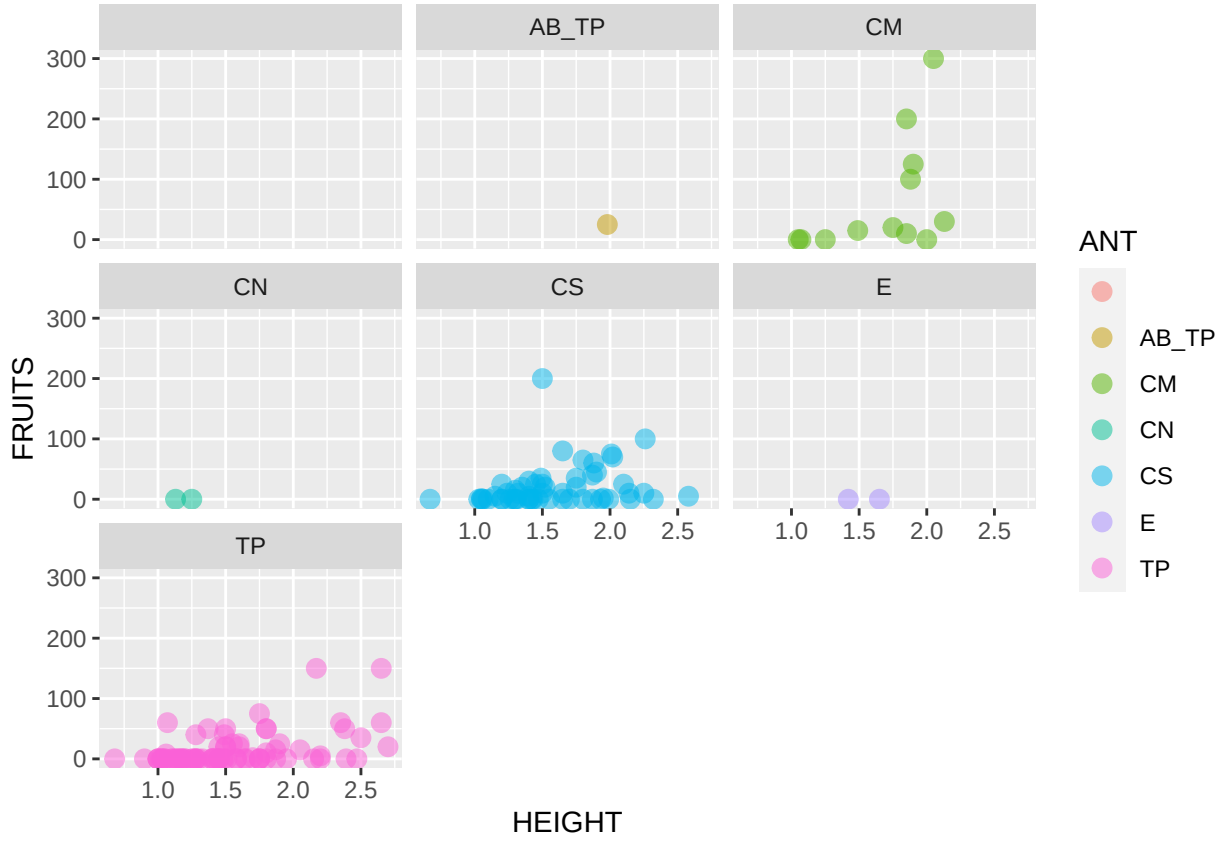
```
acacia <- read.csv(file = "../data-raw/ACACIA_DREPANOLOBIUM_SURVEY.txt",
                   sep = "\t",
                   na.strings = 'dead')
```

```
head(acacia)
```

```
##   SURVEY YEAR  SITE BLOCK TREATMENT    PLOT   ID HEIGHT AXIS1 AXIS2 CIRC
## 1      1 2012 SOUTH     1     TOTAL S1TOTAL  581   2.25  2.75  2.15   20
## 2      1 2012 SOUTH     1     TOTAL S1TOTAL  582   2.65  4.10  3.90   28
## 3      1 2012 SOUTH     1     TOTAL S1TOTAL 3111   1.50  1.70  0.85   17
## 4      1 2012 SOUTH     1     TOTAL S1TOTAL 3112   2.01  1.80  1.60   12
## 5      1 2012 SOUTH     1     TOTAL S1TOTAL 3113   1.75  1.84  1.42   13
## 6      1 2012 SOUTH     1     TOTAL S1TOTAL 3114   1.65  1.62  0.85   15
##   FLOWERS BUDS FRUITS ANT
## 1       0    0     10  CS
## 2       0    0    150  TP
## 3       2    1     50  TP
## 4       0    0     75  CS
## 5       0    0     20  CS
## 6       0    0      0   E
```

```
library(ggplot2)
ggplot(data = acacia, mapping = aes(x = HEIGHT, y = FRUITS, color = ANT)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_wrap(~ANT)
```

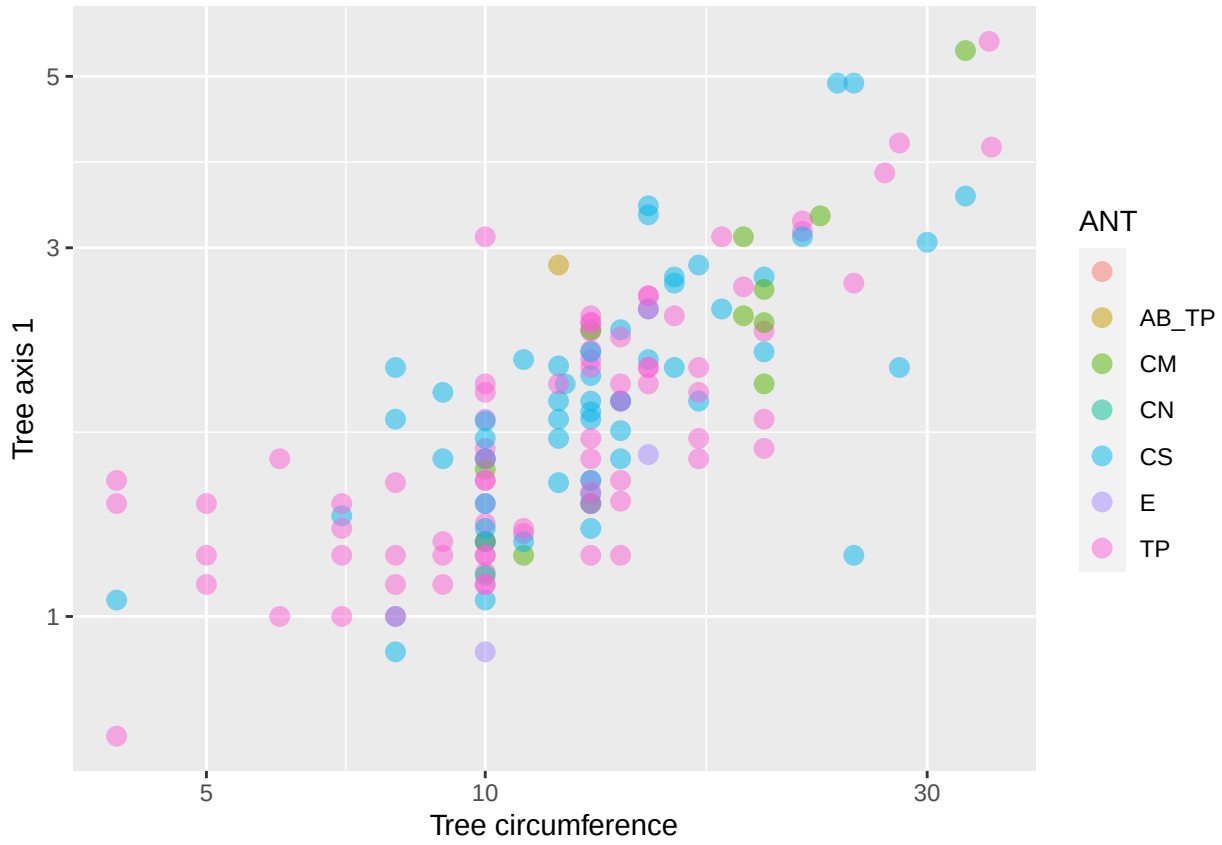
```
## Warning: Removed 4 rows containing missing values (`geom_point()`).
```



Exercise 1.

```
library(ggplot2)
ggplot(data = acacia, mapping = aes(x = CIRC, y = AXIS1, color = ANT)) +
  geom_point(size = 3, alpha = 0.5) +
  scale_y_log10() +
  scale_x_log10() +
  labs(x = "Tree circumference", y = "Tree axis 1")
```

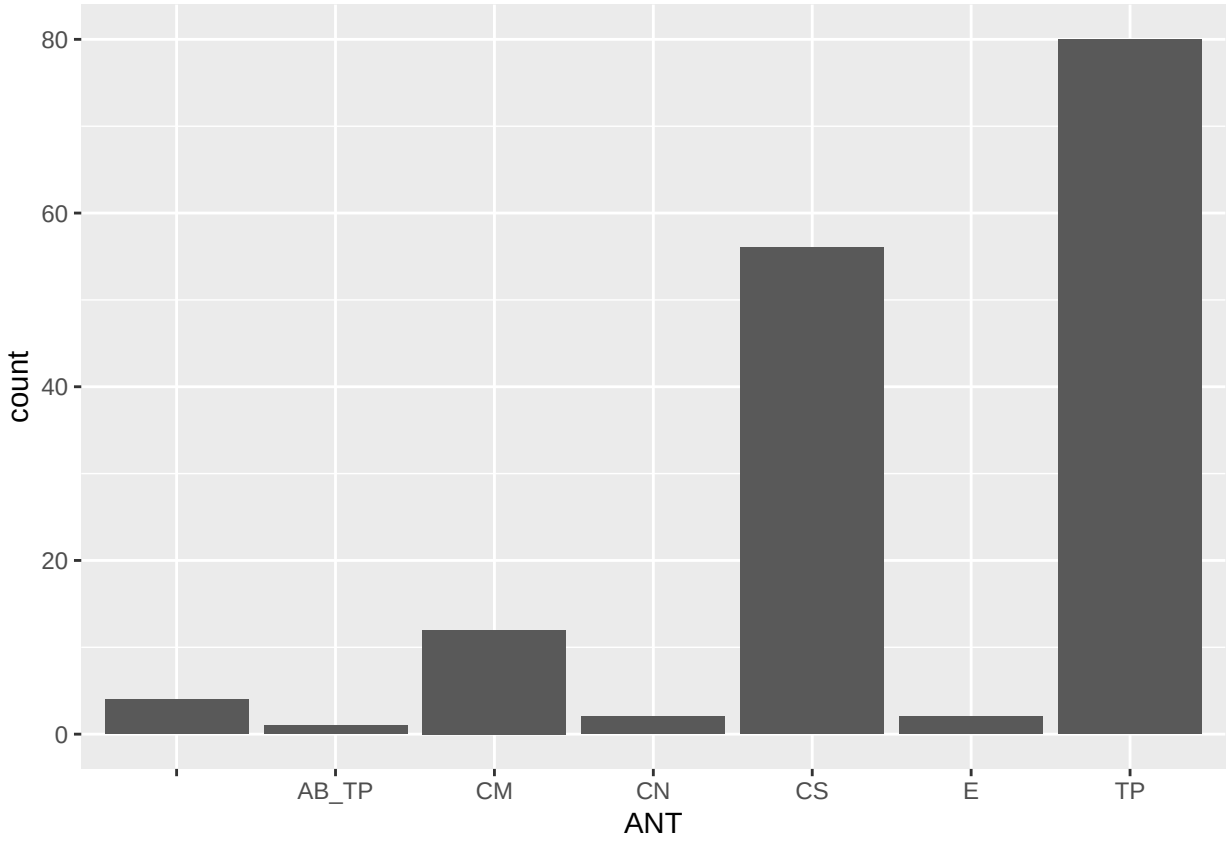
```
## Warning: Removed 4 rows containing missing values (`geom_point()`).
```



#Exercise 2

```
library(ggplot2)

ggplot(data = acacia, mapping = aes(x = ANT)) +
  geom_bar()
```

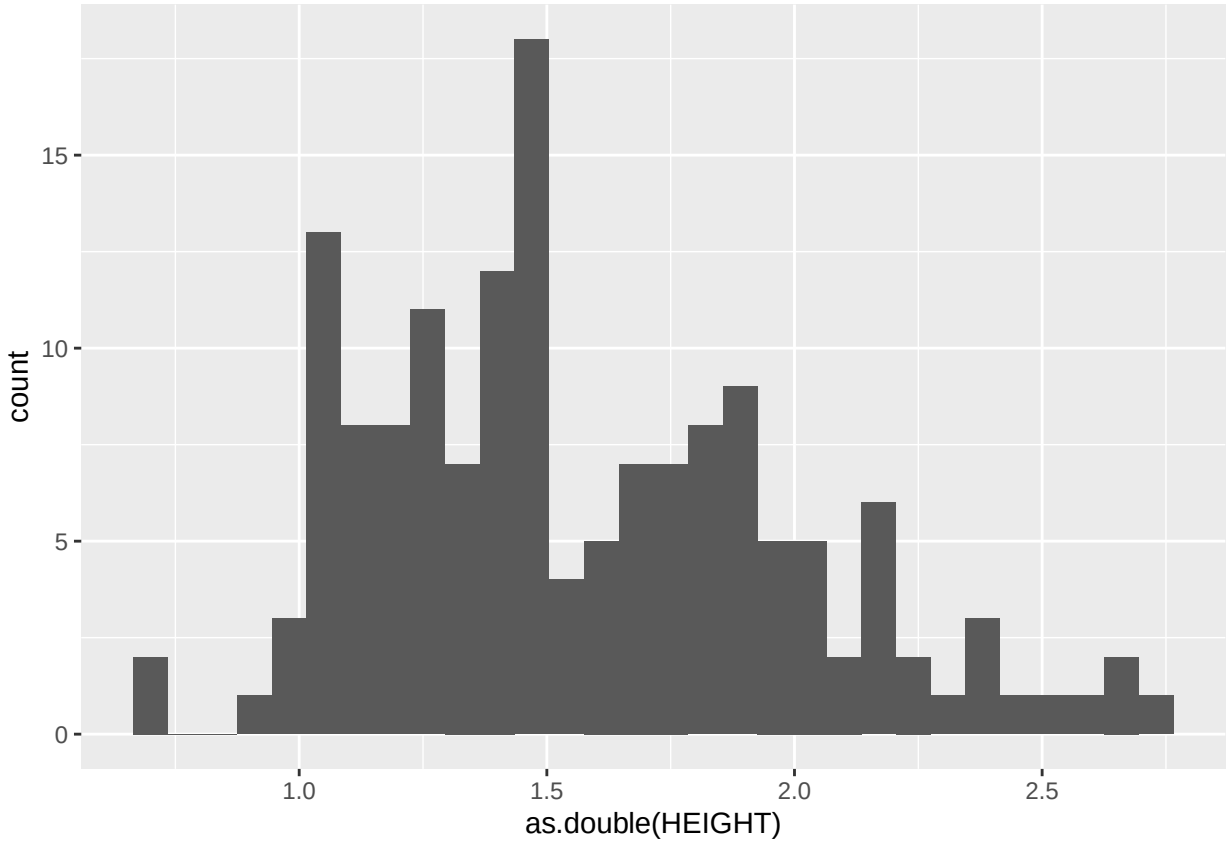



```
library(ggplot2)

ggplot(data = acacia, mapping = aes(x = as.double(HEIGHT))) +
  geom_histogram()
```

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

## Warning: Removed 4 rows containing non-finite values (`stat_bin()`).
```




```
library(ggplot2)

ggplot() +
  geom_histogram(data = acacia,
                 mapping = aes(x = AXIS1, fill = "red"),
                 alpha = 0.3) +
  geom_histogram(data = acacia,
                 mapping = aes(x = AXIS2, fill = "black"),
                 alpha = 0.3)
```

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

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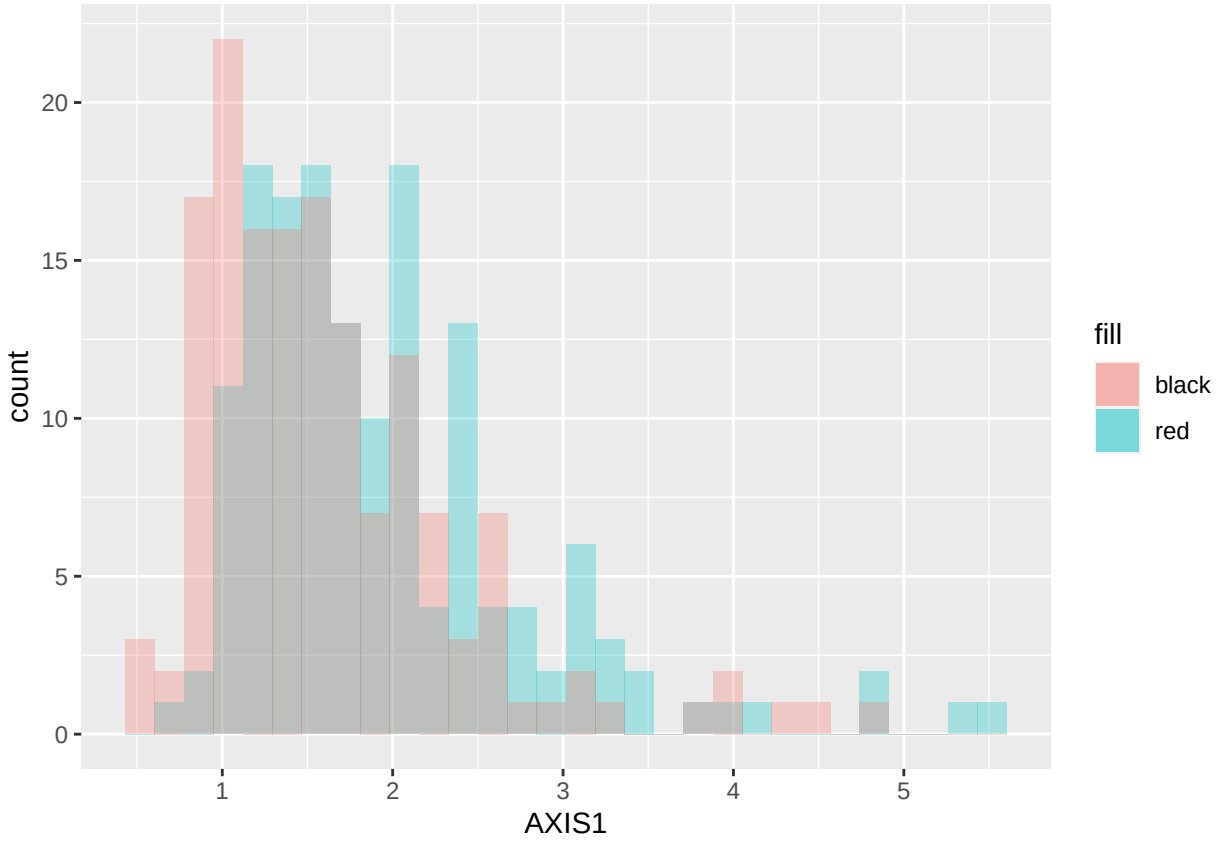


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ggplot() +
  geom_histogram(data = acacia,
                 mapping = aes(x = AXIS1, fill = "red"),
                 alpha = 0.3) +
  geom_histogram(data = acacia,
                 mapping = aes(x = AXIS2, fill = "black"),
                 alpha = 0.3) +
  facet_wrap(~TREATMENT)
```

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

## Warning: Removed 4 rows containing non-finite values (`stat_bin()`).

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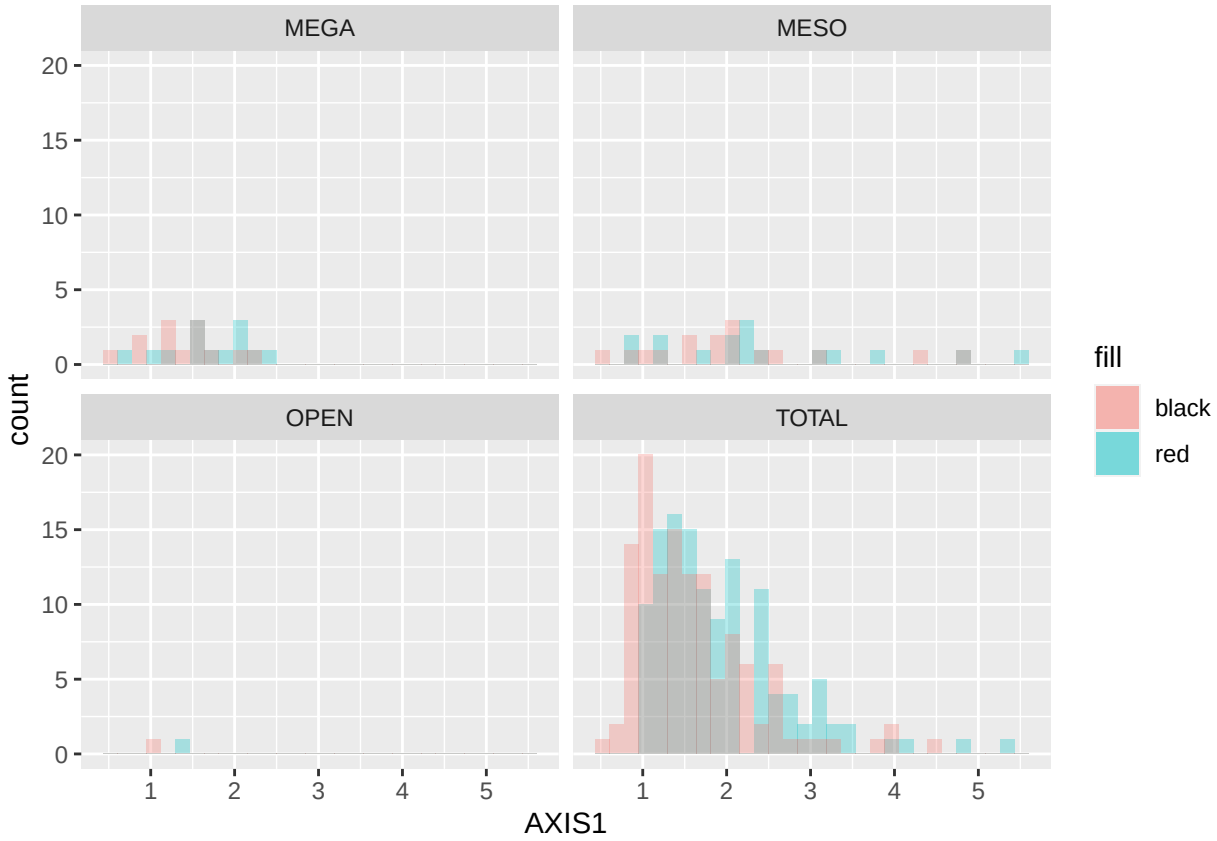
MEGA
MESO
OPEN
TOTAL
count
AXIS1
fill
black
red
0
5
10
15
20
1
2
3
4
5