

uhuru-dataset-visualization.Rmd

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1. Describing the data we are using

add a picture of an acacia ### 2. reading the data table into R

```
getwd()
```

```
## [1] "/Users/marcos/Desktop/BIO 197/Data_Science_Project/scripts"
```

```
acacia <- read.csv(file = "/Users/marcos/Desktop/BIO 197/Data_Science_Project/raw_data/ACACIA_DREPANOLOLO")
```

3. explore our data

```
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 1.5 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
```

```
tail(acacia)
```

```
## SURVEY YEAR SITE BLOCK TREATMENT PLOT ID HEIGHT AXIS1 AXIS2 CIRC
## 152 1 2012 SOUTH 3 TOTAL S3TOTAL 2175 1.42 1.45 1.30 13
## 153 1 2012 SOUTH 3 TOTAL S3TOTAL 2176 1.02 1.20 1.00 8
## 154 1 2012 SOUTH 3 TOTAL S3TOTAL 2177 1.4 1.20 1.00 9
## 155 1 2012 SOUTH 3 TOTAL S3TOTAL 2178 1.45 2.10 2.05 15
## 156 1 2012 SOUTH 3 MESO S3MESO 1421 1.95 2.20 1.60 13
## 157 1 2012 SOUTH 3 MESO S3MESO 1422 dead NA NA NA
```

```
##      FLOWERS BUDS FRUITS ANT
## 152      0    0      0 TP
## 153      0    0      0 TP
## 154      0    0      0 TP
## 155      0    0     20 TP
## 156      0    0      2 CS
## 157     NA   NA     NA
```

```
summary(acacia)
```

```
##      SURVEY      YEAR      SITE      BLOCK
## Min.   :1   Min.   :2012   Length:157   Min.   :1.000
## 1st Qu.:1   1st Qu.:2012   Class :character 1st Qu.:2.000
## Median :1   Median :2012   Mode  :character Median :2.000
## Mean   :1   Mean   :2012                   Mean  :2.089
## 3rd Qu.:1   3rd Qu.:2012                   3rd Qu.:2.000
## Max.   :1   Max.   :2012                   Max.   :3.000
##
##      TREATMENT      PLOT      ID      HEIGHT
## Length:157      Length:157   Min.   : 101   Length:157
## Class :character Class :character 1st Qu.:1062   Class :character
## Mode  :character Mode  :character Median :1301   Mode  :character
##                                     Mean  :1743
##                                     3rd Qu.:3118
##                                     Max.   :3199
##
##      AXIS1      AXIS2      CIRC      FLOWERS
## Min.   :0.700   Min.   :0.550   Min.   : 4.00   Min.   : 0.0000
## 1st Qu.:1.400   1st Qu.:1.100   1st Qu.:10.00   1st Qu.: 0.0000
## Median :1.800   Median :1.490   Median :13.00   Median : 0.0000
## Mean   :1.972   Mean   :1.636   Mean   :13.76   Mean   : 0.4444
## 3rd Qu.:2.350   3rd Qu.:2.000   3rd Qu.:16.00   3rd Qu.: 0.0000
## Max.   :5.550   Max.   :4.820   Max.   :35.20   Max.   :40.0000
## NA's   :4      NA's   :4      NA's   :4      NA's   :4
##      BUDS      FRUITS      ANT
## Min.   : 0.0000   Min.   : 0.00   Length:157
## 1st Qu.: 0.0000   1st Qu.: 0.00   Class :character
## Median : 0.0000   Median : 0.00   Mode  :character
## Mean   : 0.3595   Mean   : 20.03
## 3rd Qu.: 0.0000   3rd Qu.: 25.00
## Max.   :50.0000   Max.   :300.00
## NA's   :4      NA's   :4
```

```
colnames(acacia)
```

```
## [1] "SURVEY" "YEAR" "SITE" "BLOCK" "TREATMENT" "PLOT"
## [7] "ID" "HEIGHT" "AXIS1" "AXIS2" "CIRC" "FLOWERS"
## [13] "BUDS" "FRUITS" "ANT"
```

```
nrow(acacia)
```

```
## [1] 157
```

make sure that everything that is a number is actually numeric use function summary to do this and check that the type of data corresponds to this another way is to use the type function

```
typeof(acacia[, "HEIGHT"])
```

```
## [1] "character"
```

```
acacia$HEIGHT
```

```
## [1] "2.25" "2.65" "1.5" "2.01" "1.75" "1.65" "1.2" "1.45" "1.87" "2.38"
## [11] "2.58" "2.65" "2.35" "1.88" "2.32" "2.39" "2.2" "1.05" "2" "1.28"
## [21] "dead" "1.4" "1.9" "1.75" "1.8" "2.7" "2.02" "1.9" "1.85" "1.65"
## [31] "1.4" "2.5" "2.05" "2.26" "2.13" "1.8" "1.85" "1.5" "1.87" "1.58"
## [41] "2.05" "1.75" "1.49" "1.28" "1.49" "1.07" "1.48" "1.25" "1.41" "1.6"
## [51] "1.2" "1.49" "1.5" "1.65" "1.13" "1.25" "1.1" "2.2" "1.45" "1.6"
## [61] "1.55" "1.5" "1.03" "2.14" "1.2" "1.05" "1.8" "1.2" "1.75" "1.45"
## [71] "1.17" "2.15" "1.7" "1.98" "1.26" "1.11" "1.14" "1.26" "1.3" "1.29"
## [81] "1.31" "1.15" "1.87" "1.47" "1.05" "2.1" "1.99" "1.42" "1.5" "1.06"
## [91] "1.49" "1.8" "1.93" "1.2" "1.65" "1.52" "1.43" "1.25" "1.88" "1.03"
## [101] "1.1" "1.4" "1.05" "1.18" "1.4" "1.37" "1.32" "1.55" "1.3" "1.24"
## [111] "1.5" "1.65" "2.17" "1.28" "1.07" "0.67" "0.68" "1.87" "1.35" "1.75"
## [121] "1.75" "1.64" "1.42" "dead" "0.9" "dead" "1.8" "2.47" "2.15" "1.7"
## [131] "1.9" "1.95" "1.8" "1.4" "1" "1.75" "1.28" "1" "1.45" "1"
## [141] "1.03" "1.51" "1.17" "1.33" "1.3" "1.13" "1.58" "1.06" "1.05" "1.45"
## [151] "1.15" "1.42" "1.02" "1.4" "1.45" "1.95" "dead"
```

identified a column that has problematic data so we need to fix it so we're gonna read the data table and assign "NA" to "dead" value in the height column

```
acacia <- read.csv(file = "/Users/marcos/Desktop/BIO 197/Data_Science_Project/raw_data/ACACIA_DREPANOLOMUS.csv",
                  sep = "\t", na.strings = "dead")
getwd()
```

```
## [1] "/Users/marcos/Desktop/BIO 197/Data_Science_Project/scripts"
```

```
acacia$HEIGHT
```

```
## [1] 2.25 2.65 1.50 2.01 1.75 1.65 1.20 1.45 1.87 2.38 2.58 2.65 2.35 1.88 2.32
## [16] 2.39 2.20 1.05 2.00 1.28 NA 1.40 1.90 1.75 1.80 2.70 2.02 1.90 1.85 1.65
## [31] 1.40 2.50 2.05 2.26 2.13 1.80 1.85 1.50 1.87 1.58 2.05 1.75 1.49 1.28 1.49
## [46] 1.07 1.48 1.25 1.41 1.60 1.20 1.49 1.50 1.65 1.13 1.25 1.10 2.20 1.45 1.60
## [61] 1.55 1.50 1.03 2.14 1.20 1.05 1.80 1.20 1.75 1.45 1.17 2.15 1.70 1.98 1.26
## [76] 1.11 1.14 1.26 1.30 1.29 1.31 1.15 1.87 1.47 1.05 2.10 1.99 1.42 1.50 1.06
## [91] 1.49 1.80 1.93 1.20 1.65 1.52 1.43 1.25 1.88 1.03 1.10 1.40 1.05 1.18 1.40
## [106] 1.37 1.32 1.55 1.30 1.24 1.50 1.65 2.17 1.28 1.07 0.67 0.68 1.87 1.35 1.75
## [121] 1.75 1.64 1.42 NA 0.90 NA 1.80 2.47 2.15 1.70 1.90 1.95 1.80 1.40 1.00
## [136] 1.75 1.28 1.00 1.45 1.00 1.03 1.51 1.17 1.33 1.30 1.13 1.58 1.06 1.05 1.45
## [151] 1.15 1.42 1.02 1.40 1.45 1.95 NA
```

4. visualize our data

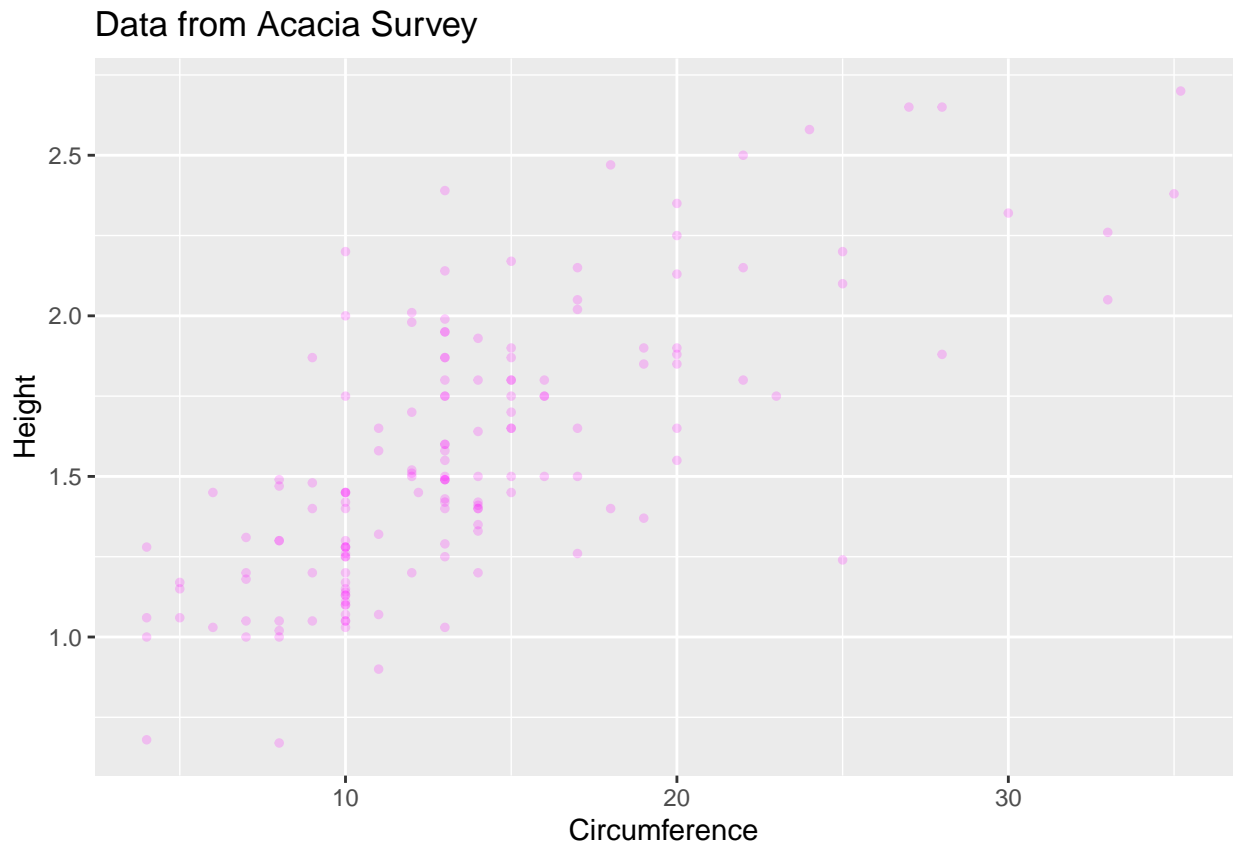
for this we use ggplot package let install it first

```
#install.packages("ggplot2")  
library(ggplot2)
```

now we are gonna creat oiuur first plotting layer with ggplot function

```
ggplot(data = acacia, mapping = aes(x = CIRC, y = HEIGHT)) +  
  geom_point(size = 1, col= "magenta", alpha = 0.2) +  
  labs(x = "Circumference", y = "Height", title = "Data from Acacia Survey")
```

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

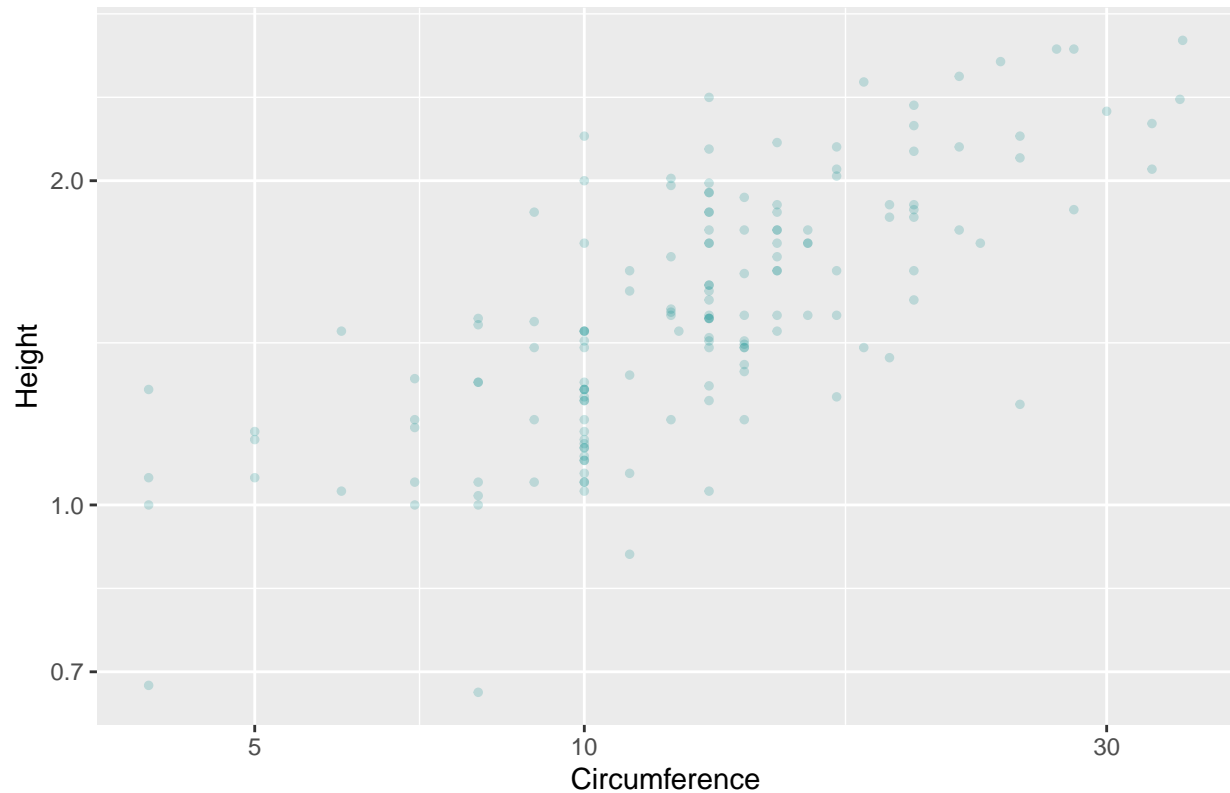


to rescale the plotting of the axis to log scale we use the function `scale_y_log10()`

```
ggplot(data = acacia, mapping = aes(x = CIRC, y = HEIGHT)) +  
  geom_point(size = 1, col= "cyan4", alpha = 0.2) +  
  scale_x_log10() +  
  scale_y_log10() +  
  labs(x = "Circumference", y = "Height", title = "Data from Acacia Survey")
```

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

Data from Acacia Survey



we have the information on experimental treatment in treatment column

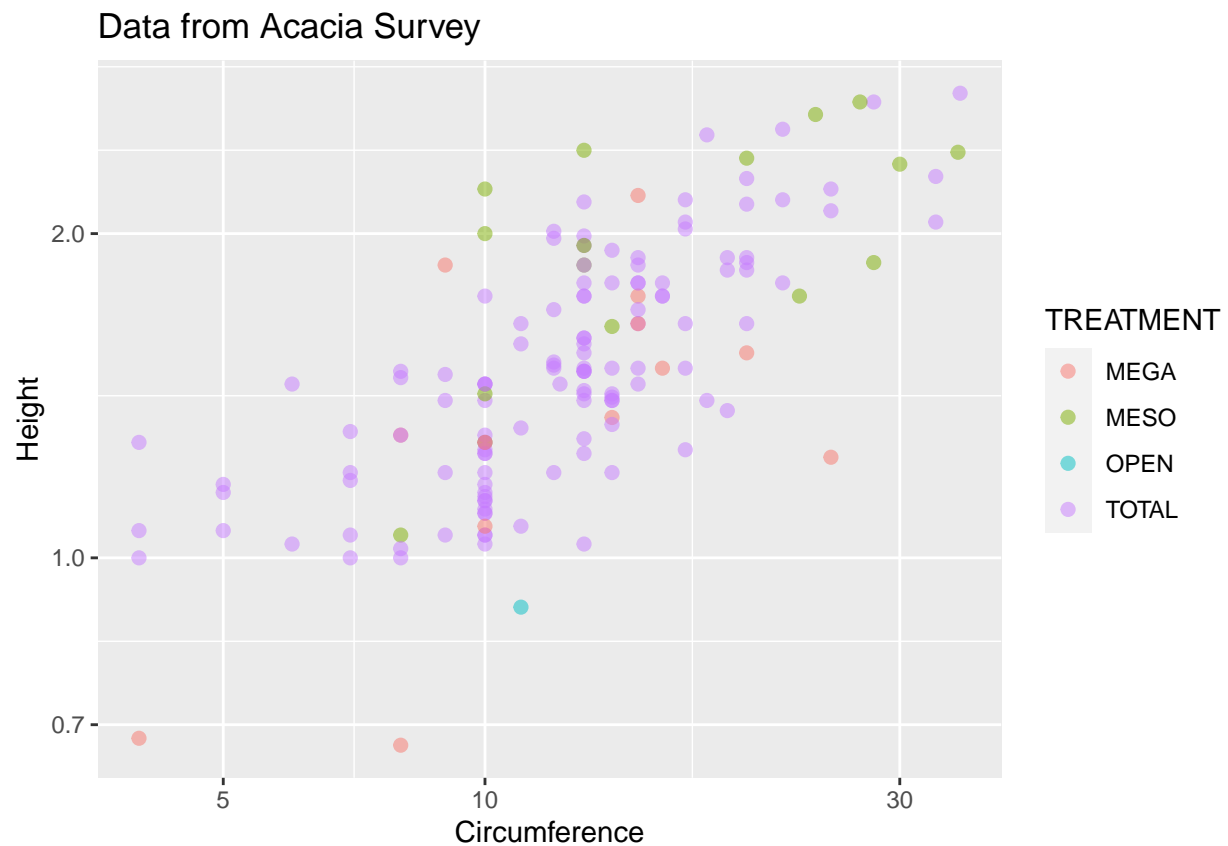
```
acacia$TREATMENT
```

```
## [1] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "MESO"
## [10] "MESO" "MESO" "MESO" "MESO" "MESO" "MESO" "MESO" "MESO" "MESO" "MESO"
## [19] "MESO" "MESO" "OPEN" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [28] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [37] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [46] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [55] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [64] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [73] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [82] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [91] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [100] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "MEGA"
## [109] "MEGA" "MEGA" "MEGA" "MEGA" "MEGA" "MEGA" "MEGA" "MEGA" "MEGA" "MEGA"
## [118] "MEGA" "MEGA" "MEGA" "MESO" "MESO" "MESO" "OPEN" "OPEN" "TOTAL"
## [127] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [136] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [145] "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL" "TOTAL"
## [154] "TOTAL" "TOTAL" "MESO" "MESO"
```

lets add this information to our plot:

```
ggplot(acacia, mapping = aes (x = CIRC, y = HEIGHT, color = TREATMENT)) +
  geom_point(size = 2, alpha = 0.5) +
  labs(x = "Circumference", y = "Height", title = "Data from Acacia Survey") +
  scale_x_log10() +
  scale_y_log10()
```

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



4.2 visualize a statistical analysis of correlation