

# uhuru-dataset-visualization.Rmd

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## 1. Describing the data we are using

This data was gathered through the UHURU experiment which consisted of enclosures of various sizes to gauge the ecological impacts that may occur to Acacia trees in Kenya. Firstly there is the mega-herbivore fence which is designed to keep larger herbivores outside the enclosure such as giraffes and elephants. Then there is <https://esapubs.org/archive/ecol/E095/064/metadata.php>

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

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

## 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 in 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",
                  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

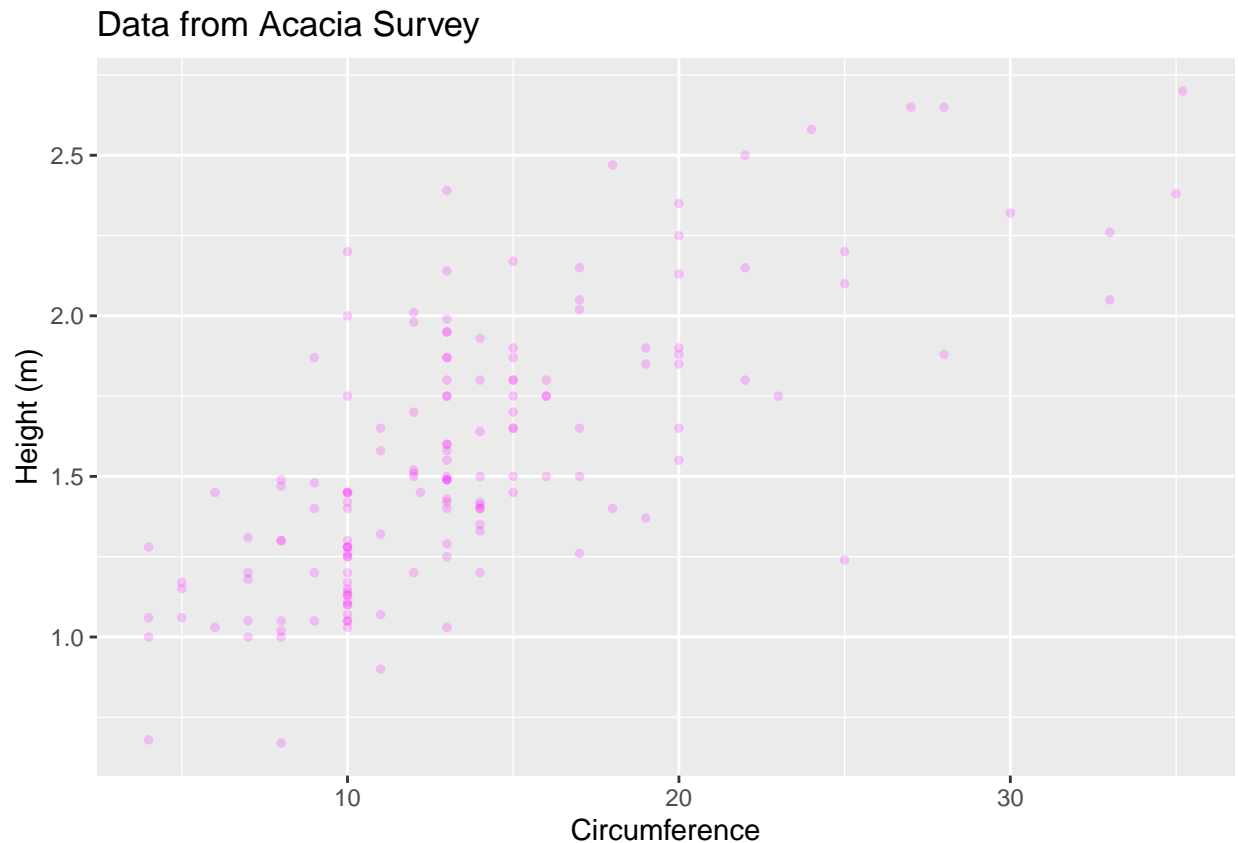
for this we use ggplot package let install it first

```
#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 (m)", title = "Data from Acacia Survey")
```

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

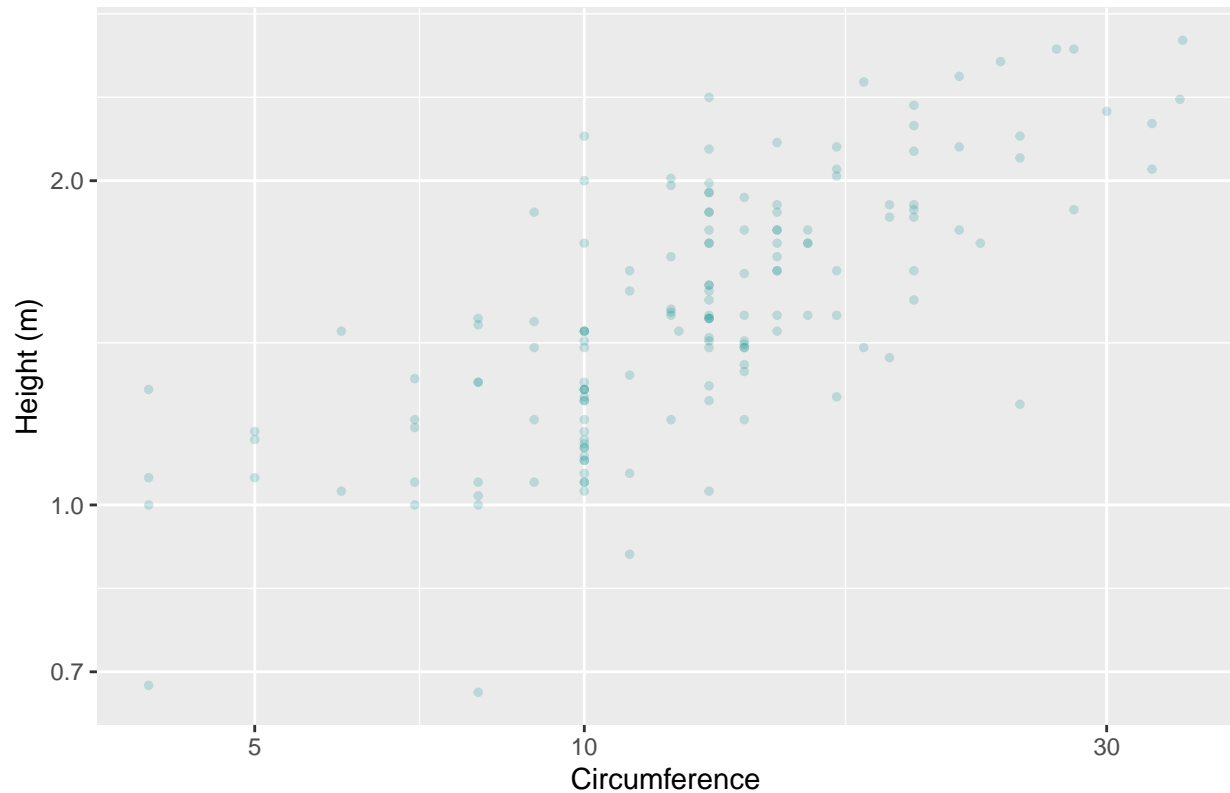


to rescale the plotting of the axis to log scale we use the function `scale_y_log10()`

```
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 (m)", 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

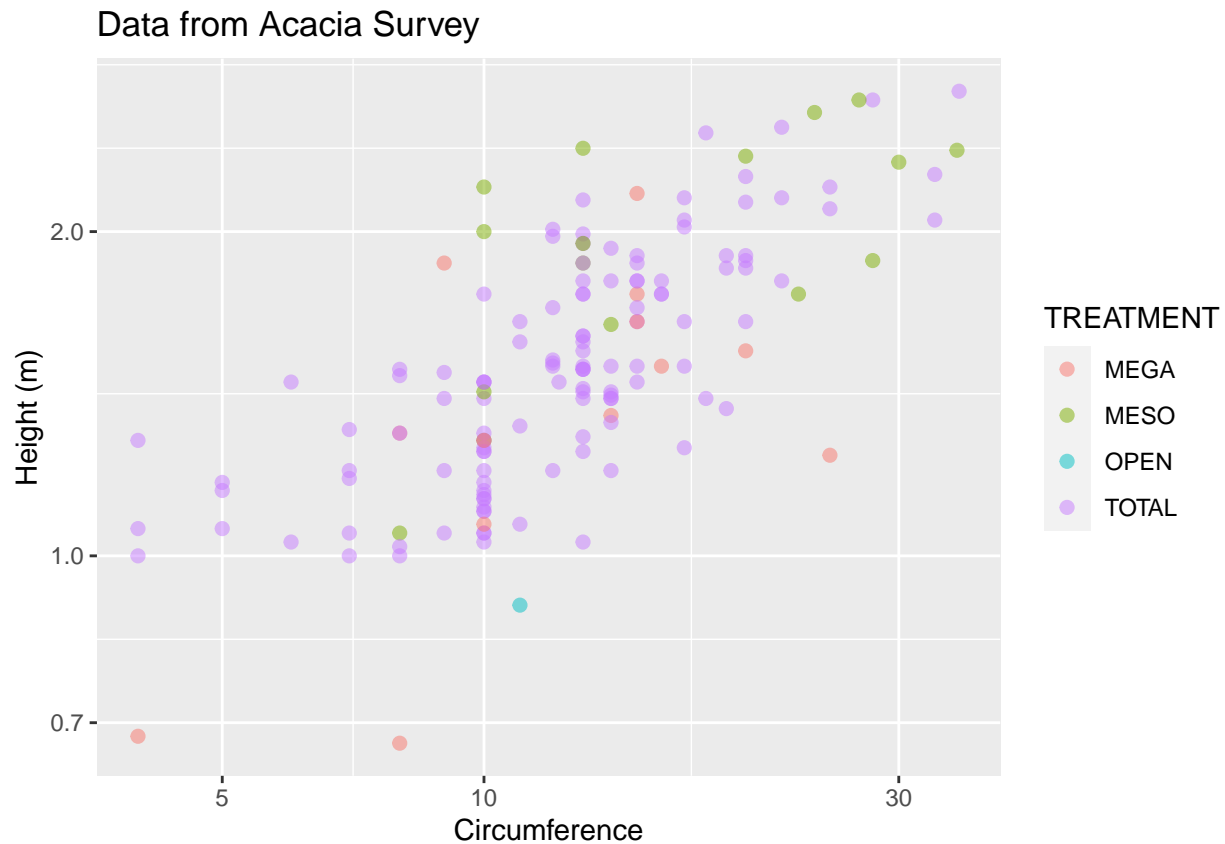
```
acacia$TREATMENT
```

```
## [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 (m)", title = "Data from Acacia Survey") +
  scale_x_log10() +
  scale_y_log10()
```

## Warning: Removed 4 rows containing missing values (geom\_point).



a scatter plot function can be created using function geom point

```
colors()
```

```
## [1] "white" "aliceblue" "antiquewhite"
## [4] "antiquewhite1" "antiquewhite2" "antiquewhite3"
## [7] "antiquewhite4" "aquamarine" "aquamarine1"
## [10] "aquamarine2" "aquamarine3" "aquamarine4"
## [13] "azure" "azure1" "azure2"
## [16] "azure3" "azure4" "beige"
## [19] "bisque" "bisque1" "bisque2"
## [22] "bisque3" "bisque4" "black"
## [25] "blanchedalmond" "blue" "blue1"
## [28] "blue2" "blue3" "blue4"
## [31] "blueviolet" "brown" "brown1"
## [34] "brown2" "brown3" "brown4"
```

## [37]	"burlywood"	"burlywood1"	"burlywood2"
## [40]	"burlywood3"	"burlywood4"	"cadetblue"
## [43]	"cadetblue1"	"cadetblue2"	"cadetblue3"
## [46]	"cadetblue4"	"chartreuse"	"chartreuse1"
## [49]	"chartreuse2"	"chartreuse3"	"chartreuse4"
## [52]	"chocolate"	"chocolate1"	"chocolate2"
## [55]	"chocolate3"	"chocolate4"	"coral"
## [58]	"coral1"	"coral2"	"coral3"
## [61]	"coral4"	"cornflowerblue"	"cornsilk"
## [64]	"cornsilk1"	"cornsilk2"	"cornsilk3"
## [67]	"cornsilk4"	"cyan"	"cyan1"
## [70]	"cyan2"	"cyan3"	"cyan4"
## [73]	"darkblue"	"darkcyan"	"darkgoldenrod"
## [76]	"darkgoldenrod1"	"darkgoldenrod2"	"darkgoldenrod3"
## [79]	"darkgoldenrod4"	"darkgray"	"darkgreen"
## [82]	"darkgrey"	"darkkhaki"	"darkmagenta"
## [85]	"darkolivegreen"	"darkolivegreen1"	"darkolivegreen2"
## [88]	"darkolivegreen3"	"darkolivegreen4"	"darkorange"
## [91]	"darkorange1"	"darkorange2"	"darkorange3"
## [94]	"darkorange4"	"darkorchid"	"darkorchid1"
## [97]	"darkorchid2"	"darkorchid3"	"darkorchid4"
## [100]	"darkred"	"darksalmon"	"darkseagreen"
## [103]	"darkseagreen1"	"darkseagreen2"	"darkseagreen3"
## [106]	"darkseagreen4"	"darkslateblue"	"darkslategray"
## [109]	"darkslategray1"	"darkslategray2"	"darkslategray3"
## [112]	"darkslategray4"	"darkslategrey"	"darkturquoise"
## [115]	"darkviolet"	"deeppink"	"deeppink1"
## [118]	"deeppink2"	"deeppink3"	"deeppink4"
## [121]	"deepskyblue"	"deepskyblue1"	"deepskyblue2"
## [124]	"deepskyblue3"	"deepskyblue4"	"dimgray"
## [127]	"dimgrey"	"dodgerblue"	"dodgerblue1"
## [130]	"dodgerblue2"	"dodgerblue3"	"dodgerblue4"
## [133]	"firebrick"	"firebrick1"	"firebrick2"
## [136]	"firebrick3"	"firebrick4"	"floralwhite"
## [139]	"forestgreen"	"gainsboro"	"ghostwhite"
## [142]	"gold"	"gold1"	"gold2"
## [145]	"gold3"	"gold4"	"goldenrod"
## [148]	"goldenrod1"	"goldenrod2"	"goldenrod3"
## [151]	"goldenrod4"	"gray"	"gray0"
## [154]	"gray1"	"gray2"	"gray3"
## [157]	"gray4"	"gray5"	"gray6"
## [160]	"gray7"	"gray8"	"gray9"
## [163]	"gray10"	"gray11"	"gray12"
## [166]	"gray13"	"gray14"	"gray15"
## [169]	"gray16"	"gray17"	"gray18"
## [172]	"gray19"	"gray20"	"gray21"
## [175]	"gray22"	"gray23"	"gray24"
## [178]	"gray25"	"gray26"	"gray27"
## [181]	"gray28"	"gray29"	"gray30"
## [184]	"gray31"	"gray32"	"gray33"
## [187]	"gray34"	"gray35"	"gray36"
## [190]	"gray37"	"gray38"	"gray39"
## [193]	"gray40"	"gray41"	"gray42"
## [196]	"gray43"	"gray44"	"gray45"

## [199]	"gray46"	"gray47"	"gray48"
## [202]	"gray49"	"gray50"	"gray51"
## [205]	"gray52"	"gray53"	"gray54"
## [208]	"gray55"	"gray56"	"gray57"
## [211]	"gray58"	"gray59"	"gray60"
## [214]	"gray61"	"gray62"	"gray63"
## [217]	"gray64"	"gray65"	"gray66"
## [220]	"gray67"	"gray68"	"gray69"
## [223]	"gray70"	"gray71"	"gray72"
## [226]	"gray73"	"gray74"	"gray75"
## [229]	"gray76"	"gray77"	"gray78"
## [232]	"gray79"	"gray80"	"gray81"
## [235]	"gray82"	"gray83"	"gray84"
## [238]	"gray85"	"gray86"	"gray87"
## [241]	"gray88"	"gray89"	"gray90"
## [244]	"gray91"	"gray92"	"gray93"
## [247]	"gray94"	"gray95"	"gray96"
## [250]	"gray97"	"gray98"	"gray99"
## [253]	"gray100"	"green"	"green1"
## [256]	"green2"	"green3"	"green4"
## [259]	"greenyellow"	"grey"	"grey0"
## [262]	"grey1"	"grey2"	"grey3"
## [265]	"grey4"	"grey5"	"grey6"
## [268]	"grey7"	"grey8"	"grey9"
## [271]	"grey10"	"grey11"	"grey12"
## [274]	"grey13"	"grey14"	"grey15"
## [277]	"grey16"	"grey17"	"grey18"
## [280]	"grey19"	"grey20"	"grey21"
## [283]	"grey22"	"grey23"	"grey24"
## [286]	"grey25"	"grey26"	"grey27"
## [289]	"grey28"	"grey29"	"grey30"
## [292]	"grey31"	"grey32"	"grey33"
## [295]	"grey34"	"grey35"	"grey36"
## [298]	"grey37"	"grey38"	"grey39"
## [301]	"grey40"	"grey41"	"grey42"
## [304]	"grey43"	"grey44"	"grey45"
## [307]	"grey46"	"grey47"	"grey48"
## [310]	"grey49"	"grey50"	"grey51"
## [313]	"grey52"	"grey53"	"grey54"
## [316]	"grey55"	"grey56"	"grey57"
## [319]	"grey58"	"grey59"	"grey60"
## [322]	"grey61"	"grey62"	"grey63"
## [325]	"grey64"	"grey65"	"grey66"
## [328]	"grey67"	"grey68"	"grey69"
## [331]	"grey70"	"grey71"	"grey72"
## [334]	"grey73"	"grey74"	"grey75"
## [337]	"grey76"	"grey77"	"grey78"
## [340]	"grey79"	"grey80"	"grey81"
## [343]	"grey82"	"grey83"	"grey84"
## [346]	"grey85"	"grey86"	"grey87"
## [349]	"grey88"	"grey89"	"grey90"
## [352]	"grey91"	"grey92"	"grey93"
## [355]	"grey94"	"grey95"	"grey96"
## [358]	"grey97"	"grey98"	"grey99"



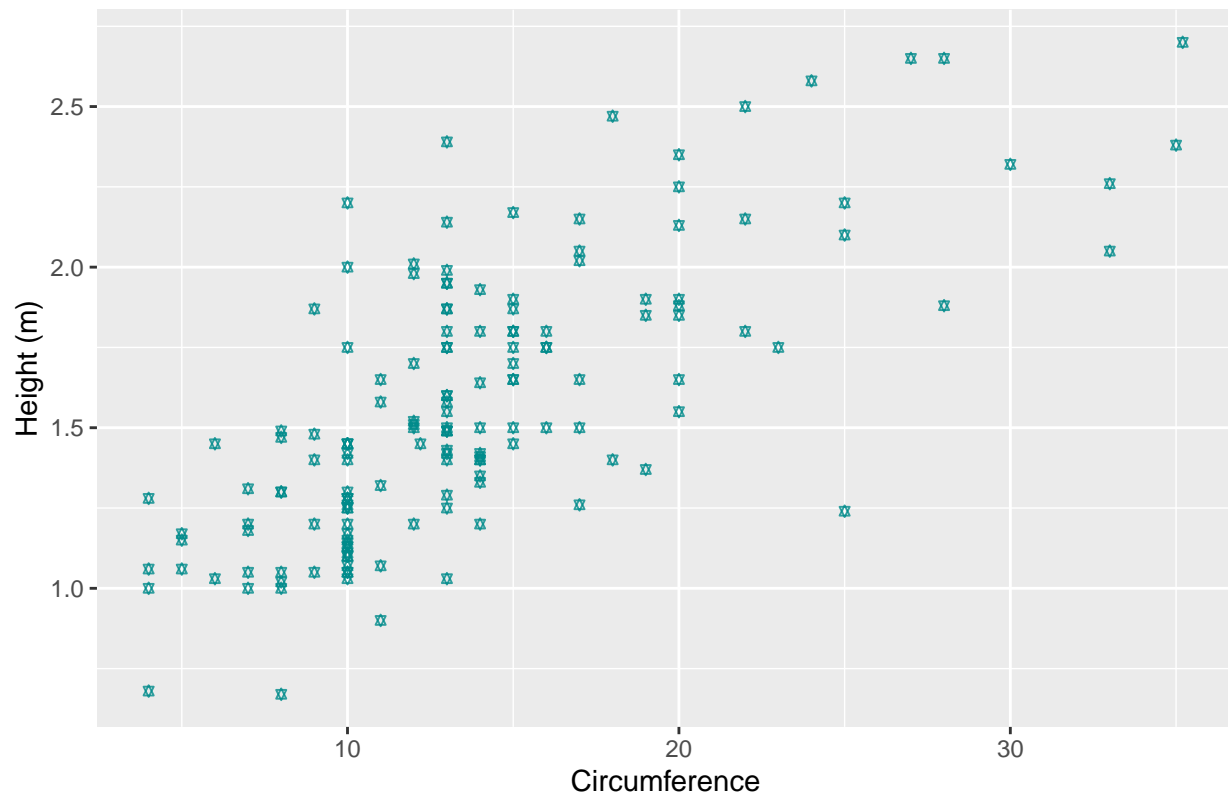
## [361]	"grey100"	"honeydew"	"honeydew1"
## [364]	"honeydew2"	"honeydew3"	"honeydew4"
## [367]	"hotpink"	"hotpink1"	"hotpink2"
## [370]	"hotpink3"	"hotpink4"	"indianred"
## [373]	"indianred1"	"indianred2"	"indianred3"
## [376]	"indianred4"	"ivory"	"ivory1"
## [379]	"ivory2"	"ivory3"	"ivory4"
## [382]	"khaki"	"khaki1"	"khaki2"
## [385]	"khaki3"	"khaki4"	"lavender"
## [388]	"lavenderblush"	"lavenderblush1"	"lavenderblush2"
## [391]	"lavenderblush3"	"lavenderblush4"	"lawngreen"
## [394]	"lemonchiffon"	"lemonchiffon1"	"lemonchiffon2"
## [397]	"lemonchiffon3"	"lemonchiffon4"	"lightblue"
## [400]	"lightblue1"	"lightblue2"	"lightblue3"
## [403]	"lightblue4"	"lightcoral"	"lightcyan"
## [406]	"lightcyan1"	"lightcyan2"	"lightcyan3"
## [409]	"lightcyan4"	"lightgoldenrod"	"lightgoldenrod1"
## [412]	"lightgoldenrod2"	"lightgoldenrod3"	"lightgoldenrod4"
## [415]	"lightgoldenrodyellow"	"lightgray"	"lightgreen"
## [418]	"lightgrey"	"lightpink"	"lightpink1"
## [421]	"lightpink2"	"lightpink3"	"lightpink4"
## [424]	"lightsalmon"	"lightsalmon1"	"lightsalmon2"
## [427]	"lightsalmon3"	"lightsalmon4"	"lightseagreen"
## [430]	"lightskyblue"	"lightskyblue1"	"lightskyblue2"
## [433]	"lightskyblue3"	"lightskyblue4"	"lightslateblue"
## [436]	"lightslategray"	"lightslategrey"	"lightsteelblue"
## [439]	"lightsteelblue1"	"lightsteelblue2"	"lightsteelblue3"
## [442]	"lightsteelblue4"	"lightyellow"	"lightyellow1"
## [445]	"lightyellow2"	"lightyellow3"	"lightyellow4"
## [448]	"limegreen"	"linen"	"magenta"
## [451]	"magenta1"	"magenta2"	"magenta3"
## [454]	"magenta4"	"maroon"	"maroon1"
## [457]	"maroon2"	"maroon3"	"maroon4"
## [460]	"mediumaquamarine"	"mediumblue"	"mediumorchid"
## [463]	"mediumorchid1"	"mediumorchid2"	"mediumorchid3"
## [466]	"mediumorchid4"	"mediumpurple"	"mediumpurple1"
## [469]	"mediumpurple2"	"mediumpurple3"	"mediumpurple4"
## [472]	"mediumseagreen"	"mediumslateblue"	"mediumspringgreen"
## [475]	"mediumturquoise"	"mediumvioletred"	"midnightblue"
## [478]	"mintcream"	"mistyrose"	"mistyrose1"
## [481]	"mistyrose2"	"mistyrose3"	"mistyrose4"
## [484]	"moccasin"	"navajowhite"	"navajowhite1"
## [487]	"navajowhite2"	"navajowhite3"	"navajowhite4"
## [490]	"navy"	"navyblue"	"oldlace"
## [493]	"olivedrab"	"olivedrab1"	"olivedrab2"
## [496]	"olivedrab3"	"olivedrab4"	"orange"
## [499]	"orange1"	"orange2"	"orange3"
## [502]	"orange4"	"orangered"	"orangered1"
## [505]	"orangered2"	"orangered3"	"orangered4"
## [508]	"orchid"	"orchid1"	"orchid2"
## [511]	"orchid3"	"orchid4"	"palegoldenrod"
## [514]	"palegreen"	"palegreen1"	"palegreen2"
## [517]	"palegreen3"	"palegreen4"	"paleturquoise"
## [520]	"paleturquoise1"	"paleturquoise2"	"paleturquoise3"

## [523]	"paleturquoise4"	"palevioletred"	"palevioletred1"
## [526]	"palevioletred2"	"palevioletred3"	"palevioletred4"
## [529]	"papayawhip"	"peachpuff"	"peachpuff1"
## [532]	"peachpuff2"	"peachpuff3"	"peachpuff4"
## [535]	"peru"	"pink"	"pink1"
## [538]	"pink2"	"pink3"	"pink4"
## [541]	"plum"	"plum1"	"plum2"
## [544]	"plum3"	"plum4"	"powderblue"
## [547]	"purple"	"purple1"	"purple2"
## [550]	"purple3"	"purple4"	"red"
## [553]	"red1"	"red2"	"red3"
## [556]	"red4"	"rosybrown"	"rosybrown1"
## [559]	"rosybrown2"	"rosybrown3"	"rosybrown4"
## [562]	"royalblue"	"royalblue1"	"royalblue2"
## [565]	"royalblue3"	"royalblue4"	"saddlebrown"
## [568]	"salmon"	"salmon1"	"salmon2"
## [571]	"salmon3"	"salmon4"	"sandybrown"
## [574]	"seagreen"	"seagreen1"	"seagreen2"
## [577]	"seagreen3"	"seagreen4"	"seashell"
## [580]	"seashell1"	"seashell2"	"seashell3"
## [583]	"seashell4"	"sienna"	"sienna1"
## [586]	"sienna2"	"sienna3"	"sienna4"
## [589]	"skyblue"	"skyblue1"	"skyblue2"
## [592]	"skyblue3"	"skyblue4"	"slateblue"
## [595]	"slateblue1"	"slateblue2"	"slateblue3"
## [598]	"slateblue4"	"slategray"	"slategray1"
## [601]	"slategray2"	"slategray3"	"slategray4"
## [604]	"slategrey"	"snow"	"snow1"
## [607]	"snow2"	"snow3"	"snow4"
## [610]	"springgreen"	"springgreen1"	"springgreen2"
## [613]	"springgreen3"	"springgreen4"	"steelblue"
## [616]	"steelblue1"	"steelblue2"	"steelblue3"
## [619]	"steelblue4"	"tan"	"tan1"
## [622]	"tan2"	"tan3"	"tan4"
## [625]	"thistle"	"thistle1"	"thistle2"
## [628]	"thistle3"	"thistle4"	"tomato"
## [631]	"tomato1"	"tomato2"	"tomato3"
## [634]	"tomato4"	"turquoise"	"turquoise1"
## [637]	"turquoise2"	"turquoise3"	"turquoise4"
## [640]	"violet"	"violetred"	"violetred1"
## [643]	"violetred2"	"violetred3"	"violetred4"
## [646]	"wheat"	"wheat1"	"wheat2"
## [649]	"wheat3"	"wheat4"	"whitesmoke"
## [652]	"yellow"	"yellow1"	"yellow2"
## [655]	"yellow3"	"yellow4"	"yellowgreen"

```
ggplot(data = acacia, mapping = aes(x = CIRC, y = HEIGHT)) +
  geom_point(size = 1, col= "cyan4", alpha = 0.8, shape = 11) +
  labs(x = "Circumference", y = "Height (m)", title = "Data from Acacia Survey")
```

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

Data from Acacia Survey

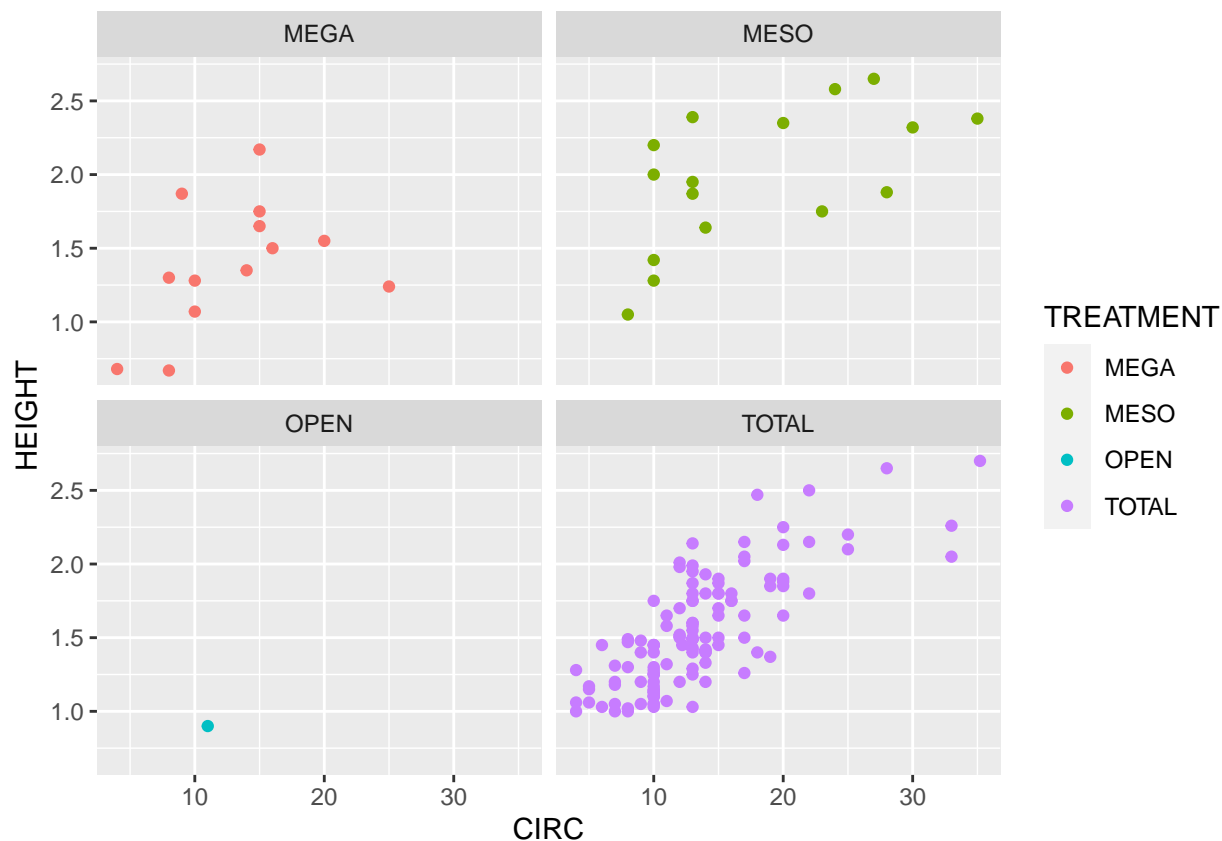


#subplots or facets

function to create subplots is called `facet_wrap()`

```
ggplot(data = acacia, mapping = aes(x = CIRC, y = HEIGHT, color = TREATMENT)) +
  geom_point() +
  facet_wrap(~TREATMENT)
```

## Warning: Removed 4 rows containing missing values (geom\_point).



The plot above indicates that acacia trees within the megaherbivore fence enclosure were typically smaller both in height and in circumference in comparison to the acacia trees within the mesoherbivore fence enclosure.

When comparing the open and total we can see that in an open enclosure there are very few trees whereas in an entirely closed off enclosure contained much more trees.

how to test these hypotheses

## model fitting functions

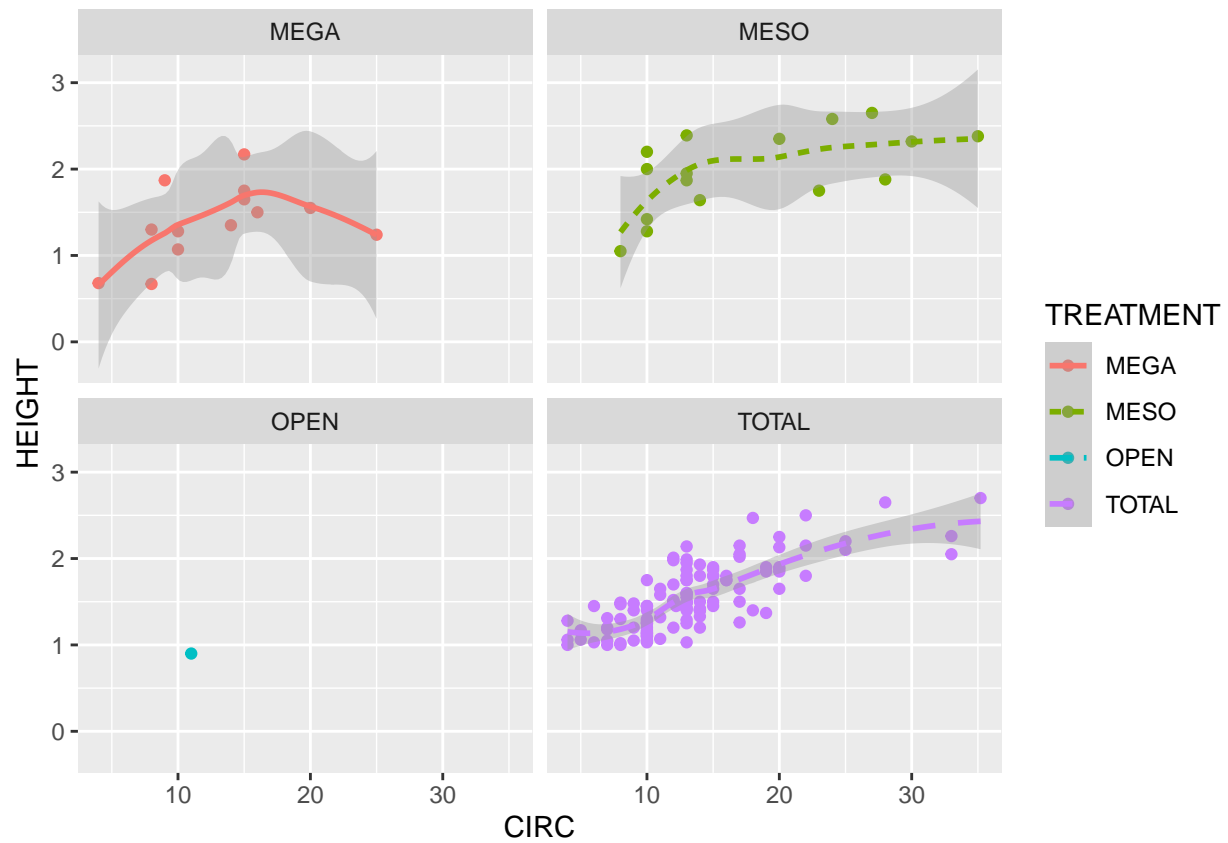
the `geom_smooth()` function allows us to fit linear models to a set of points

```
ggplot(data = acacia, mapping = aes(x = CIRC, y = HEIGHT, color = TREATMENT,
linetype = TREATMENT)) +
  geom_point() +
  geom_smooth(method = "loess") +
  facet_wrap(~TREATMENT)
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

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

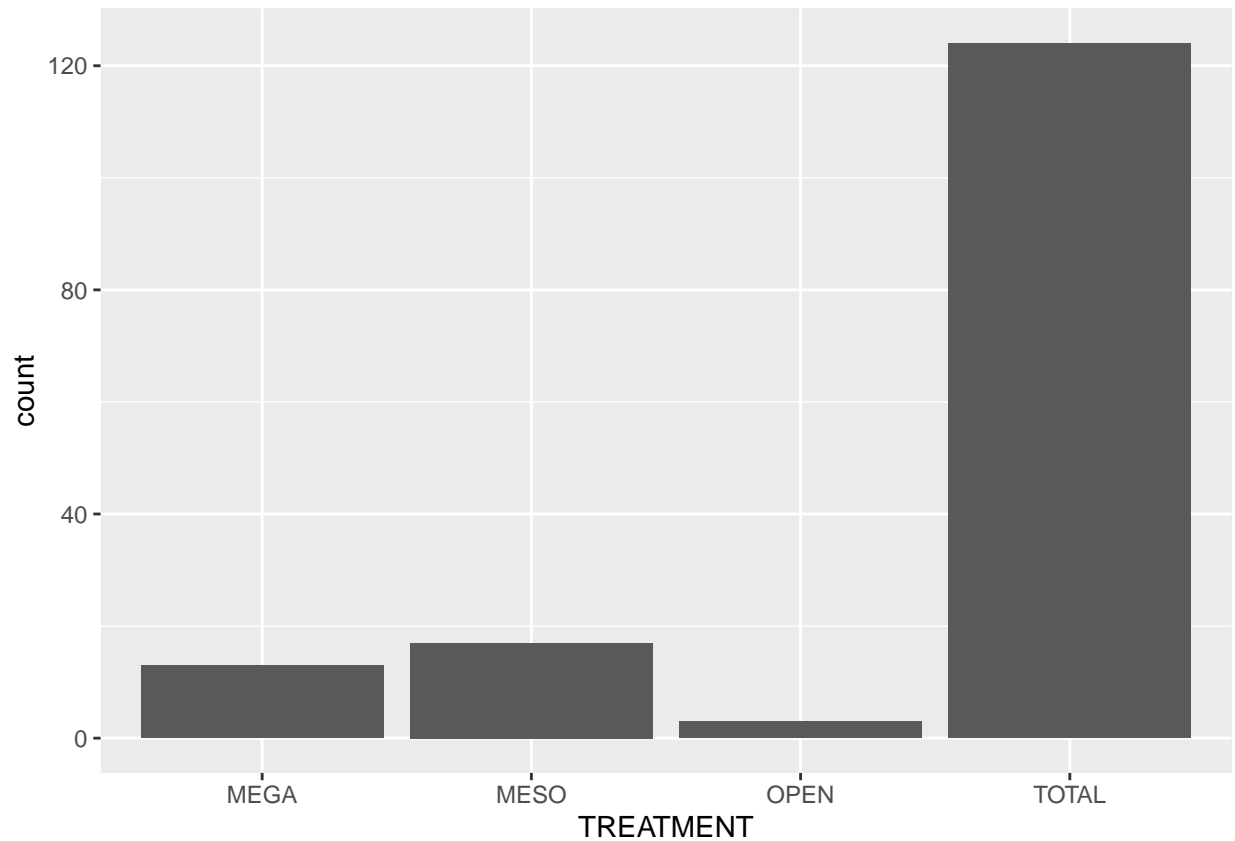
```
## Warning: Removed 4 rows containing missing values (geom_point).
```



## histograms and barplots

for bar plots we use `geom_bar()` function:

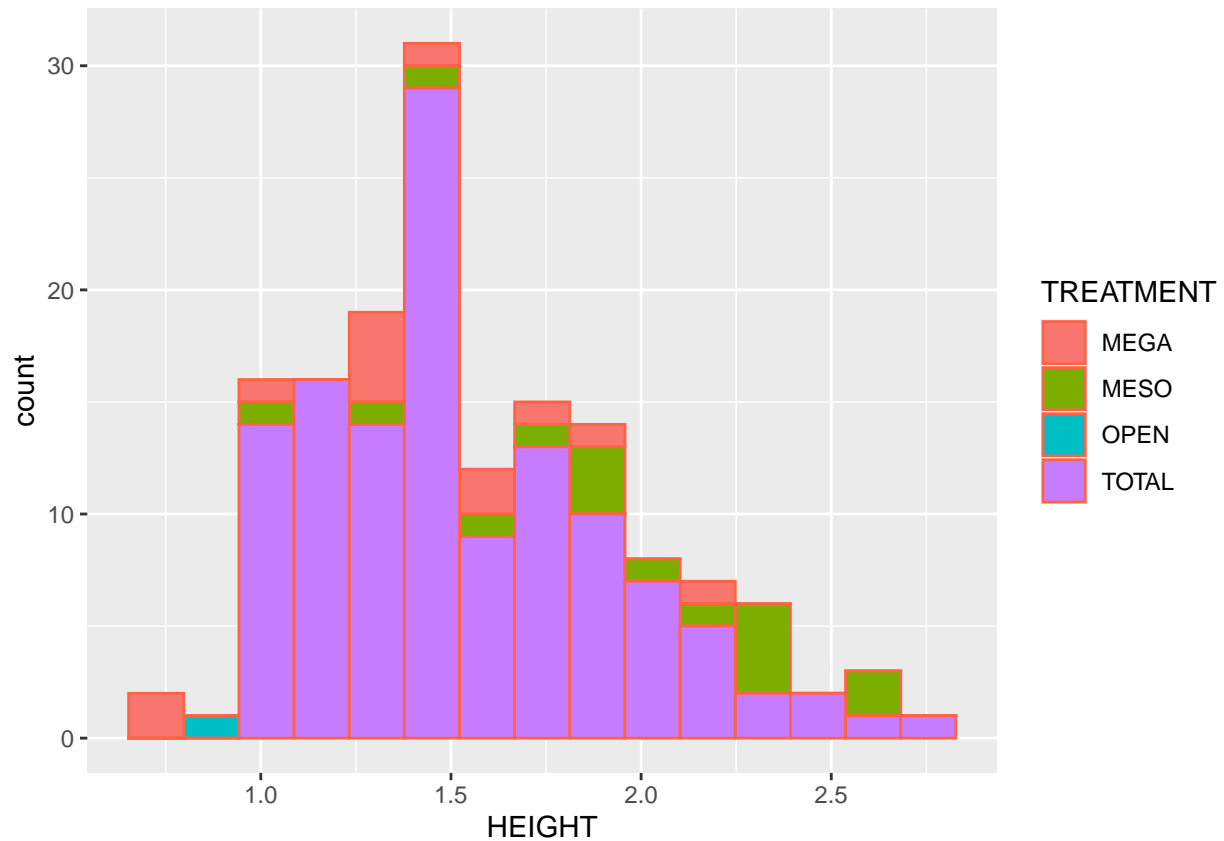
```
ggplot(data = acacia, mapping = aes(x = TREATMENT)) +  
  geom_bar()
```



if we want to see the distribution of a continuous variable like height or circ we use `geom_histogram()` function

```
ggplot(data = acacia, mapping = aes(x = HEIGHT, fill = TREATMENT)) +  
  geom_histogram(bins = 15, col = "tomato")
```

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



layer multiple data from the same or different data sets

```
ggplot() +
  geom_point(data = acacia,
            mapping = aes(x = CIRC, y = HEIGHT,
                          color = TREATMENT)) +
  geom_smooth(data = acacia, mapping = aes(x = CIRC, y = HEIGHT)) +
  geom_histogram(data = acacia,
                mapping = aes(x = CIRC, col = TREATMENT), alpha = 0.1)
```

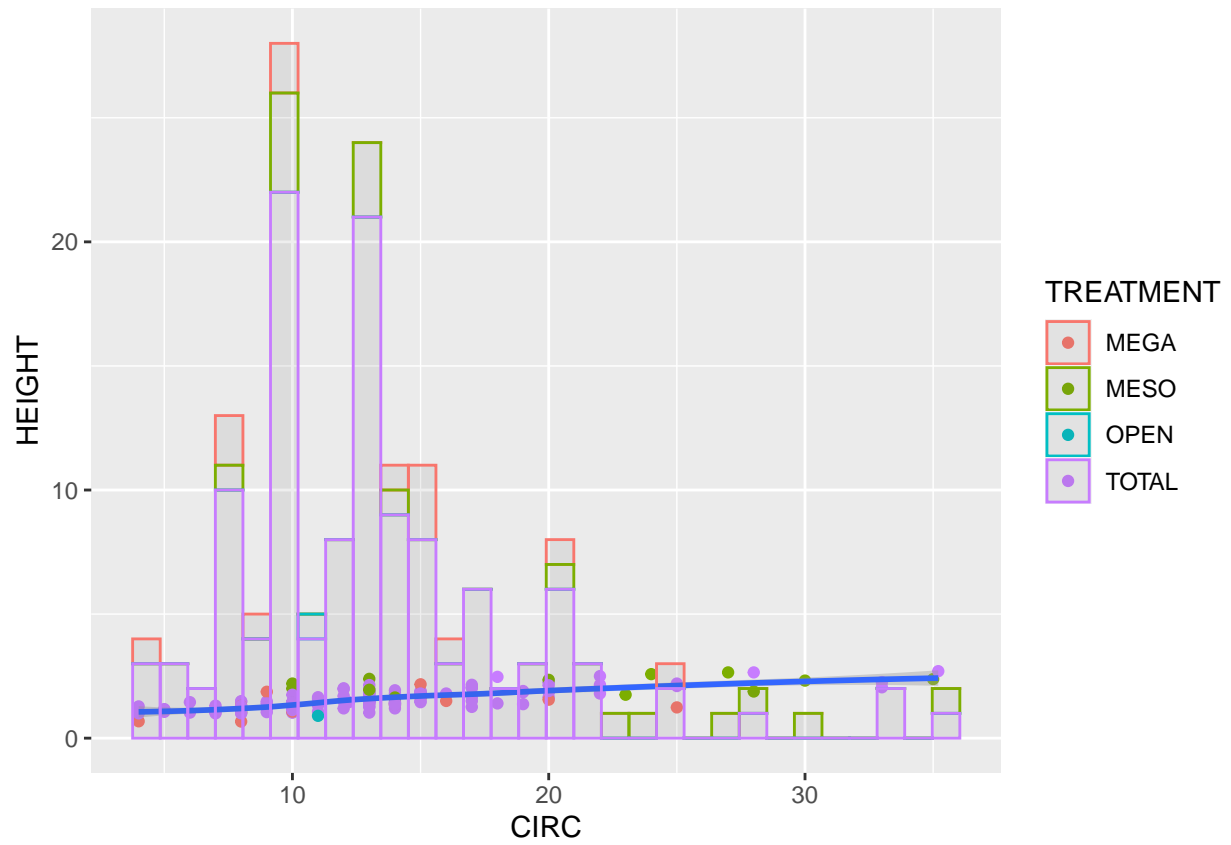
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```

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

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

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

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



#### 4.2 visualize a statistical analysis of correlation