Data Visualization Homework - Acacia Vs Trees

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Exercise 3

Read the data

```
trees <- read_tsv(file = "../data-raw/TREE_SURVEYS.txt")
```

```
## Rows: 7508 Columns: 16
## -- Column specification --------------------------------------------------------
## Delimiter: "\t"
## chr (9): SITE, TREATMENT, PLOT, SPECIES, DEAD, HEIGHT, AXIS_2, MEASUREMENT, ...
## dbl (7): SURVEY, YEAR, BLOCK, ORIGINAL_TAG, NEW_TAG, AXIS_1, CIRC
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
head(trees)
```

```
## # A tibble: 6 x 16
##   SURVEY  YEAR SITE  TREATMENT BLOCK PLOT   SPECIES ORIGI~1 NEW_TAG DEAD  HEIGHT
##    <dbl> <dbl> <chr> <chr>     <dbl> <chr>  <chr>     <dbl>   <dbl> <chr> <chr>
## 1      1  2009 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N     3.4
## 2      2  2010 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N     3.32
## 3      3  2011 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N     3.65
## 4      4  2012 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N     3.74
## 5      5  2013 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N     3.59
## 6      1  2009 SOUTH TOTAL         2 S2TOT~ Acacia~       2      NA N     2.3
## # ... with 5 more variables: AXIS_1 <dbl>, AXIS_2 <chr>, CIRC <dbl>,
## #   MEASUREMENT <chr>, STEMS <chr>, and abbreviated variable name
## #   1: ORIGINAL_TAG
```

Quality assurance

After visually inspecting the variables, it looks like height is character type and it should be numeric

```
str(trees)
```

```
## spc_tbl_ [7,508 x 16] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
##  $ SURVEY      : num [1:7508] 1 2 3 4 5 1 2 3 4 5 ...
##  $ YEAR        : num [1:7508] 2009 2010 2011 2012 2013 ...
##  $ SITE        : chr [1:7508] "SOUTH" "SOUTH" "SOUTH" "SOUTH" ...
##  $ TREATMENT   : chr [1:7508] "TOTAL" "TOTAL" "TOTAL" "TOTAL" ...
##  $ BLOCK       : num [1:7508] 2 2 2 2 2 2 2 2 2 2 ...
##  $ PLOT        : chr [1:7508] "S2TOTAL" "S2TOTAL" "S2TOTAL" "S2TOTAL" ...
##  $ SPECIES     : chr [1:7508] "Acacia_etbaica" "Acacia_etbaica" "Acacia_etbaica" "Acacia_etbaica" ..
##  $ ORIGINAL_TAG: num [1:7508] 1 1 1 1 1 2 2 2 2 2 ...
##  $ NEW_TAG     : num [1:7508] NA NA NA NA NA NA NA NA NA NA ...
##  $ DEAD        : chr [1:7508] "N" "N" "N" "N" ...
##  $ HEIGHT      : chr [1:7508] "3.4" "3.32" "3.65" "3.74" ...
##  $ AXIS_1      : num [1:7508] 6.1 8.25 8.85 5.5 5 2.2 2.75 3.3 NA 3.7 ...
##  $ AXIS_2      : chr [1:7508] "5" "8.45" "9" "7.1" ...
##  $ CIRC        : num [1:7508] 37.8 18.8 57 60 55 14.2 18.4 25 NA 31 ...
##  $ MEASUREMENT : chr [1:7508] "D" "D" "C" "C" ...
##  $ STEMS       : chr [1:7508] "1" "1" "1" "1" ...
##  - attr(*, "spec")=
##   .. cols(
##   ..   SURVEY = col_double(),
##   ..   YEAR = col_double(),
##   ..   SITE = col_character(),
##   ..   TREATMENT = col_character(),
##   ..   BLOCK = col_double(),
##   ..   PLOT = col_character(),
##   ..   SPECIES = col_character(),
##   ..   ORIGINAL_TAG = col_double(),
##   ..   NEW_TAG = col_double(),
##   ..   DEAD = col_character(),
##   ..   HEIGHT = col_character(),
##   ..   AXIS_1 = col_double(),
##   ..   AXIS_2 = col_character(),
##   ..   CIRC = col_double(),
##   ..   MEASUREMENT = col_character(),
##   ..   STEMS = col_character()
##   .. )
##  - attr(*, "problems")=<externalptr>
```

```
head(trees$HEIGHT)
```

```
## [1] "3.4"  "3.32" "3.65" "3.74" "3.59" "2.3"
```

```
trees$HEIGHT <- as.numeric(trees$HEIGHT)
```

```
## Warning: NAs introduced by coercion
```

```
head(trees)
```

```
## # A tibble: 6 x 16
##   SURVEY  YEAR SITE  TREATMENT BLOCK PLOT   SPECIES ORIGI~1 NEW_TAG DEAD  HEIGHT
##    <dbl> <dbl> <chr> <chr>     <dbl> <chr>  <chr>     <dbl>   <dbl> <chr>  <dbl>
## 1      1  2009 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.4
## 2      2  2010 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.32
## 3      3  2011 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.65
## 4      4  2012 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.74
## 5      5  2013 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.59
## 6      1  2009 SOUTH TOTAL         2 S2TOT~ Acacia~       2      NA N       2.3
## # ... with 5 more variables: AXIS_1 <dbl>, AXIS_2 <chr>, CIRC <dbl>,
## #   MEASUREMENT <chr>, STEMS <chr>, and abbreviated variable name
## #   1: ORIGINAL_TAG
```

Alternatively, we can force variables to be assigned a specific type when we read them:

```
trees <- read_tsv("../data-raw/TREE_SURVEYS.txt",
               col_types = list(HEIGHT = col_double(),
                                AXIS_2 = col_double()))
```

```
## Warning: One or more parsing issues, call `problems()` on your data frame for details,
## e.g.:
##   dat <- vroom(...)
##   problems(dat)
```

```
canopy_area <- trees$AXIS_1 * trees$AXIS_2
head(trees)
```

```
## # A tibble: 6 x 16
##   SURVEY  YEAR SITE  TREATMENT BLOCK PLOT   SPECIES ORIGI~1 NEW_TAG DEAD  HEIGHT
##    <dbl> <dbl> <chr> <chr>     <dbl> <chr>  <chr>     <dbl>   <dbl> <chr>  <dbl>
## 1      1  2009 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.4
## 2      2  2010 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.32
## 3      3  2011 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.65
## 4      4  2012 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.74
## 5      5  2013 SOUTH TOTAL         2 S2TOT~ Acacia~       1      NA N       3.59
## 6      1  2009 SOUTH TOTAL         2 S2TOT~ Acacia~       2      NA N       2.3
## # ... with 5 more variables: AXIS_1 <dbl>, AXIS_2 <dbl>, CIRC <dbl>,
## #   MEASUREMENT <chr>, STEMS <chr>, and abbreviated variable name
## #   1: ORIGINAL_TAG
```

```
trees$canopy_area <- canopy_area
trees$area <- canopy_area
```

```
numbers <- -10:10
letters[-4]
```

```
##  [1] "a" "b" "c" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q" "r" "s" "t"
## [20] "u" "v" "w" "x" "y" "z"
```

```
numbers[c(1:3,5:10)]
```

```
## [1] -10  -9  -8  -6  -5  -4  -3  -2  -1
```

```
numbers[-4]
```

```
##  [1] -10  -9  -8  -6  -5  -4  -3  -2  -1   0   1   2   3   4   5   6   7   8   9
## [20]  10
```

```
trees[1:3,-(5:10)]
```

```
## # A tibble: 3 x 12
##   SURVEY  YEAR SITE  TREATMENT HEIGHT AXIS_1 AXIS_2  CIRC MEASUR~1 STEMS canop~2
##    <dbl> <dbl> <chr> <chr>      <dbl>  <dbl>  <dbl> <dbl> <chr>    <chr>   <dbl>
## 1      1  2009 SOUTH TOTAL       3.4    6.1    5     37.8 D        1        30.5
## 2      2  2010 SOUTH TOTAL       3.32   8.25   8.45  18.8 D        1        69.7
## 3      3  2011 SOUTH TOTAL       3.65   8.85   9     57   C        1        79.6
## # ... with 1 more variable: area <dbl>, and abbreviated variable names
## #   1: MEASUREMENT, 2: canopy_area
```

```
trees
```

```
## # A tibble: 7,508 x 18
##    SURVEY  YEAR SITE  TREATMENT BLOCK PLOT  SPECIES ORIGI~1 NEW_TAG DEAD  HEIGHT
##     <dbl> <dbl> <chr> <chr>     <dbl> <chr> <chr>     <dbl>   <dbl> <chr>  <dbl>
##  1      1  2009 SOUTH TOTAL         2 S2TO~ Acacia~       1      NA N       3.4
##  2      2  2010 SOUTH TOTAL         2 S2TO~ Acacia~       1      NA N       3.32
##  3      3  2011 SOUTH TOTAL         2 S2TO~ Acacia~       1      NA N       3.65
##  4      4  2012 SOUTH TOTAL         2 S2TO~ Acacia~       1      NA N       3.74
##  5      5  2013 SOUTH TOTAL         2 S2TO~ Acacia~       1      NA N       3.59
##  6      1  2009 SOUTH TOTAL         2 S2TO~ Acacia~       2      NA N       2.3
##  7      2  2010 SOUTH TOTAL         2 S2TO~ Acacia~       2      NA N       2.32
##  8      3  2011 SOUTH TOTAL         2 S2TO~ Acacia~       2      NA N       2.75
##  9      4  2012 SOUTH TOTAL         2 S2TO~ Acacia~       2      NA Y      NA
## 10      5  2013 SOUTH TOTAL         2 S2TO~ Acacia~       2      NA N       2.86
## # ... with 7,498 more rows, 7 more variables: AXIS_1 <dbl>, AXIS_2 <dbl>,
## #   CIRC <dbl>, MEASUREMENT <chr>, STEMS <chr>, canopy_area <dbl>, area <dbl>,
## #   and abbreviated variable name 1: ORIGINAL_TAG
```

Create a subset of the `trees` data frame with just the `SURVEY`, `YEAR`, `SITE`, and `canopy_area` columns:

```
trees_test <- subset(trees, select=c(SURVEY, YEAR, SITE, canopy_area))
str(trees_test)
```

```
## tibble [7,508 x 4] (S3: tbl_df/tbl/data.frame)
##  $ SURVEY     : num [1:7508] 1 2 3 4 5 1 2 3 4 5 ...
##  $ YEAR       : num [1:7508] 2009 2010 2011 2012 2013 ...
##  $ SITE       : chr [1:7508] "SOUTH" "SOUTH" "SOUTH" "SOUTH" ...
##  $ canopy_area: num [1:7508] 30.5 69.7 79.6 39 40.8 ...
```

```
trees_test <- data.frame(SURVEY = trees$SURVEY,
                         YEAR = trees$YEAR,
                         SITE = trees$SITE,
                         canopy_area = trees$canopy_area)
str(trees_test)
```

```
## 'data.frame':    7508 obs. of  4 variables:
##  $ SURVEY     : num  1 2 3 4 5 1 2 3 4 5 ...
##  $ YEAR       : num  2009 2010 2011 2012 2013 ...
##  $ SITE       : chr  "SOUTH" "SOUTH" "SOUTH" "SOUTH" ...
##  $ canopy_area: num  30.5 69.7 79.6 39 40.8 ...
```

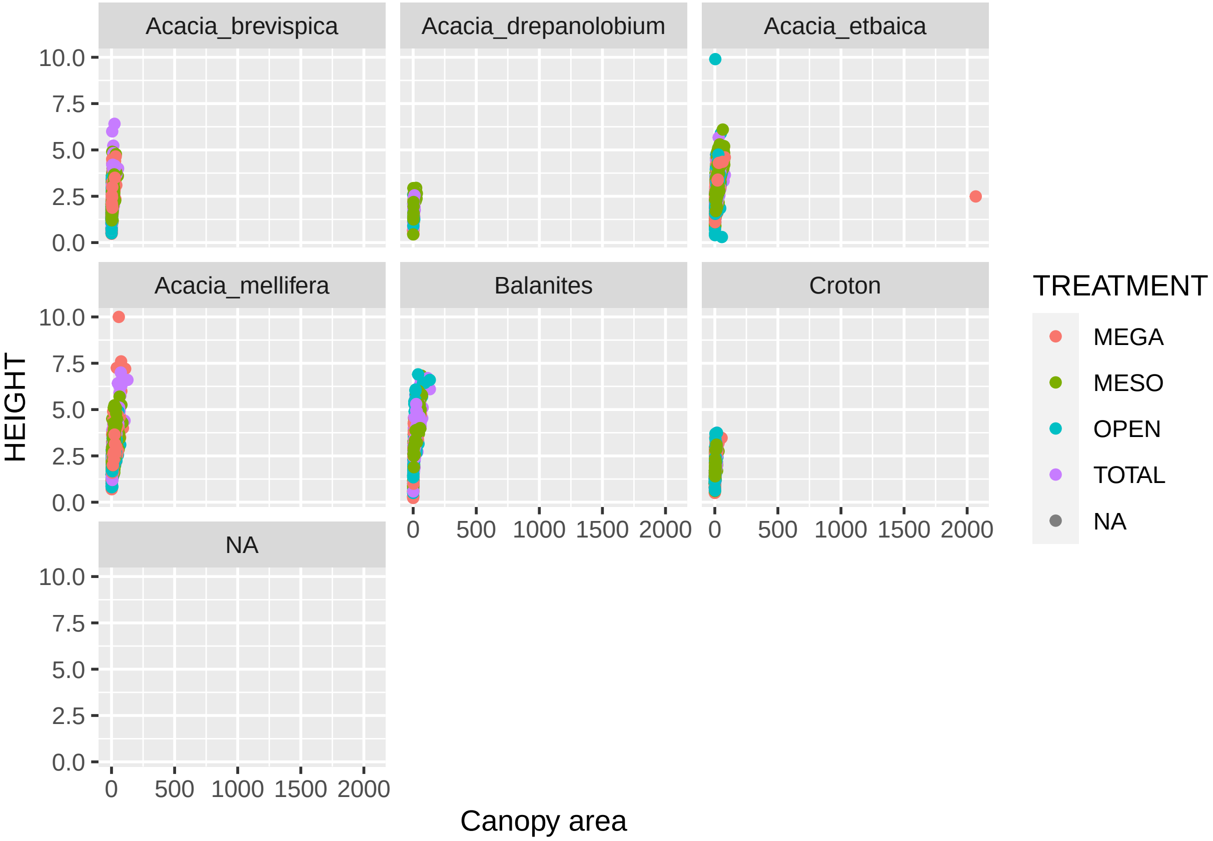
```
trees2 <- trees[,c("SURVEY", "YEAR", "SITE", "canopy_area")]
str(trees2)
```

```
## tibble [7,508 x 4] (S3: tbl_df/tbl/data.frame)
##  $ SURVEY     : num [1:7508] 1 2 3 4 5 1 2 3 4 5 ...
##  $ YEAR       : num [1:7508] 2009 2010 2011 2012 2013 ...
##  $ SITE       : chr [1:7508] "SOUTH" "SOUTH" "SOUTH" "SOUTH" ...
##  $ canopy_area: num [1:7508] 30.5 69.7 79.6 39 40.8 ...
```

Make a scatter plot with `canopy_area` on the x axis and `HEIGHT` on the y axis. Color the points by `TREATMENT` and create a subplot per species uding the function `facet_wrap()`. This will plot the points for each variable in the `SPECIES` column in a separate subplot. Label the x axis `"Canopy Area (m)"` and the y axis `"Height (m)"`. Make the point size 2.

```
ggplot(data = trees, mapping = aes(x = canopy_area, y = HEIGHT, color = TREATMENT)) +
  geom_point() +
  labs(x = "Canopy area") +
  facet_wrap(~SPECIES)
```

```
## Warning: Removed 215 rows containing missing values (`geom_point()`).
```



That's a big outlier in the plot from (2). 50 by 50 meters is a little too big for a real acacia tree, so filter the data to remove any values for AXIS_1 and AXIS_2 that are over 20 and update the data frame. Then, remake the graph.

```
# we can do this with the subset function
trees3 <- subset(trees, canopy_area <= 400)
# which(is.na(trees4$TREATMENT))

# OR finding the actual value that is the outlier
which(trees$canopy_area > 200)
```

```
## [1] 3839
```

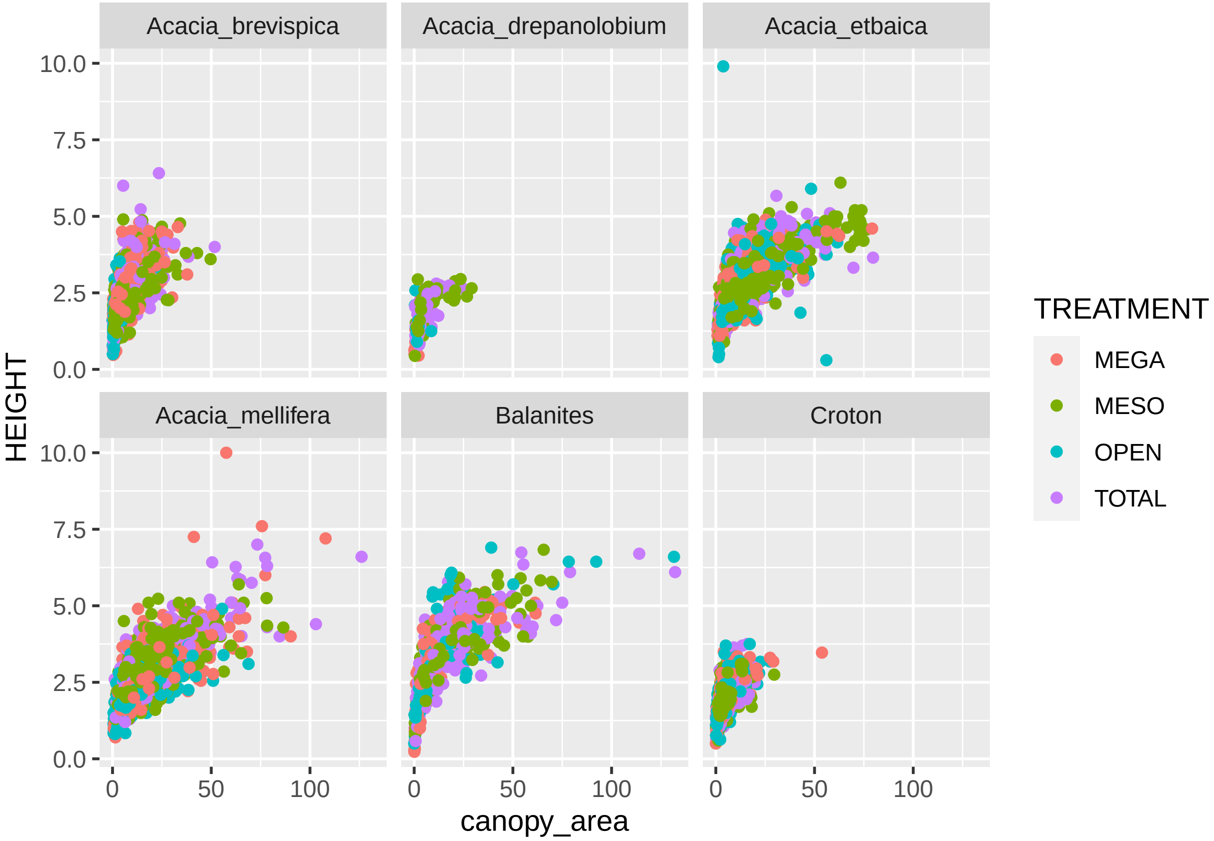
```
trees[3839,]
```

```
## # A tibble: 1 x 18
##   SURVEY  YEAR SITE    TREATM~1 BLOCK PLOT  SPECIES ORIGI~2 NEW_TAG DEAD  HEIGHT
##    <dbl> <dbl> <chr>   <chr>    <dbl> <chr> <chr>     <dbl>   <dbl> <chr>  <dbl>
## 1      5  2013 CENTRAL MEGA         2 C2ME~ Acacia~    1941      NA N       2.49
## # ... with 7 more variables: AXIS_1 <dbl>, AXIS_2 <dbl>, CIRC <dbl>,
## #   MEASUREMENT <chr>, STEMS <chr>, canopy_area <dbl>, area <dbl>, and
## #   abbreviated variable names 1: TREATMENT, 2: ORIGINAL_TAG
```

```
trees4 <- trees[-3839,]
# n <- which(is.na(trees4$TREATMENT))
# trees4[n,]
```

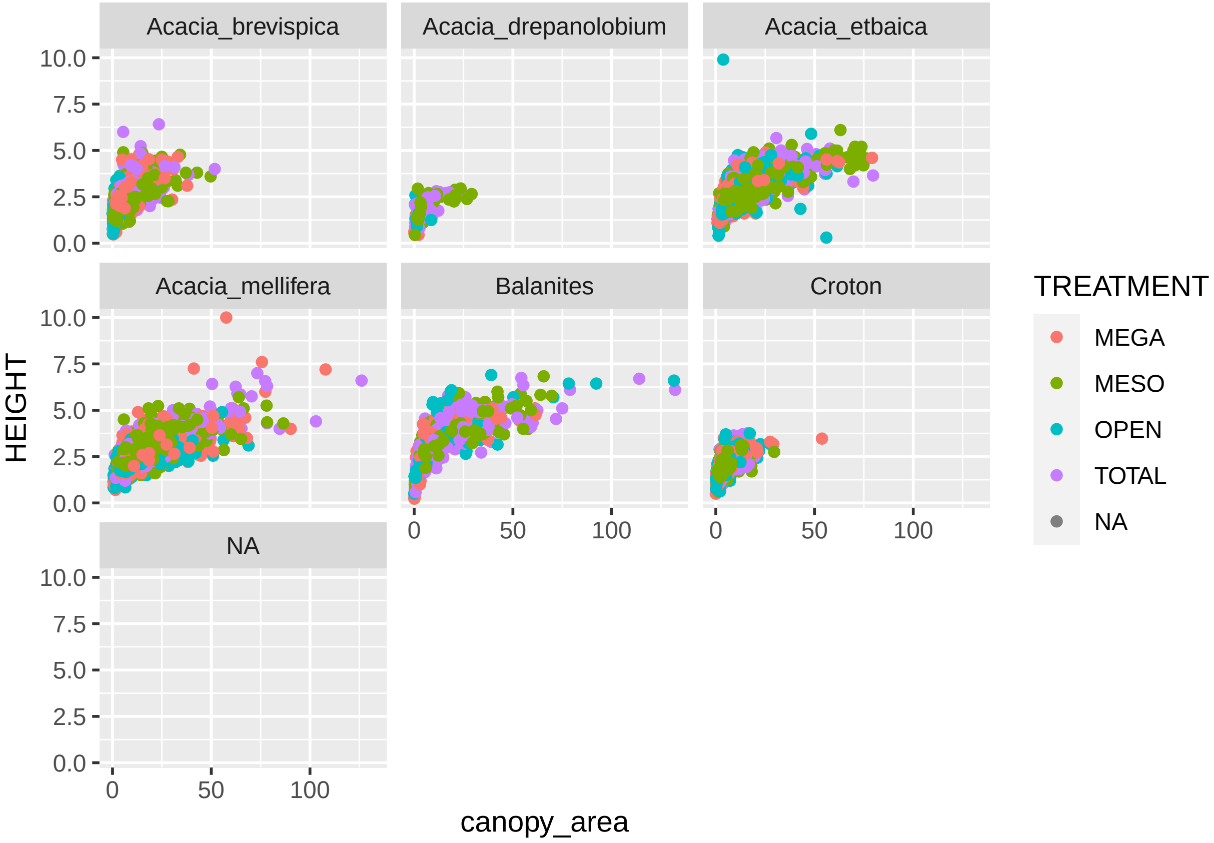
The two tables are the same:

```
ggplot(data = trees3, mapping = aes(x = canopy_area, y = HEIGHT, color = TREATMENT)) +
  geom_point() +
  facet_wrap(~SPECIES)
```



```
ggplot(data = trees4, mapping = aes(x = canopy_area, y = HEIGHT, color = TREATMENT)) +
  geom_point() +
  facet_wrap(~SPECIES)
```

```
## Warning: Removed 215 rows containing missing values (`geom_point()`).
```



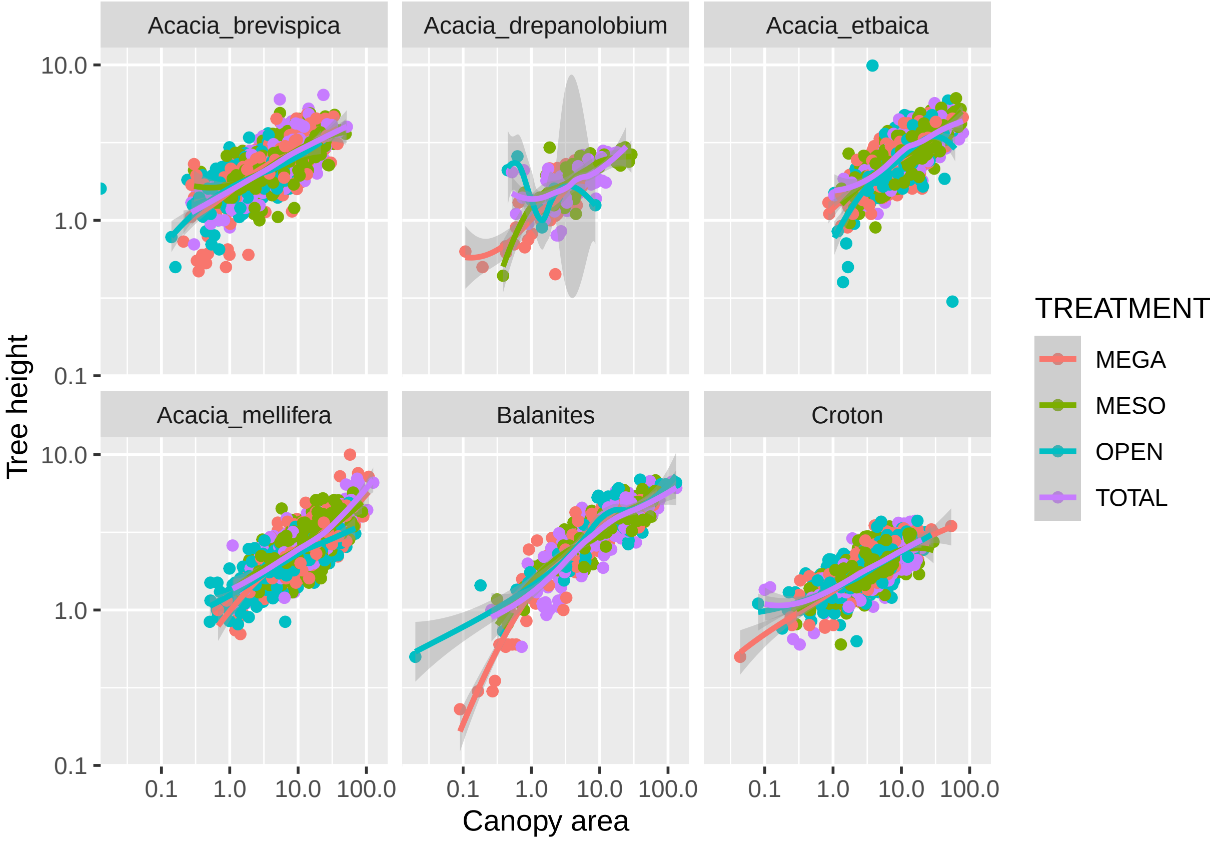
Final plot:

```r
ggplot(data = trees3, mapping = aes(x = canopy_area, y = HEIGHT, color = TREATMENT)) +
  geom_point() +
  scale_x_log10() +
  scale_y_log10() +
  facet_wrap(~SPECIES) +
  geom_smooth() +
  labs(x = "Canopy area", y = "Tree height")
```

```
## Warning: Transformation introduced infinite values in continuous x-axis
## Transformation introduced infinite values in continuous x-axis
```

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

```
## Warning: Removed 1 rows containing non-finite values (`stat_smooth()`).
```


Acacia_brevispica
Acacia_drepanolobium
Acacia_etbaica
Acacia_mellifera
Balanites
Croton
Tree height
10.0
1.0
0.1
0.1
1.0
10.0
100.0
Canopy area
TREATMENT
MEGA
MESO
OPEN
TOTAL