

# TREE SURVEYS manipulations

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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.

```
library(readr)
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)
```

```
trees$canopy_area <- trees$AXIS_1 * trees$AXIS_2
```

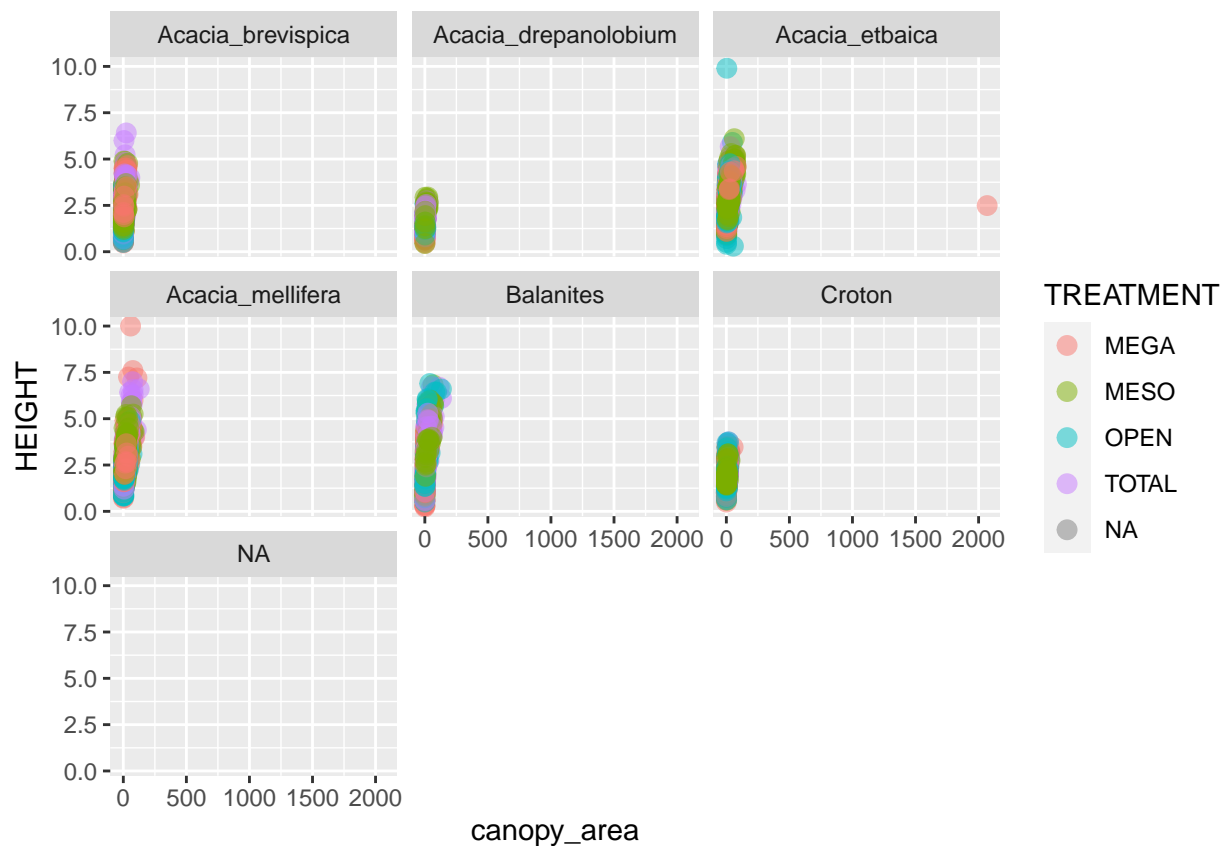
```
subset(trees, select = c(SURVEY, YEAR, SITE, canopy_area))
```

```
## # A tibble: 7,508 x 4
##   SURVEY YEAR SITE canopy_area
##   <dbl> <dbl> <chr>    <dbl>
## 1     1     1 2009 SOUTH     30.5
## 2     2     2 2010 SOUTH     69.7
## 3     3     3 2011 SOUTH     79.6
## 4     4     4 2012 SOUTH     39.0
## 5     5     5 2013 SOUTH     40.8
```

```
## 6      1  2009 SOUTH      6.16
## 7      2  2010 SOUTH      7.29
## 8      3  2011 SOUTH     12.5
## 9      4  2012 SOUTH     NA
## 10     5  2013 SOUTH      9.62
## # ... with 7,498 more rows
```

```
library(ggplot2)
ggplot(data = trees, mapping = aes(x = canopy_area, y = HEIGHT, color = TREATMENT)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_wrap(~SPECIES)
```

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



```
treesmod <- subset(trees, canopy_area <= 400)
```

```
library(ggplot2)
ggplot(data = treesmod, mapping = aes(x = canopy_area, y = HEIGHT, color = TREATMENT)) +
  geom_point(size = 3, alpha = 0.5) +
  facet_wrap(~SPECIES)
```

