

## shrub volume data

### Exercise 1

Create a new Rmd file called “shrub\_volume.Rmd”. Write a short paragraph describing the data set before starting your analysis. Include a figure.

The dataset is based on a study of the factors that control the size and carbon storage of shrubs. An experiment in which the effects of three various treatments on shrub volume located in four different areas is seen. The site describes the area in which the scrubs are seen. The experiment describes thich type of treatment is implemented on the shrubs. The length, width, and height, constitute measurement factprs that are utilized to determine the volume of each of the shrubs.

```
knitr::include_graphics("../fig/shrubs-image.jpeg")
```



Import the data set using `read.csv()`. Assign it to an object called `shrubs`.

```
shrubs <- read.csv(file = "../data-raw/shrub-volume-data.csv")
```

Select the data from the “length” column and print it out (using `select()`).

```
# select(shrubs, length) %>% print()
```

Select the data from the site and experiment columns and print it out (using `select()`).

```
# select(shrubs, site, experiment) %>% print()
```

Add a new column named “area” containing the area of the shrub, which is the length times the width (using `mutate()`).

```
# mutate(shrubs, area = length*width)
```

Sort the data by length (using `arrange()`).

```
# arrange(shrubs, length)
```

Filter the data to include only plants with heights greater than 5 (using `filter()`).

```
# filter(shrubs, height > 5)
```

Filter the data to include only plants with heights greater than 4 and widths greater than 2 (using `,` or `&` to include two conditions).

```
# filter(shrubs, height > 4 & width > 2)
```

Filter the data to include only plants from Experiment 1 or Experiment 3 (using `|` for “or”).

```
# filter(shrubs, experiment == 1 | experiment == 3)
```

Filter the data to remove rows with null values in the height column (using `!is.na`)

```
# filter(shrubs, !is.na(height))
```

Create a new data frame called `shrub_volumes` that includes all of the original data and a new column containing the volumes (`length * width * height`), and display it.

```
# mutate(shrubs, volume = length*width*height) %>%  
# select(site, experiment, length, width, height, volume)
```

## Exercise 2

Modify the code to calculate and print the average height of a plant in each experiment.

```
# shrub_dims <- read.csv('../data-raw/shrub-volume-data.csv')  
# by_experiment <- group_by(shrub_dims, experiment)  
# avg_height_by_experiment <- summarize(by_experiment, avg_height = mean(height))  
# avg_height_by_experiment
```

Use `max()` to determine the maximum height of a plant at each site.

```
# shrub_dims <- read.csv('../data-raw/shrub-volume-data.csv')  
# by_site <- group_by(shrub_dims, site)  
# max_height <- summarize(by_site, max_height = max(height))  
# max_height
```

Write the same code but as a pipeline (using the pipe `|>` or `>`) to get the same result.

```
# shrub_dims <- read.csv('../data-raw/shrub-volume-data.csv')  
# avg_height <- shrub_dims %>%  
#   group_by(site) %>%  
#   summarize(avg_height = mean(height))
```

```
# shrub_dims <- read.csv('../data-raw/shrub-volume-data.csv')  
# avg_height_by_experiment <- shrub_dims %>%  
#   group_by(experiment) %>%  
#   summarize(avg_height = mean(height))  
# avg_height_by_experiment
```

```
# shrub_dims <- read.csv('../data-raw/shrub-volume-data.csv')
# max_height <- shrub_dims %>%
#   group_by(site) %>%
#   summarize(max_height = max(height))
# max_height
```

## Exercise 3

Fix the errors in the code so that it does what it's supposed to.

Add a comment to the end of each line of code explaining what it does.

When importing the data we need to ensure that we show the location of where it is, so our R studio can know where to find the file or dataset.

```
read.csv("../data-raw/shrub-volume-data.csv")
```

##	site	experiment	length	width	height
## 1	1	1	2.2	1.3	9.6
## 2	1	2	2.1	2.2	7.6
## 3	1	3	2.7	1.5	2.2
## 4	2	1	3.0	4.5	1.5
## 5	2	2	3.1	3.1	4.0
## 6	2	3	2.5	2.8	3.0
## 7	3	1	1.9	1.8	4.5
## 8	3	2	1.1	0.5	2.3
## 9	3	3	3.5	2.0	7.5
## 10	4	1	2.9	2.7	3.2
## 11	4	2	4.5	4.8	6.5
## 12	4	3	1.2	1.8	2.7

We need to create a new object labeled as `shrub_data` using the data. After importing the data using the `read.csv` function, it is important to assign it to an object; in this case, `shrub_data`.

```
shrub_data <- read.csv("../data-raw/shrub-volume-data.csv")
```

After assigning the dataset to an object we can use the object and pipeline to start it off

```
# shrub_data <- read.csv("../data-raw/shrub-volume-data.csv")
# shrub_volume_site <- shrub_data %>%
#   mutate(volume = length * width * height) %>%
#   group_by(site) %>%
#   summarize(mean_volume = mean(volume))
```

When using `summarize`, instead of the mean volume taking the average of the volumes, it took the maximum of the volumes, which is incorrect. To fix this, the `max` function was changed to the `mean` function.

```
# shrub_data <- read.csv("../data-raw/shrub-volume-data.csv")
# shrub_volume_experiment <- shrub_data %>%
#   mutate(volume = length * width * height) %>%
#   group_by(experiment) %>%
#   summarize(mean_volume = mean(volume))
```

This shows the correct code to import the shrub volume data and calculate the average shrub volume for each site and, separately, for each experiment.