R_Homework_2_RK

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Load packages

```r
library(tidyverse)
```

```
## Warning in as.POSIXlt.POSIXct(Sys.time()): unknown timezone 'zone/tz/2019c.1.0/
## zoneinfo/America/New_York'
```

```
## -- Attaching packages ------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.0     v purrr   0.3.3
## v tibble  3.0.1     v dplyr   0.8.5
## v tidyr   1.0.2     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

```
## Warning: package 'readr' was built under R version 3.4.4
```

```
## Warning: package 'stringr' was built under R version 3.4.4
```

```
## -- Conflicts ---------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```r
library(readxl)
```

```
## Warning: package 'readxl' was built under R version 3.4.4
```

```r
library(readr)
library(janitor)
```

```
## Warning: package 'janitor' was built under R version 3.4.4
```

Load data

```r
# Load agua chinon vegetation transect data
ac_data_raw <- read_xlsx("OCWR_AC_2019_Data.xlsx")
ac_data <- clean_names(ac_data_raw)

# Load oak restoration data
oak_data_raw <- read_csv("Weir_Oak_Restoration_Data_winter19_2.csv")
```

```
## Parsed with column specification:
## cols(
##   `Short ID` = col_character(),
##   Survival = col_logical(),
##   Quantity = col_double(),
```

```
##    `Height (cm)` = col_double(),
##    `Open Closed` = col_character(),
##    `Location UML` = col_character(),
##    `Water Yes No` = col_character(),
##    `Sampling Group` = col_character()
## )
oak_data <- clean_names(oak_data_raw)
```

Refer to specific columns

```
# Refer to height columns (2 ways)
oak_data$height_cm
```

```
##     [1]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##    [15]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##    [29]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##    [43]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##    [57]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##    [71]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##    [85]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##    [99]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [113]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [127]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [141]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [155]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [169]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [183]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [197]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [211]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [225]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [239]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [253]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [267]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [281]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [295]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [309]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [323]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [337]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [351]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [365]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [379]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [393]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [407]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [421]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [435]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [449]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [463]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [477]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [491]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [505]   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0
##   [519]   0.0   0.0   0.0   1.0   1.5   1.7   3.0   3.1   4.0   4.0   4.5   5.0   5.0   5.0
##   [533]   5.0   5.0   5.0   5.5   6.0   6.0   6.0   6.0   6.0   6.0   6.0   6.0   6.0   6.0
```

```
## [547]  6.0  6.0  6.0  6.0  6.0  6.5  6.5  6.5  6.5  6.5  7.0  7.0  7.0  7.0
## [561]  7.0  7.0  7.0  7.0  7.0  7.5  7.5  7.5  8.0  8.0  8.0  8.0  8.0  8.0
## [575]  8.0  8.0  8.0  8.0  8.0  8.0  8.0  8.0  8.0  8.0  8.1  8.1  8.5  8.7
## [589]  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0
## [603]  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.0  9.5  9.5  9.5  9.5  9.5
## [617]  9.8  9.8  9.9  9.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0
## [631] 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0
## [645] 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0
## [659] 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.6 10.7 10.9 11.0 11.0 11.0 11.0
## [673] 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0
## [687] 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0 11.0
## [701] 11.0 11.0 11.0 11.0 11.0 11.0 11.2 11.4 11.5 11.5 11.5 11.5 11.5 11.5
## [715] 11.6 11.7 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0
## [729] 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0
## [743] 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.3 12.3 12.3
## [757] 12.5 12.5 12.5 12.5 12.7 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0
## [771] 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0
## [785] 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0
## [799] 13.0 13.2 13.2 13.3 13.5 13.5 13.5 13.9 14.0 14.0 14.0 14.0 14.0 14.0
## [813] 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0
## [827] 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0 14.0
## [841] 14.0 14.0 14.0 14.0 14.1 14.1 14.2 14.3 14.5 14.5 14.5 14.5 14.5 14.5
## [855] 14.5 14.5 14.5 14.9 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0
## [869] 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0
## [883] 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0
## [897] 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.3
## [911] 15.5 15.5 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0
## [925] 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0
## [939] 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.0 16.1 16.2 16.3 16.3 16.3
## [953] 16.5 16.5 16.5 16.5 16.5 16.5 16.7 16.8 17.0 17.0 17.0 17.0 17.0 17.0
## [967] 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0
## [981] 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17.1 17.2
## [995] 17.5 17.5 17.5 17.5 17.5 17.5 17.5 17.5 17.7 17.8 18.0 18.0 18.0 18.0
## [1009] 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0
## [1023] 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.0 18.4 18.5 18.5
## [1037] 18.5 18.5 18.5 18.5 18.6 18.9 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0
## [1051] 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.3 19.4 19.5
## [1065] 19.5 19.5 19.5 19.6 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0
## [1079] 20.0 20.0 20.1 20.3 20.5 20.5 20.5 20.5 20.9 21.0 21.0 21.0 21.0 21.0
## [1093] 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.5
## [1107] 21.5 21.5 21.5 21.5 21.6 22.0 22.0 22.0 22.0 22.0 22.0 22.0 22.0 22.0
## [1121] 22.0 22.0 22.0 22.0 22.0 22.0 22.0 22.0 22.0 22.0 22.1 22.3 22.3 22.4
## [1135] 22.5 22.5 22.5 23.0 23.0 23.0 23.0 23.0 23.0 23.0 23.0 23.0 23.2 23.5
## [1149] 23.8 24.0 24.0 24.0 24.0 24.0 24.0 24.0 24.0 24.0 24.0 24.0 24.2 24.5
## [1163] 24.5 24.5 24.5 24.5 24.9 25.0 25.0 25.0 25.0 25.0 25.5 25.5 25.5 25.6
## [1177] 26.0 26.0 26.0 26.0 26.0 26.5 27.0 27.0 27.0 27.0 27.0 27.0 28.0 28.0
## [1191] 29.0 29.0 30.5 31.6 31.7 35.0 37.0 40.0 40.0 46.0 46.5 63.0
```

```r
oak_data[4]
```

```
## # A tibble: 1,202 x 1
##    height_cm
##        <dbl>
## 1          0
## 2          0
```

```
## 3          0
## 4          0
## 5          0
## 6          0
## 7          0
## 8          0
## 9          0
## 10         0
## # ... with 1,192 more rows
```

```
# Refer to location_uml through sampling group
oak_data[6:8]
```

```
## # A tibble: 1,202 x 3
##    location_uml water_yes_no sampling_group
##    <chr>        <chr>        <chr>
##  1 Lower        No           L_C
##  2 Lower        Yes          L_C
##  3 Lower        Yes          L_C
##  4 Lower        Yes          L_C
##  5 Lower        No           L_C
##  6 Lower        No           L_C
##  7 Lower        No           L_C
##  8 Lower        Yes          L_C
##  9 Lower        No           L_C
## 10 Lower        No           L_C
## # ... with 1,192 more rows
```

```
# Refer to columns 2,5,6,7
oak_data[c(2,5,6,7)]
```

```
## # A tibble: 1,202 x 4
##    survival open_closed location_uml water_yes_no
##    <lgl>    <chr>       <chr>        <chr>
##  1 FALSE    Closed      Lower        No
##  2 FALSE    Closed      Lower        Yes
##  3 FALSE    Closed      Lower        Yes
##  4 FALSE    Closed      Lower        Yes
##  5 FALSE    Closed      Lower        No
##  6 FALSE    Closed      Lower        No
##  7 FALSE    Closed      Lower        No
##  8 FALSE    Closed      Lower        Yes
##  9 FALSE    Closed      Lower        No
## 10 FALSE    Closed      Lower        No
## # ... with 1,192 more rows
```

```
# Refer to all columns except 3 and 8
oak_data[-c(3,8)]
```

```
## # A tibble: 1,202 x 6
##    short_id survival height_cm open_closed location_uml water_yes_no
##    <chr>    <lgl>        <dbl> <chr>       <chr>        <chr>
##  1 L_C_01_4 FALSE            0 Closed      Lower        No
##  2 L_C_02_1 FALSE            0 Closed      Lower        Yes
##  3 L_C_02_2 FALSE            0 Closed      Lower        Yes
##  4 L_C_02_3 FALSE            0 Closed      Lower        Yes
```

```
##  5 L_C_02_4 FALSE               0 Closed      Lower        No
##  6 L_C_03_3 FALSE               0 Closed      Lower        No
##  7 L_C_03_4 FALSE               0 Closed      Lower        No
##  8 L_C_04_1 FALSE               0 Closed      Lower        Yes
##  9 L_C_04_3 FALSE               0 Closed      Lower        No
## 10 L_C_05_1 FALSE               0 Closed      Lower        No
## # ... with 1,192 more rows
```

Change the names of columns and observations

```r
# Create a new dataframe with the oak data
oak_data2 <- oak_data

# Change the names in the sampling groups from short form to long form
oak_data2$sampling_group[which(oak_data2$sampling_group=="L_C")] <- "lower_closed"

oak_data2$sampling_group[which(oak_data2$sampling_group=="L_O")] <- "lower_open"

oak_data2$sampling_group[which(oak_data2$sampling_group=="M_C")] <- "middle_closed"

oak_data2$sampling_group[which(oak_data2$sampling_group=="M_O")] <- "middle_open"

oak_data2$sampling_group[which(oak_data2$sampling_group=="U_C")] <- "upper_closed"

oak_data2$sampling_group[which(oak_data2$sampling_group=="U_O")] <- "upper_open"

# Rename columns 7 (four methods) Note – We must reset the dataframe every time we use another method t

# Method 1
oak_data2 <- oak_data
names(oak_data2)[7] <- "supplementary_watering"

# Method 2
oak_data2 <- oak_data
colnames(oak_data2)[7] <- "supplementary_watering"

# Method 3
oak_data2 <- oak_data
rename(oak_data2, "supplementary_watering" = "water_yes_no")
```

```
## # A tibble: 1,202 x 8
##     short_id survival quantity height_cm open_closed location_uml
##     <chr>    <lgl>       <dbl>     <dbl> <chr>       <chr>
##  1 L_C_01_4 FALSE           0         0 Closed      Lower
##  2 L_C_02_1 FALSE           0         0 Closed      Lower
##  3 L_C_02_2 FALSE           0         0 Closed      Lower
##  4 L_C_02_3 FALSE           0         0 Closed      Lower
##  5 L_C_02_4 FALSE           0         0 Closed      Lower
##  6 L_C_03_3 FALSE           0         0 Closed      Lower
##  7 L_C_03_4 FALSE           0         0 Closed      Lower
##  8 L_C_04_1 FALSE           0         0 Closed      Lower
##  9 L_C_04_3 FALSE           0         0 Closed      Lower
## 10 L_C_05_1 FALSE           0         0 Closed      Lower
```

```
## # ... with 1,192 more rows, and 2 more variables: supplementary_watering <chr>,
## #   sampling_group <chr>
```

```r
# Method 4
oak_data2 <- oak_data
oak_data2 %>%
  rename("supplementary_watering" = "water_yes_no")
```

```
## # A tibble: 1,202 x 8
##    short_id survival quantity height_cm open_closed location_uml
##    <chr>    <lgl>       <dbl>     <dbl> <chr>       <chr>
##  1 L_C_01_4 FALSE           0         0 Closed      Lower
##  2 L_C_02_1 FALSE           0         0 Closed      Lower
##  3 L_C_02_2 FALSE           0         0 Closed      Lower
##  4 L_C_02_3 FALSE           0         0 Closed      Lower
##  5 L_C_02_4 FALSE           0         0 Closed      Lower
##  6 L_C_03_3 FALSE           0         0 Closed      Lower
##  7 L_C_03_4 FALSE           0         0 Closed      Lower
##  8 L_C_04_1 FALSE           0         0 Closed      Lower
##  9 L_C_04_3 FALSE           0         0 Closed      Lower
## 10 L_C_05_1 FALSE           0         0 Closed      Lower
## # ... with 1,192 more rows, and 2 more variables: supplementary_watering <chr>,
## #   sampling_group <chr>
```

Create new columns

```r
# Create a new dataframe with the agua chinon data
ac_data2 <- ac_data

# Create a new column using "$" that divides pin number by two
ac_data2$pin2 <- ac_data2$pin_number/2

# Create a new column using mutate() that returns a 1 for native species and a 0 for anything else
ac_data2 %>%
  mutate(binary_native_non = ifelse(native_non_native == "Native", 1,0))
```

```
## # A tibble: 1,732 x 12
##    desired_habitat polygon_id transect pin_number data_type species_code
##    <chr>           <chr>         <dbl>      <dbl> <chr>     <chr>
##  1 Weedy Control   Weedy Con~        1         NA A.Belt    SOLSPP
##  2 Weedy Control   Weedy Con~        1         NA A.Belt    AMBACA
##  3 Weedy Control   Weedy Con~        1         NA A.Belt    AMBPSI
##  4 Weedy Control   Weedy Con~        1         NA A.Belt    ERIFAS
##  5 Weedy Control   Weedy Con~        1         NA A.Belt    ISOMEN
##  6 Weedy Control   Weedy Con~        1         NA A.Belt    LACSER
##  7 Mulefat Scrub/~ OW-M7            1          1 T.PI      NoNatVeg
##  8 Mulefat Scrub/~ OW-M7            1          2 T.PI      EROCIC
##  9 Mulefat Scrub/~ OW-M7            1          3 T.PI      FESMYU
## 10 Mulefat Scrub/~ OW-M7            1          4 T.PI      ERIFAS
## # ... with 1,722 more rows, and 6 more variables: scientific_name <chr>,
## #   native_non_native <chr>, functional_group <chr>, layer <chr>, pin2 <dbl>,
## #   binary_native_non <dbl>
```

```r
# Create a new column that rounds the numbers in step 1
ac_data2$pin2round <- round(ac_data2$pin2)
```

Create tables

```r
# Diversity1 table
ac_data %>%
  filter(data_type == "T.PI") %>%
  group_by(polygon_id, transect, native_non_native) %>%
  count(species_code)
```

```
## # A tibble: 245 x 5
## # Groups:   polygon_id, transect, native_non_native [49]
##    polygon_id transect native_non_native species_code     n
##    <chr>         <dbl> <chr>             <chr>        <int>
##  1 5M Buffer         2 Native            ACMGLA           1
##  2 5M Buffer         2 Native            ARTCAL          21
##  3 5M Buffer         2 Native            ARTDRA           1
##  4 5M Buffer         2 Native            CALMAC           2
##  5 5M Buffer         2 Native            DEIFAS           5
##  6 5M Buffer         2 Native            ERIFAS          32
##  7 5M Buffer         2 Native            ISOMEN           6
##  8 5M Buffer         2 Native            MALLAU           6
##  9 5M Buffer         2 Native            RAFCAL           1
## 10 5M Buffer         2 Native            STIPUL           2
## # ... with 235 more rows
```

```r
# Functional1 table
func1 <- ac_data %>%
  filter(data_type == "T.PI", native_non_native == "Native") %>%
  group_by(polygon_id, transect) %>%
  count(functional_group)
```

Create plots

```r
# Plot 1
plot1 <- ggplot(ac_data, aes(layer, fill=functional_group)) +
  geom_bar(position="dodge") +
  xlab("Layer") +
  ylab("Count") +
  ggtitle("Vegetation at Agua Chinon by layer and functional group") +
  scale_x_discrete(expand=c(0.2,0), labels = c("No vegetation", "Herb", "Large\nshrub/tree", "Shrub")) +
  scale_y_continuous(expand=c(0,0)) +
  theme_classic() +
  theme(plot.title=element_text(face="bold"), axis.text.x = element_text(size = 8), legend.text = element
  scale_fill_manual(name="Functional Groups", labels = c("no vegetation", "Annual forb\n(late flowering)
  guides(fill=guide_legend(nrow=7))

plot1
```

Vegetation at Agua Chinon by layer and functional group
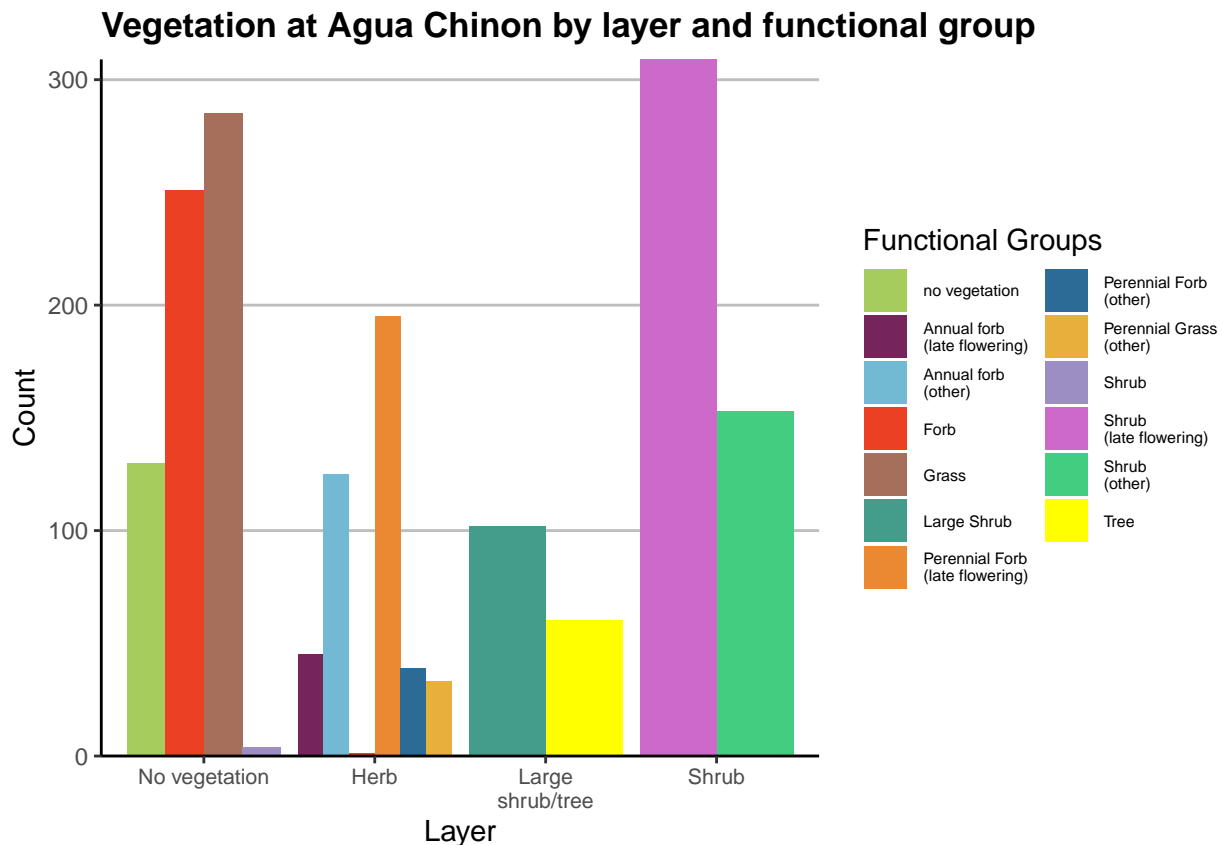

```
# Plot 2 (Note that I am fixing the error with the capitalization of 5M Buffer in advance of making my
ac_data$polygon_id[which(ac_data$polygon_id=="5M Buffer")] <- "5M BUFFER"

plot2 <- ggplot(ac_data, aes(polygon_id, fill=native_non_native)) +
  geom_bar(position="fill") +
  xlab("Polygon ID") +
  ylab("Count") +
  ggtitle("Vegetation at Agua Chinon by native status") +
  scale_x_discrete(expand=c(0.1,0)) +
  scale_y_continuous(expand=c(0,0)) +
  theme_classic() +
  theme(plot.title=element_text(face="bold"), axis.text.x = element_text(size = 7, angle = 90, hjust = 
  scale_fill_manual(name="Legend", labels = c("Native", "No vegetation", "Non-native"), values = c("#a6
  guides(fill=guide_legend(nrow=7))

plot2
```

Vegetation at Agua Chinon by native status

Legend
- Native
- No vegetation
- Non−native