

Coding_Challenge_DataWrangling

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Coding Challenge __ Data Wrangling

```
#install.packages("tidyverse")  
library(tidyverse)
```

```
## Warning: package 'ggplot2' was built under R version 4.4.3
```

```
## Warning: package 'purrr' was built under R version 4.4.2
```

```
## Warning: package 'lubridate' was built under R version 4.4.2
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
## v dplyr      1.1.4      v readr      2.1.5
```

```
## v forcats   1.0.0      v stringr   1.5.1
```

```
## v ggplot2    3.5.1      v tibble    3.2.1
```

```
## v lubridate  1.9.4      v tidyr     1.3.1
```

```
## v purrr      1.0.4
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag()     masks stats::lag()
```

```
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

1. 3 pts. Download two .csv files from Canvas called Diversity-Data.csv and Metadata.csv, and read them into R using relative file paths.

```
DiversityData <- read.csv("DiversityData.csv")  
str(DiversityData)
```

```
## 'data.frame':   70 obs. of  5 variables:
```

```
## $ Code      : chr  "S01_13" "S02_16" "S03_19" "S04_22" ...
```

```
## $ shannon    : num  6.62 6.61 6.66 6.66 6.61 ...
```

```
## $ invsimpson : num  211 207 213 205 200 ...
```

```
## $ simpson    : num  0.995 0.995 0.995 0.995 0.995 ...
```

```
## $ richness   : int  3319 3079 3935 3922 3196 3481 3250 3170 3657 3177 ...
```

```
Metadata <- read.csv("Metadata.csv")
```

```
str(Metadata)
```

```
## 'data.frame': 70 obs. of 5 variables:
## $ Code : chr "S01_13" "S02_16" "S03_19" "S04_22" ...
## $ Crop : chr "Soil" "Soil" "Soil" "Soil" ...
## $ Time_Point : int 0 0 0 0 0 6 6 6 6 ...
## $ Replicate : int 1 2 3 4 5 6 1 2 3 4 ...
## $ Water_Imbibed: chr "na" "na" "na" "na" ...
```

2. 4 pts. Join the two dataframes together by the common column 'Code'. Name the resulting dataframe alpha.

```
alpha <- left_join(Metadata, DiversityData, by = "Code")
```

3. 4 pts. Calculate Pielou's evenness index: Pielou's evenness is an ecological parameter calculated by the Shannon diversity index (column Shannon) divided by the log of the richness column.

#a. Using mutate, create a new column to calculate Pielou's evenness index. #b. Name the resulting dataframe alpha_even.

```
# Creating a new column
alpha_even <- mutate(alpha, Pielou_evenness = shannon / log(richness))
```

4 4. Pts. Using tidyverse language of functions and the pipe, use the summarise function and tell me the mean and standard error evenness grouped by crop over time.

#a. Start with the alpha_even dataframe #b. Group the data: group the data by Crop and Time_Point. #c. Summarize the data: Calculate the mean, count, standard deviation, and standard error for the even variable within each group. #d. Name the resulting dataframe alpha_average

```
#summary statistics
```

```
alpha_average <- alpha_even %>%
  group_by(Crop, Time_Point) %>%
  summarise(mean_even = mean(Pielou_evenness), # calculating the mean richness, stdeviation, and stand
            n = n(),
            sd.dev = sd(Pielou_evenness)) %>%
  mutate(std.err = sd.dev/sqrt(n))
```

```
## 'summarise()' has grouped output by 'Crop'. You can override using the
## '.groups' argument.
```

5. 4. Pts. Calculate the difference between the soybean column, the soil column, and the difference between the cotton column and the soil column

#a. Start with the `alpha_average` dataframe #b. Select relevant columns: select the columns `Time_Point`, `Crop`, and `mean.even`. #c. Reshape the data: Use the `pivot_wider` function to transform the data from long to wide format, creating new columns for each `Crop` with values from `mean.even`. #d. Calculate differences: Create new columns named `diff.cotton.even` and `diff.soybean.even` by calculating the difference between `Soil` and `Cotton`, and `Soil` and `Soybean`, respectively. #e. Name the resulting dataframe `alpha_average2`

```
alpha_average2 <- alpha_average %>%
  select(Time_Point, Crop, mean.even) %>%
  pivot_wider(names_from = Crop, values_from = mean.even) %>%
  mutate(diff.cotton.even = Soil - Cotton) %>%
  mutate(diff.soybean.even = Soil - Soybean)
```

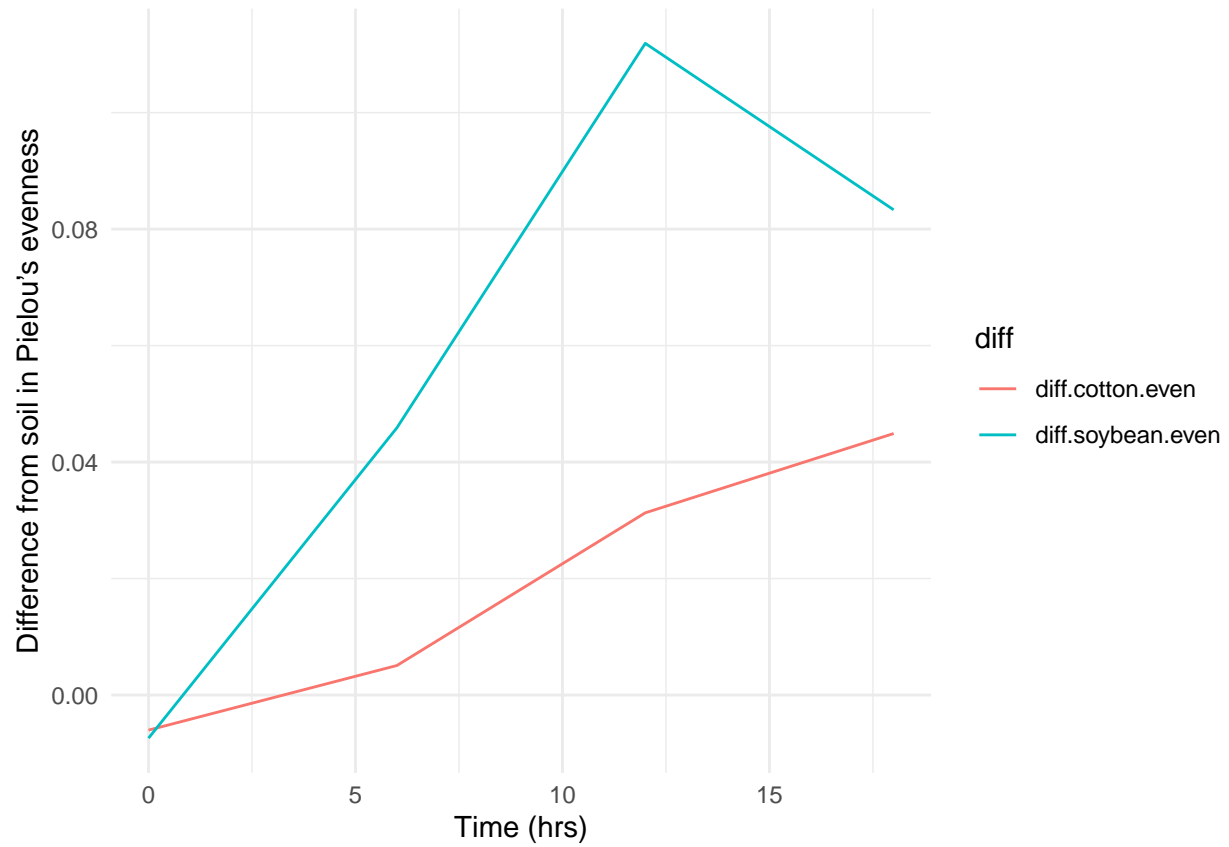
6. 4 pts. Connecting it to plots

#a. Start with the `alpha_average2` dataframe #b. Select relevant columns: select the columns `Time_Point`, `diff.cotton.even`, and `diff.soybean.even`. #c. Reshape the data: Use the `pivot_longer` function to transform the data from wide to long format, creating a new column named `diff` that contains the values from `diff.cotton.even` and `diff.soybean.even`. #i. This might be challenging, so I'll give you a break. The code is below.

```
#pivot_longer(c(diff.cotton.even, diff.soybean.even), names_to = "diff")
```

#d. Create the plot: Use `ggplot` and `geom_line()` with '`Time_Point`' on the x-axis, the column '`values`' on the y-axis, and different colors for each '`diff`' category. The column named '`values`' come from the `pivot_longer`. The resulting plot should look like the one to the right.

```
alpha_average2 %>%
  select(Time_Point, diff.cotton.even, diff.soybean.even) %>%
  pivot_longer(c(diff.cotton.even, diff.soybean.even), names_to = "diff") %>%
  ggplot(aes(x = Time_Point, y = value, color=diff)) + # Plot it
  geom_line() +
  theme_minimal() +
  xlab("Time (hrs)") +
  ylab("Difference from soil in Pielou's evenness")
```



Below is the clickable link to manuscript where these data are published

[Coding_challenge_5 Folder](#)