2025_3_27_DataWrangling_CodeChallenge5_mer0127

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Contents

Question 1

Download two .csv files from Canvas called DiversityData.csv and Metadata.csv, and read them into R using relative file paths.

```
library(tidyverse)
```

```
## -- 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     1.0.2
## -- 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
```

```
diversitydata <-read.csv("DiversityData.csv", na.strings= "na")
metadata <- read.csv("Metadata.csv", na.strings= "na")
```

Question 2

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

```
alpha <-left_join(diversitydata, metadata, by= "Code")
head(alpha)
```

```
##     Code  shannon invsimpson   simpson richness Crop Time_Point Replicate
## 1 S01_13 6.624921   210.7279 0.9952545     3319 Soil          0         1
## 2 S02_16 6.612413   206.8666 0.9951660     3079 Soil          0         2
## 3 S03_19 6.660853   213.0184 0.9953056     3935 Soil          0         3
## 4 S04_22 6.660671   204.6908 0.9951146     3922 Soil          0         4
## 5 S05_25 6.610965   200.2552 0.9950064     3196 Soil          0         5
## 6 S06_28 6.650812   199.3211 0.9949830     3481 Soil          0         6
##   Water_Imbibed
## 1            NA
## 2            NA
## 3            NA
## 4            NA
## 5            NA
## 6            NA
```

Question 3

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.

```
alpha_even<-alpha%>%
 mutate(even=shannon/log(richness))

head(alpha_even)
```

```
##     Code  shannon invsimpson   simpson richness Crop Time_Point Replicate
## 1 S01_13 6.624921   210.7279 0.9952545     3319 Soil          0         1
## 2 S02_16 6.612413   206.8666 0.9951660     3079 Soil          0         2
## 3 S03_19 6.660853   213.0184 0.9953056     3935 Soil          0         3
## 4 S04_22 6.660671   204.6908 0.9951146     3922 Soil          0         4
## 5 S05_25 6.610965   200.2552 0.9950064     3196 Soil          0         5
## 6 S06_28 6.650812   199.3211 0.9949830     3481 Soil          0         6
##   Water_Imbibed      even
## 1            NA 0.8171431
## 2            NA 0.8232216
## 3            NA 0.8046776
## 4            NA 0.8049774
## 5            NA 0.8192376
## 6            NA 0.8155427
```

Question 4

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

```
alpha_average<- alpha_even%>%
  group_by(Crop, Time_Point)%>%  #grouping data by Crop and Time_Point
  summarise(mean.even=mean(even),
    n=n(),  #Count
    std.dev=sd(even), #Standard Deviation
    std.err = (std.dev/sqrt(n)),  #Standard Error
    .groups = 'drop'  # This will drop the grouping after, added due to warning
    )

head(alpha_average)
```

```
## # A tibble: 6 x 6
##   Crop   Time_Point mean.even     n std.dev std.err
##   <chr>       <int>     <dbl> <int>   <dbl>   <dbl>
## 1 Cotton          0     0.820     6 0.00556 0.00227
## 2 Cotton          6     0.805     6 0.00920 0.00376
## 3 Cotton         12     0.767     6 0.0157  0.00640
## 4 Cotton         18     0.755     5 0.0169  0.00755
## 5 Soil            0     0.814     6 0.00765 0.00312
## 6 Soil            6     0.810     6 0.00587 0.00240
```

Question 5

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)
head(alpha_average2)
```

```
## # A tibble: 4 x 6
##   Time_Point Cotton  Soil Soybean diff.cotton.even diff.soybean.even
##        <int>  <dbl> <dbl>   <dbl>            <dbl>             <dbl>
## 1          0  0.820 0.814   0.822         -0.00602          -0.00740
```

```
## 2          6  0.805 0.810   0.764          0.00507          0.0459
## 3         12  0.767 0.798   0.687          0.0313           0.112
## 4         18  0.755 0.800   0.716          0.0449           0.0833
```

Question 6

Connecting it to plots.

a. Start with the alpha_average2 dataframe

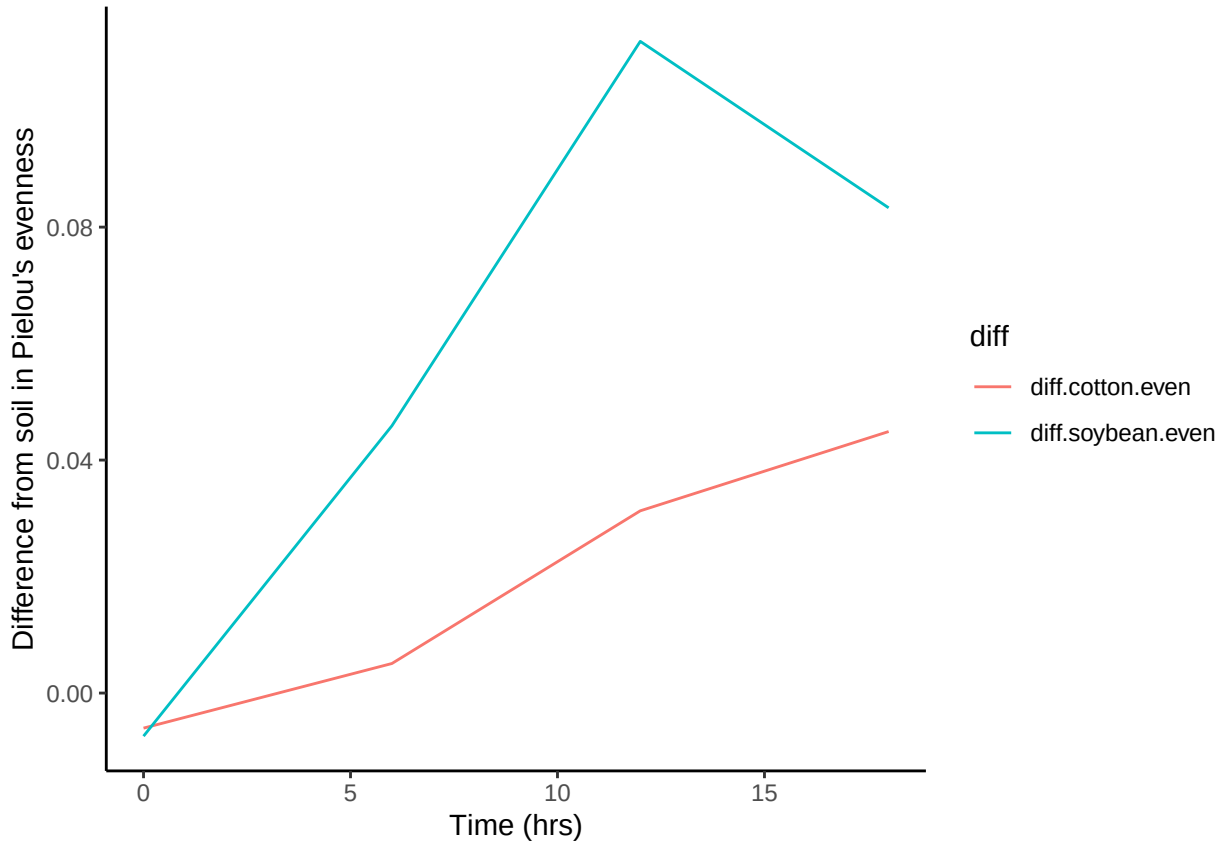
b. Select relevant columns: select the columns Time_Point, diff.cotton.even, and diff.soybean.even

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. Code given.

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 name '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)%>%  #grouping data
  pivot_longer(c(diff.cotton.even, diff.soybean.even), #reshaping data
               names_to = "diff")%>%
  ggplot( aes(x = Time_Point, y = value, color = diff, group = diff))+
  geom_line()+    #creating plot to express the data
  xlab("Time (hrs)")+
  ylab ("Difference from soil in Pielou's evenness")+
  theme_classic()
```



Question 7

Commit and push a gfm .md file to GitHub inside a directory called Coding Challenge 5. Provide me a link to your github written as a clickable link in your .pdf or .docx

Coding Challenge Five