CodingChallenge5

Kylie Blake

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Contents

Question 1

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

```
#Loading in necessary packages
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
```

```
library(ggplot2)

#Loading in DiversityData and Metadata
Metadata <- read.csv("CodingChallenge5//Metadata.csv", na.strings = "na")
DiversityData <-  read.csv("CodingChallenge5//DiversityData.csv")
```

Question 2

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

```
#Combining the two datasets by column "Code"
alpha <- left_join(Metadata,DiversityData, by = "Code")
head(alpha) #viewing first few rows of dataframe
```

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

Question 3

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 Pielous's evenness index column, named PEI
alpha_even <- mutate(alpha, PEI = shannon/log(richness))
head(alpha_even) #viewing first few rows of dataframe
```

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

Question 4

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.

```r
#caluculate summary statistics for evenness grouped by crop over time
alpha_average <-  alpha_even %>%
  group_by(Crop, Time_Point) %>% #viewing data grouped by crop and time_point
  summarise(mean.even = mean(PEI), #calculate mean evenness
            count = n(), #count number of values by crop over time
            sd.even = sd(PEI), #calculate std dev evenness
            se.even = sd.even/sqrt(count)) #calculate std error evenness
```

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

```r
head(alpha_average) #view some of the resulting alpha_average dataframe
```

```
## # A tibble: 6 x 6
## # Groups:   Crop [2]
##   Crop   Time_Point mean.even count sd.even se.even
##   <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

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

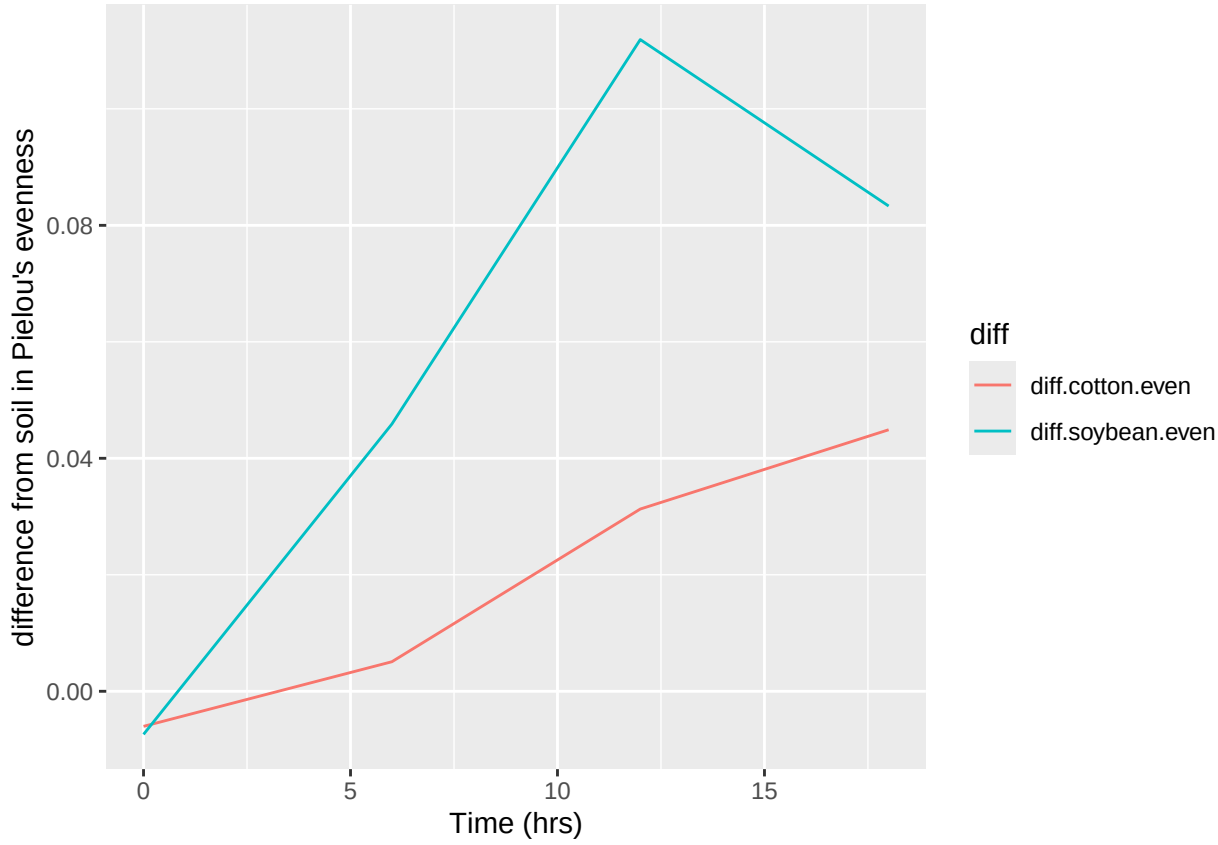
```r
alpha_average2 <- alpha_average %>%
  select(Time_Point, Crop, mean.even) %>% #only select the three columns (Time_Point, Crop, mean.even)
  pivot_wider(names_from = Crop, values_from = mean.even) %>%  #put multiple observations in one row fo
  mutate(diff.cotton.even = Soil - Cotton,
         diff.soybean.even = Soil - Soybean) #create new columns
head(alpha_average2) #view some of the resulting alpha_average2 dataframe
```

```
## # 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

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. 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) %>%#selecting only relevant columns
  pivot_longer(c(diff.cotton.even, diff.soybean.even), names_to = "diff") %>% #putting data in long for
  ggplot(aes(x = Time_Point, y = value, color = diff)) + # adding in a ggplot
  geom_line() + #make line bar
  xlab("Time (hrs)") + #label x-axis
  ylab("difference from soil in Pielou's evenness") #label y-axis
```



Question 7

7. 2 pts. 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

Click here to my GitHub