Data wrangling

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Contents

```
install.packages('tinytex')
tinytex::install_tinytex()
```

```
library(tidyverse)
```

```
## Warning: package 'ggplot2' was built under R version 4.3.2
```

```
## Warning: package 'tidyr' was built under R version 4.3.2
```

```
## -- 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 1.9.3     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
```

```
microbiome.fungi <- read.csv("Data_Folder/Bull_richness.csv")
str(microbiome.fungi)
```

```
## 'data.frame':    287 obs. of  16 variables:
##  $ SampleID       : chr  "Corn2017LeafObjective2Collection1T1R1CAH2" "Corn2017LeafObjective2Collecti
##  $ Crop           : chr  "Corn" "Corn" "Corn" "Corn" ...
##  $ Objective      : chr  "Objective 2" "Objective 2" "Objective 2" "Objective 2" ...
##  $ Collection     : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ Compartment    : chr  "Leaf" "Leaf" "Leaf" "Leaf" ...
##  $ DateSampled    : chr  "6/26/17" "6/26/17" "6/26/17" "6/26/17" ...
##  $ GrowthStage    : chr  "V6" "V6" "V6" "V6" ...
##  $ Treatment      : chr  "Conv." "Conv." "Conv." "Conv." ...
##  $ Rep            : chr  "R1" "R1" "R1" "R1" ...
##  $ Sample         : chr  "A" "B" "C" "A" ...
##  $ Fungicide      : chr  "C" "C" "C" "F" ...
##  $ Target_organism: chr  "Fungi" "Fungi" "Fungi" "Fungi" ...
##  $ Location       : chr  "Kellogg Biological Station" "Kellogg Biological Station" "Kellogg Biologica
##  $ Experiment     : chr  "LTER" "LTER" "LTER" "LTER" ...
##  $ Year           : int  2017 2017 2017 2017 2017 2017 2017 2017 2017 2017 ...
##  $ richness       : int  9 6 5 7 4 2 3 8 4 4 ...
```

Data Exploration

Select Function select() to select the column you are interested in your data.

```
microbiome.fungi2 <- select(microbiome.fungi, SampleID, Crop, Compartment:Fungicide, richness)
```

Subsetting/filtering data (i.e., selecting certain rows)

using filter function filter()

```
head(filter(microbiome.fungi2, Treatment == "Conv."))
```

```
##                                     SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf     6/26/17
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf     6/26/17
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf     6/26/17
## 4 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf     6/26/17
## 5 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf     6/26/17
## 6 Corn2017LeafObjective2Collection1T1R1FCE3 Corn        Leaf     6/26/17
##   GrowthStage Treatment Rep Sample Fungicide richness
## 1          V6     Conv.  R1      A         C        9
## 2          V6     Conv.  R1      B         C        6
## 3          V6     Conv.  R1      C         C        5
## 4          V6     Conv.  R1      A         F        7
## 5          V6     Conv.  R1      B         F        4
## 6          V6     Conv.  R1      C         F        2
```

```
# A more complex using &
head(filter(microbiome.fungi2, Treatment == "Conv." & Fungicide == "C")) # & means addition of that dat
```

```
##                                     SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf     6/26/17
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf     6/26/17
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf     6/26/17
## 4 Corn2017LeafObjective2Collection1T1R2CAF3 Corn        Leaf     6/26/17
## 5 Corn2017LeafObjective2Collection1T1R2CBG3 Corn        Leaf     6/26/17
## 6 Corn2017LeafObjective2Collection1T1R2CCH3 Corn        Leaf     6/26/17
##   GrowthStage Treatment Rep Sample Fungicide richness
## 1          V6     Conv.  R1      A         C        9
## 2          V6     Conv.  R1      B         C        6
## 3          V6     Conv.  R1      C         C        5
## 4          V6     Conv.  R2      A         C        3
## 5          V6     Conv.  R2      B         C        8
## 6          V6     Conv.  R2      C         C        4
```

```
head(filter(microbiome.fungi2, Sample == "A" | Sample == "B")) # means | sample A or sample B
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf     6/26/17
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf     6/26/17
## 3 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf     6/26/17
## 4 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf     6/26/17
## 5 Corn2017LeafObjective2Collection1T1R2CAF3 Corn        Leaf     6/26/17
## 6 Corn2017LeafObjective2Collection1T1R2CBG3 Corn        Leaf     6/26/17
##   GrowthStage Treatment Rep Sample Fungicide richness
## 1          V6     Conv.  R1      A         C        9
## 2          V6     Conv.  R1      B         C        6
## 3          V6     Conv.  R1      A         F        7
## 4          V6     Conv.  R1      B         F        4
## 5          V6     Conv.  R2      A         C        3
## 6          V6     Conv.  R2      B         C        8
```

Creating a new colum

using mutate function mutate()

```
# Create a new column called logRich
head(mutate(microbiome.fungi2, logRich = log(richness))) # create new column named logRich that has the
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf     6/26/17
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf     6/26/17
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf     6/26/17
## 4 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf     6/26/17
## 5 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf     6/26/17
## 6 Corn2017LeafObjective2Collection1T1R1FCE3 Corn        Leaf     6/26/17
##   GrowthStage Treatment Rep Sample Fungicide richness   logRich
## 1          V6     Conv.  R1      A         C        9 2.1972246
## 2          V6     Conv.  R1      B         C        6 1.7917595
## 3          V6     Conv.  R1      C         C        5 1.6094379
## 4          V6     Conv.  R1      A         F        7 1.9459101
## 5          V6     Conv.  R1      B         F        4 1.3862944
## 6          V6     Conv.  R1      C         F        2 0.6931472
```

```
# Creating a new column which combines Crop and Treatment
head(mutate(microbiome.fungi2, Crop_Treatment = paste(Crop, Treatment)))
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf     6/26/17
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf     6/26/17
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf     6/26/17
## 4 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf     6/26/17
## 5 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf     6/26/17
## 6 Corn2017LeafObjective2Collection1T1R1FCE3 Corn        Leaf     6/26/17
##   GrowthStage Treatment Rep Sample Fungicide richness Crop_Treatment
## 1          V6     Conv.  R1      A         C        9     Corn Conv.
## 2          V6     Conv.  R1      B         C        6     Corn Conv.
## 3          V6     Conv.  R1      C         C        5     Corn Conv.
## 4          V6     Conv.  R1      A         F        7     Corn Conv.
## 5          V6     Conv.  R1      B         F        4     Corn Conv.
## 6          V6     Conv.  R1      C         F        2     Corn Conv.
```

Using The pipe %>% function

it combine output of one function into input of another function,by connecting them with

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>% # selecting columns
  filter(Treatment == "Conv.") %>% # subsetting to only include the conventional treatment
  mutate(logRich = log(richness)) %>% # creating a new column of the log richness
  head() # displaying the first six rows
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf     6/26/17
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf     6/26/17
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf     6/26/17
## 4 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf     6/26/17
## 5 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf     6/26/17
## 6 Corn2017LeafObjective2Collection1T1R1FCE3 Corn        Leaf     6/26/17
##   GrowthStage Treatment Rep Sample Fungicide richness   logRich
## 1          V6     Conv.  R1      A         C        9 2.1972246
## 2          V6     Conv.  R1      B         C        6 1.7917595
## 3          V6     Conv.  R1      C         C        5 1.6094379
## 4          V6     Conv.  R1      A         F        7 1.9459101
## 5          V6     Conv.  R1      B         F        4 1.3862944
## 6          V6     Conv.  R1      C         F        2 0.6931472
```

summarising data using summarise() function

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>% # selecting columns
  filter(Treatment == "Conv.") %>% # subsetting to only include the conventional treatment
  mutate(logRich = log(richness)) %>% # creating a new column of the log richness
  summarise(Mean.rich = mean(logRich)) # calculating overall mean log richness within the conventionally
```

```
##   Mean.rich
## 1  2.304395
```

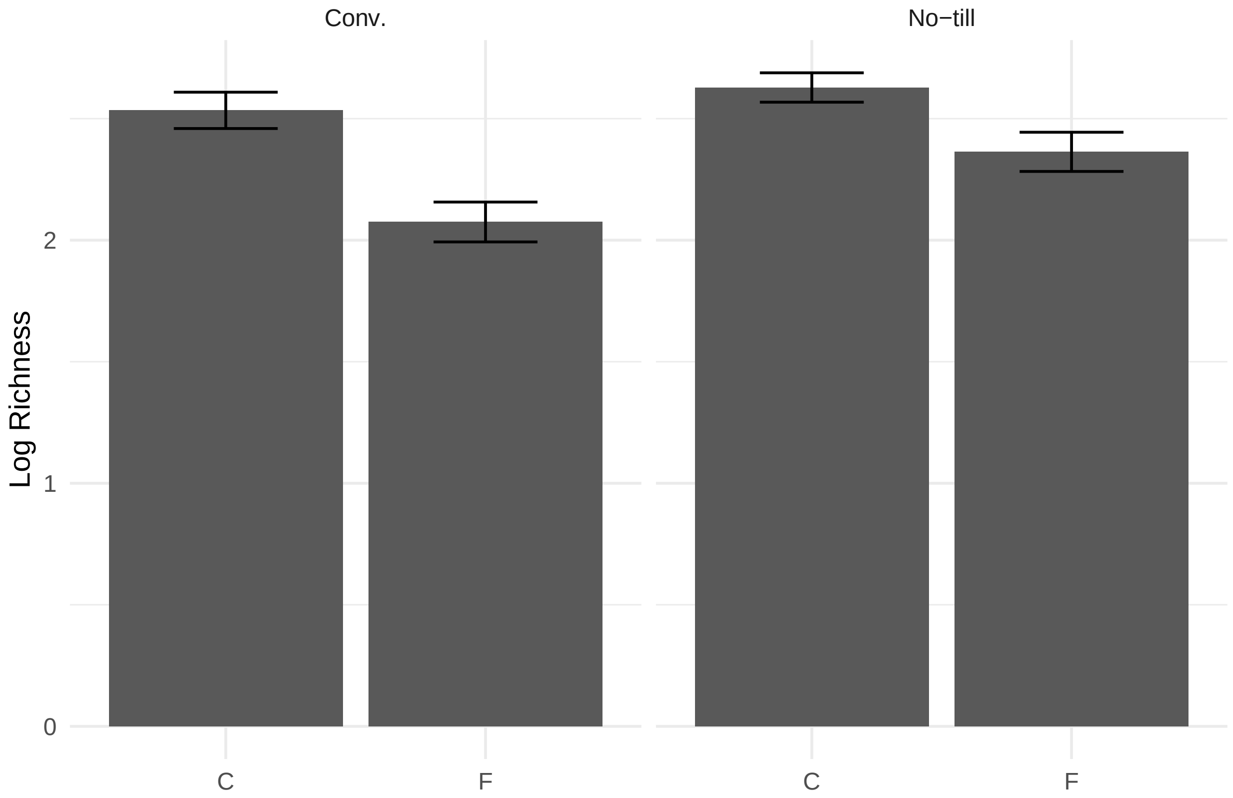
```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>% # selecting columns
  filter(Treatment == "Conv.") %>% # subsetting to only include the conventional treatment
  mutate(logRich = log(richness)) %>% # creating a new column of the log richness
  summarise(Mean.rich = mean(logRich), # calculating the mean richness, stdeviation, and standard error
            n = n(),
            sd.dev = sd(logRich)) %>%
  mutate(std.err = sd.dev/sqrt(n))
```

```
##   Mean.rich   n    sd.dev   std.err
## 1  2.304395 144 0.7024667 0.0585389
```

connnecting to plotting

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>% # selecting columns
  group_by(Treatment, Fungicide) %>% # grouping by treatment and fungicide to later calculate summary s
  mutate(logRich = log(richness)) %>% # creating a new column of the log richness
  summarise(Mean.rich = mean(logRich), # calculating the mean richness, stdeviation, and standard error
            n = n(),
            sd.dev = sd(logRich)) %>%
  mutate(std.err = sd.dev/sqrt(n)) %>%
  ggplot(aes(x = Fungicide, y = Mean.rich)) + # adding in a ggplot
  geom_bar(stat="identity") +
  geom_errorbar( aes(x=Fungicide, ymin=Mean.rich-std.err, ymax=Mean.rich+std.err), width=0.4) +
  theme_minimal() +
  xlab("") +
  ylab("Log Richness") +
  facet_wrap(~Treatment)
```

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



### using Joining function

```r
# selecting just the richness and sample ID
richness <- microbiome.fungi %>%
  select(SampleID, richness)

# selecting columns that don't include the richness
metadata <- microbiome.fungi %>%
  select(SampleID, Fungicide, Crop, Compartment, GrowthStage, Treatment, Rep, Sample)

head(metadata)
```

```
##                                    SampleID Fungicide Crop Compartment
## 1 Corn2017LeafObjective2Collection1T1R1CAH2         C Corn        Leaf
## 2 Corn2017LeafObjective2Collection1T1R1CBA3         C Corn        Leaf
## 3 Corn2017LeafObjective2Collection1T1R1CCB3         C Corn        Leaf
## 4 Corn2017LeafObjective2Collection1T1R1FAC3         F Corn        Leaf
## 5 Corn2017LeafObjective2Collection1T1R1FBD3         F Corn        Leaf
## 6 Corn2017LeafObjective2Collection1T1R1FCE3         F Corn        Leaf
##   GrowthStage Treatment Rep Sample
## 1          V6     Conv.  R1      A
## 2          V6     Conv.  R1      B
## 3          V6     Conv.  R1      C
## 4          V6     Conv.  R1      A
## 5          V6     Conv.  R1      B
## 6          V6     Conv.  R1      C
```

```r
head(richness)
```

```
##                                    SampleID richness
## 1 Corn2017LeafObjective2Collection1T1R1CAH2        9
## 2 Corn2017LeafObjective2Collection1T1R1CBA3        6
## 3 Corn2017LeafObjective2Collection1T1R1CCB3        5
## 4 Corn2017LeafObjective2Collection1T1R1FAC3        7
## 5 Corn2017LeafObjective2Collection1T1R1FBD3        4
## 6 Corn2017LeafObjective2Collection1T1R1FCE3        2
```

```r
head(left_join(metadata, richness, by = "SampleID")) # adding the richness data to the metadata based o
```

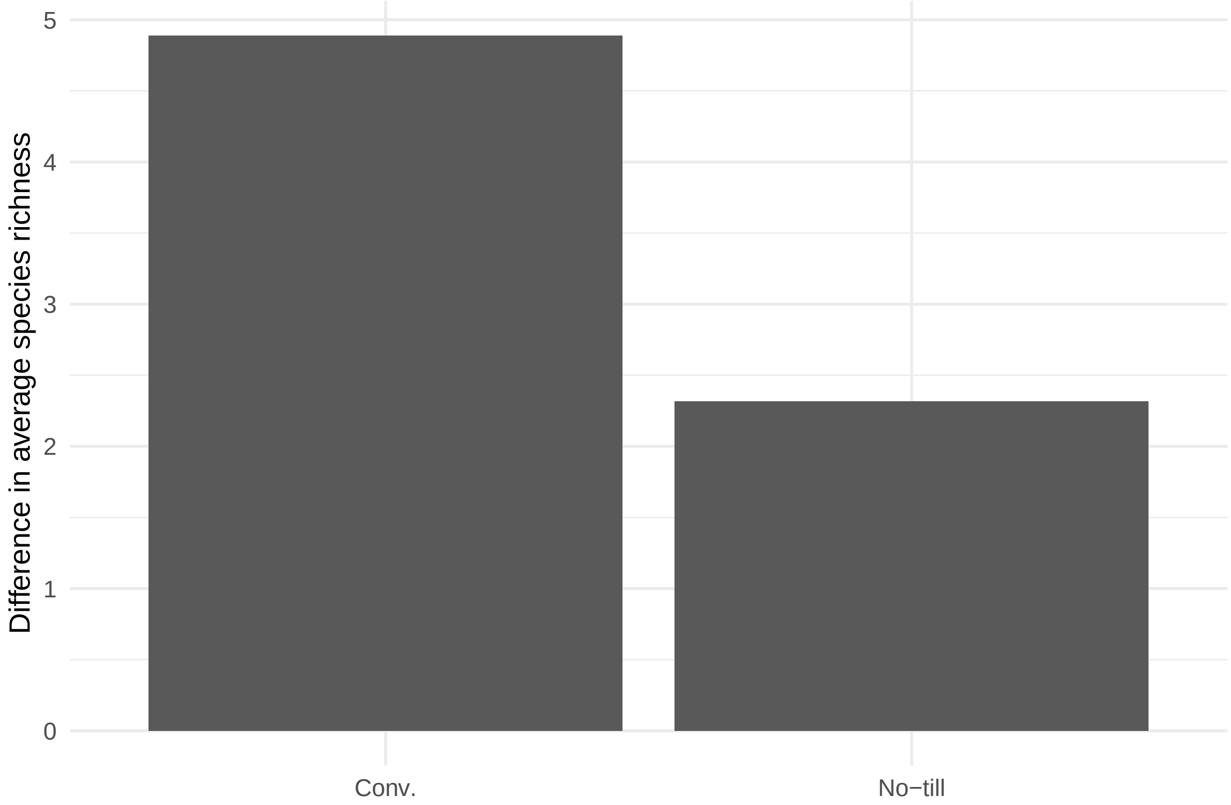
```
##                                    SampleID Fungicide Crop Compartment
## 1 Corn2017LeafObjective2Collection1T1R1CAH2         C Corn        Leaf
## 2 Corn2017LeafObjective2Collection1T1R1CBA3         C Corn        Leaf
## 3 Corn2017LeafObjective2Collection1T1R1CCB3         C Corn        Leaf
## 4 Corn2017LeafObjective2Collection1T1R1FAC3         F Corn        Leaf
## 5 Corn2017LeafObjective2Collection1T1R1FBD3         F Corn        Leaf
## 6 Corn2017LeafObjective2Collection1T1R1FCE3         F Corn        Leaf
##   GrowthStage Treatment Rep Sample richness
## 1          V6     Conv.  R1      A        9
## 2          V6     Conv.  R1      B        6
## 3          V6     Conv.  R1      C        5
## 4          V6     Conv.  R1      A        7
## 5          V6     Conv.  R1      B        4
## 6          V6     Conv.  R1      C        2
```

Pivoting using pivot_longer() and pivot_wider() Function

for pivot_wider()

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>% # selecting columns  filter(Class == "Sor
  group_by(Treatment, Fungicide) %>% # grouping by treatment and fungicide to later calculate summary s
  summarise(Mean = mean(richness)) %>% # calculates the mean per Treatment and Fungicide
pivot_wider(names_from = Fungicide, values_from = Mean) %>% # pivot to wide format
  mutate(diff.fungicide = C - F) %>%  # calculate the difference between the means.
  ggplot(aes(x = Treatment, y = diff.fungicide)) + # Plot it
  geom_col() +
  theme_minimal() +
  xlab("") +
  ylab("Difference in average species richness")
```

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


Difference in average species richness
Conv.
No−till