Data Wrangling

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Contents

```r
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 error
```

```r
microbiome.fungi <- read.csv("CodingChallenges\\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  "6/26/2017" "6/26/2017" "6/26/2017" "6/26/2017" ...
##  $ 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 ...
```

1. Select function #### "select()"

- You can use this function to select only certain columns of your data

```
microbiome.fungi2 <- select(microbiome.fungi,SampleID,Crop, Compartment:Fungicide, richness)
#colon in btw comp and fungicide, can use this if have number of columns in order to select the columns
```

2. Filter function #### “filter()”

- To filter out data by specific variables

```
#essentially does same thing a filter

head(filter(microbiome.fungi2,Treatment == "Conv.")) #filter this by where treatment is equal to conven
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf   6/26/2017
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf   6/26/2017
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf   6/26/2017
## 4 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf   6/26/2017
## 5 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf   6/26/2017
## 6 Corn2017LeafObjective2Collection1T1R1FCE3 Corn        Leaf   6/26/2017
##   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")) #filtering by two conditions
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf   6/26/2017
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf   6/26/2017
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf   6/26/2017
## 4 Corn2017LeafObjective2Collection1T1R2CAF3 Corn        Leaf   6/26/2017
## 5 Corn2017LeafObjective2Collection1T1R2CBG3 Corn        Leaf   6/26/2017
## 6 Corn2017LeafObjective2Collection1T1R2CCH3 Corn        Leaf   6/26/2017
##   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
```

```
#Another more complex example using or |
head(filter(microbiome.fungi2, Sample == "A" | Sample == "B")) #samples A or B
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf   6/26/2017
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf   6/26/2017
## 3 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf   6/26/2017
## 4 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf   6/26/2017
## 5 Corn2017LeafObjective2Collection1T1R2CAF3 Corn        Leaf   6/26/2017
## 6 Corn2017LeafObjective2Collection1T1R2CBG3 Corn        Leaf   6/26/2017
##   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
```

3. Mutate function #### “mutate()”

- Allows us to quickly create new columns

```
microbiome.fungi2$logRich <- log(microbiome.fungi2$richness)  #is the same as:

#Create a new column called logRich
head(mutate(microbiome.fungi2, logRich = log(richness))) #format (dataset, name of column = function)
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf   6/26/2017
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf   6/26/2017
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf   6/26/2017
## 4 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf   6/26/2017
## 5 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf   6/26/2017
## 6 Corn2017LeafObjective2Collection1T1R1FCE3 Corn        Leaf   6/26/2017
##   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   6/26/2017
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf   6/26/2017
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf   6/26/2017
## 4 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf   6/26/2017
## 5 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf   6/26/2017
## 6 Corn2017LeafObjective2Collection1T1R1FCE3 Corn        Leaf   6/26/2017
##   GrowthStage Treatment Rep Sample Fungicide richness   logRich Crop_Treatment
## 1          V6     Conv.  R1      A         C        9 2.1972246     Corn Conv.
## 2          V6     Conv.  R1      B         C        6 1.7917595     Corn Conv.
## 3          V6     Conv.  R1      C         C        5 1.6094379     Corn Conv.
## 4          V6     Conv.  R1      A         F        7 1.9459101     Corn Conv.
## 5          V6     Conv.  R1      B         F        4 1.3862944     Corn Conv.
## 6          V6     Conv.  R1      C         F        2 0.6931472     Corn Conv.
```

4. The pipe #### “%>%” The pipe allows you to string multiple commands together, and helps to visualize what you are doing to your data step by step.

- Allows you to input previous data from the right side of the pope into the function on the left (or next line)

```
#take orig dataset then the pipe: (do not need to define dataset in each command)
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() #display the first six rows
```

```
##                                    SampleID Crop Compartment DateSampled
## 1 Corn2017LeafObjective2Collection1T1R1CAH2 Corn        Leaf   6/26/2017
## 2 Corn2017LeafObjective2Collection1T1R1CBA3 Corn        Leaf   6/26/2017
## 3 Corn2017LeafObjective2Collection1T1R1CCB3 Corn        Leaf   6/26/2017
## 4 Corn2017LeafObjective2Collection1T1R1FAC3 Corn        Leaf   6/26/2017
## 5 Corn2017LeafObjective2Collection1T1R1FBD3 Corn        Leaf   6/26/2017
## 6 Corn2017LeafObjective2Collection1T1R1FCE3 Corn        Leaf   6/26/2017
##   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
```

5. Summarise #### “summarise()” We can use this function to calculate mean, std dev and errors

```
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 withing the conventionally
```

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

```
#This will only give one calculation, which is the average log(richness)

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 withing the conventionally
            n=n(), #calculates the number of rows, give column name of n
            sd.dev = sd(logRich)) %>% #give column name sd.dev, calculate std.dev
  mutate(std.err = sd.dev/sqrt(n)) #mutate function to calculate std error
```

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

6. Group-by #### “group_by()” Allows us to group data by a certain way

```r
#CALUCLATE MEANS AND STD DEV FOR EACH TREATMENT AND FUNGICIDE
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))
```

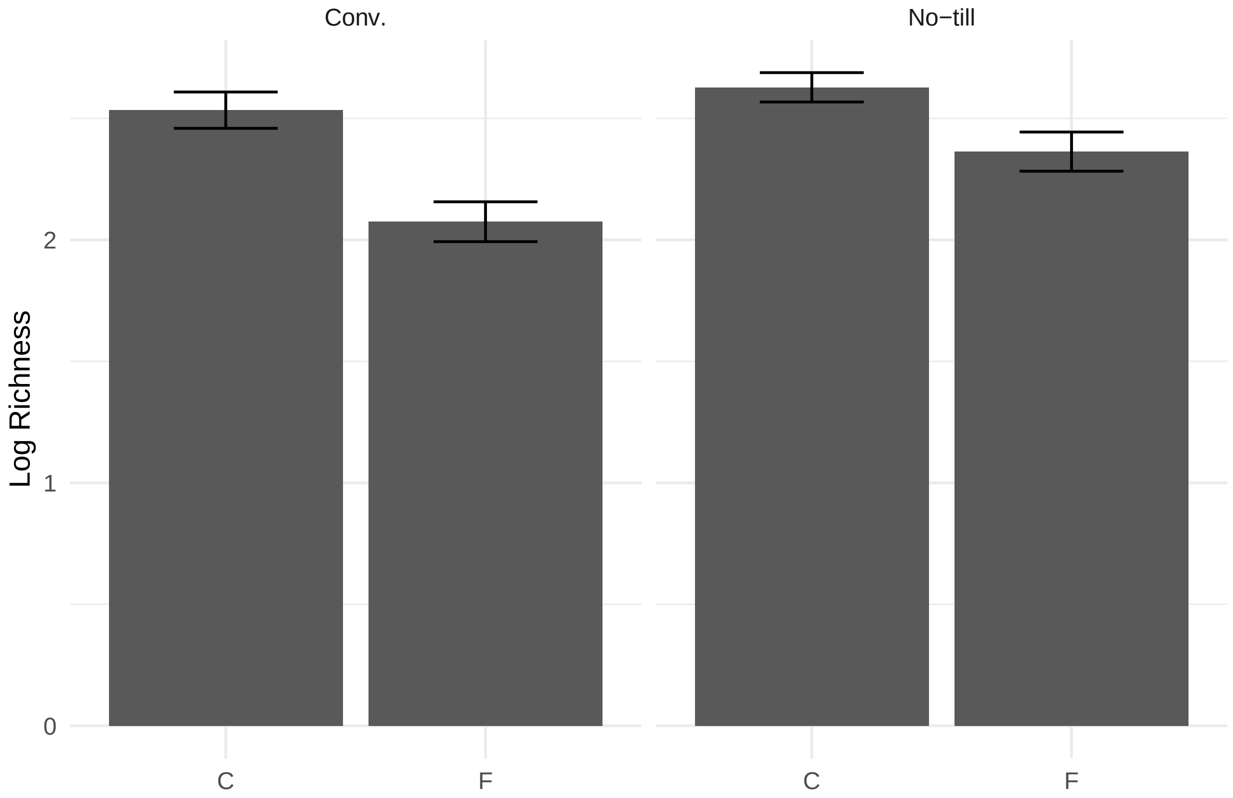
```
## ‘summarise()‘ has grouped output by ’Treatment’. You can override using the
## ‘.groups‘ argument.
```

```
## # A tibble: 4 x 6
## # Groups:   Treatment [2]
##   Treatment Fungicide Mean.rich     n sd.dev std.err
##   <chr>     <chr>         <dbl> <int>  <dbl>   <dbl>
## 1 Conv.     C              2.53    72  0.635  0.0748
## 2 Conv.     F              2.07    72  0.696  0.0820
## 3 No-till   C              2.63    72  0.513  0.0604
## 4 No-till   F              2.36    71  0.680  0.0807
```

Connnecting to plot We can use pipes directly in a ggplot!

```r
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)) %>%
  #Adding in ggplot - Do not need to specify the data set since you specified at the top
  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.
```



#### Joining Functions that allow you to combine multiple datasets based on a common set of variables - left_join() - keep all rows of X and add matching rows from Y. Any rows in Y that don't match X are excluded -right_join() -reverse of left_join() - inner_join() -only keep rows that are common to both X and Y, remove everything else -full_join() - keep any columns that are in either X or Y

```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
```

```
head(richness)
```

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

```
#Can join these two dataframes by common column == SampleID

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

```
##                                     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 long data -> one observation per sample or per row wide data -> multiple observations per row *wide-data is not wrong per say, but in general we want long-data

```
#Set up data frame
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
```

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

```
## # A tibble: 4 x 3
## # Groups:   Treatment [2]
##   Treatment Fungicide  Mean
##   <chr>     <chr>     <dbl>
## 1 Conv.     C         14.6
## 2 Conv.     F          9.75
## 3 No-till   C         15.4
## 4 No-till   F         13.1
```

```
#Change from long format (above) to wide format
#Change dataset to this: two columns C anf F column for fungicide -- we want names from fungicide colum
#values input to be taken from mean column
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
```

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

```
## # A tibble: 2 x 3
## # Groups:   Treatment [2]
##   Treatment     C     F
##   <chr>     <dbl> <dbl>
## 1 Conv.      14.6  9.75
## 2 No-till    15.4 13.1
```

Now we can easily take the difference between the fungicide and control

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness ) %>%  #selecting columns
  group_by(Treatment, Fungicide) %>%  #grouping by treatment and fungicide to later calc summary stats
  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 diff btw the means
```

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

```
## # A tibble: 2 x 4
## # Groups:   Treatment [2]
##   Treatment     C     F diff.fungicide
##   <chr>     <dbl> <dbl>          <dbl>
## 1 Conv.      14.6  9.75           4.89
## 2 No-till    15.4 13.1            2.32
```