

# Data Wrangling

Brynleigh Payne

March 19, 2025

Brynleigh Github

## Seemless data wrangling

The tidyverse is a bunch of packages and functions written by the same folks that manage Rstudio. The tidyverse builds upon base R to allow for easier use of large datasets.

If you do not have the tidyverse installed please install it and load it `install.packages("tidyverse")`

```
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  1.9.3      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
```

When you load in the tidyverse notice that it loads in 8 different packages. You will not have to load these individually.

More info and cheet sheets can be found here: <https://tidyr.tidyverse.org/index.html>

Lets demonstrate some of the most useful functionality of some tidyverse functions. **Note** that this tutorial does not cover everything and **self-learning** may be required for specific functionality. We will cover the following:

- Data wrangling & manipulation
  - mutate()
  - select()
  - filter()
  - the pipe %>%
  - summarise()
  - group\_by()
  - joining
  - pivotting
  - Integration with plotting

For this tutorial I will use the same microbiome dataset we used in previous classes for `ggplot`, except this dataset includes all fungi in the Phylum Ascomycota, not just one family.

```
microbiome.fungi <- read.csv("PLPA5820/PLPA5820/07_ggplot/Bull_richness.csv")
str(microbiome.fungi)
```

```
## 'data.frame': 287 obs. of 16 variables:
## $ SampleID : chr "Corn2017LeafObjective2Collection1T1R1CAH2" "Corn2017LeafObjective2Collection1T1R1CAH2" ...
## $ 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 Biological Station" ...
## $ 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 ...
```

Lets start exploring the data.

Sometimes you may want to only select certain columns of your data. This is accomplished with the `select` function..

**`select()`** Note: colon indicates “selecting through”

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

```
## 'data.frame': 287 obs. of 10 variables:
## $ SampleID : chr "Corn2017LeafObjective2Collection1T1R1CAH2" "Corn2017LeafObjective2Collection1T1R1CAH2" ...
## $ Crop : chr "Corn" "Corn" "Corn" "Corn" ...
## $ 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" ...
## $ richness : int 9 6 5 7 4 2 3 8 4 4 ...
```

Note the syntax. I listed all the column headers I wanted, but at the end I used `Compartment:Fungicide` because all these were in order and I can use the column to select them all.

**`filter()`** This is a convenient function that allows you to subset data fairly easily. However, I'm not sure how its much easier than other subset function

```
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"))
```

```
##                               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
```

*# 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      6/26/17
## 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
```

`mutate()` Mutate allows us to quickly create new columns.

```
# Note: Creating a new column in base R
microbiome.fungi2$logRich <- log(microbiome.fungi2$richness)
# Create a new column called logRich
head(mutate(microbiome.fungi2, logRich = log(richness)))
```

```
##                               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  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.
```

**the pipe %>%** We can also combine multiple functions together. This is an important concept and is very powerful. It helps to try to visualize what you are doing to your data at each step. Basically the pipe allows you to input the previous data from the right side of the pipe into the function on the left (or next line).

In

We will combine all previous steps into one large string of functions.

When we do this we do not have to specify the data in each function. The data from the previous step is transferred to the next step.

```
select(microbiome.fungi, SampleID, Crop, Compartment:Fungicide, richness) # before
```

##	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
## 7	Corn2017LeafObjective2Collection1T1R2CAF3	Corn	Leaf	6/26/17
## 8	Corn2017LeafObjective2Collection1T1R2CBG3	Corn	Leaf	6/26/17
## 9	Corn2017LeafObjective2Collection1T1R2CCH3	Corn	Leaf	6/26/17
## 10	Corn2017LeafObjective2Collection1T1R2FAA4	Corn	Leaf	6/26/17
## 11	Corn2017LeafObjective2Collection1T1R2FBB4	Corn	Leaf	6/26/17
## 12	Corn2017LeafObjective2Collection1T1R2FCC4	Corn	Leaf	6/26/17
## 13	Corn2017LeafObjective2Collection1T1R5CAD4	Corn	Leaf	6/26/17
## 14	Corn2017LeafObjective2Collection1T1R5CBE4	Corn	Leaf	6/26/17
## 15	Corn2017LeafObjective2Collection1T1R5CCF4	Corn	Leaf	6/26/17
## 16	Corn2017LeafObjective2Collection1T1R5FAG4	Corn	Leaf	6/26/17
## 17	Corn2017LeafObjective2Collection1T1R5FBH4	Corn	Leaf	6/26/17
## 18	Corn2017LeafObjective2Collection1T1R5FCA5	Corn	Leaf	6/26/17
## 19	Corn2017LeafObjective2Collection1T1R6CAB5	Corn	Leaf	6/26/17
## 20	Corn2017LeafObjective2Collection1T1R6CBC5	Corn	Leaf	6/26/17
## 21	Corn2017LeafObjective2Collection1T1R6CCD5	Corn	Leaf	6/26/17
## 22	Corn2017LeafObjective2Collection1T1R6FAE5	Corn	Leaf	6/26/17
## 23	Corn2017LeafObjective2Collection1T1R6FBF5	Corn	Leaf	6/26/17
## 24	Corn2017LeafObjective2Collection1T1R6FCG5	Corn	Leaf	6/26/17
## 25	Corn2017LeafObjective2Collection1T2R1CAH5	Corn	Leaf	6/26/17
## 26	Corn2017LeafObjective2Collection1T2R1CBA6	Corn	Leaf	6/26/17
## 27	Corn2017LeafObjective2Collection1T2R1CCB6	Corn	Leaf	6/26/17
## 28	Corn2017LeafObjective2Collection1T2R1FAC6	Corn	Leaf	6/26/17
## 29	Corn2017LeafObjective2Collection1T2R1FBE6	Corn	Leaf	6/26/17
## 30	Corn2017LeafObjective2Collection1T2R1FCD6	Corn	Leaf	6/26/17
## 31	Corn2017LeafObjective2Collection1T2R2CAF6	Corn	Leaf	6/26/17
## 32	Corn2017LeafObjective2Collection1T2R2CBG6	Corn	Leaf	6/26/17
## 33	Corn2017LeafObjective2Collection1T2R2CCH6	Corn	Leaf	6/26/17
## 34	Corn2017LeafObjective2Collection1T2R2FAA7	Corn	Leaf	6/26/17
## 35	Corn2017LeafObjective2Collection1T2R2FBB7	Corn	Leaf	6/26/17
## 36	Corn2017LeafObjective2Collection1T2R2FCC7	Corn	Leaf	6/26/17
## 37	Corn2017LeafObjective2Collection1T2R5CAD7	Corn	Leaf	6/26/17
## 38	Corn2017LeafObjective2Collection1T2R5CBE7	Corn	Leaf	6/26/17
## 39	Corn2017LeafObjective2Collection1T2R5CCF7	Corn	Leaf	6/26/17
## 40	Corn2017LeafObjective2Collection1T2R5FAG7	Corn	Leaf	6/26/17
## 41	Corn2017LeafObjective2Collection1T2R5FBH7	Corn	Leaf	6/26/17
## 42	Corn2017LeafObjective2Collection1T2R5FCA8	Corn	Leaf	6/26/17
## 43	Corn2017LeafObjective2Collection1T2R6CAB8	Corn	Leaf	6/26/17
## 44	Corn2017LeafObjective2Collection1T2R6CBC8	Corn	Leaf	6/26/17
## 45	Corn2017LeafObjective2Collection1T2R6CCD8	Corn	Leaf	6/26/17
## 46	Corn2017LeafObjective2Collection1T2R6FAE8	Corn	Leaf	6/26/17
## 47	Corn2017LeafObjective2Collection1T2R6FBF8	Corn	Leaf	6/26/17
## 48	Corn2017LeafObjective2Collection1T2R6FCG8	Corn	Leaf	6/26/17
## 49	Corn2017LeafObjective2Collection2T1R1CAC9	Corn	Leaf	7/5/17
## 50	Corn2017LeafObjective2Collection2T1R1CBD9	Corn	Leaf	7/5/17
## 51	Corn2017LeafObjective2Collection2T1R1CCE9	Corn	Leaf	7/5/17
## 52	Corn2017LeafObjective2Collection2T1R1FAH8	Corn	Leaf	7/5/17
## 53	Corn2017LeafObjective2Collection2T1R1FBA9	Corn	Leaf	7/5/17

## 54	Corn2017LeafObjective2Collection2T1R1FCB9	Corn	Leaf	7/5/17
## 55	Corn2017LeafObjective2Collection2T1R2CAA10	Corn	Leaf	7/5/17
## 56	Corn2017LeafObjective2Collection2T1R2CBC10	Corn	Leaf	7/5/17
## 57	Corn2017LeafObjective2Collection2T1R2CCD10	Corn	Leaf	7/5/17
## 58	Corn2017LeafObjective2Collection2T1R2FAF9	Corn	Leaf	7/5/17
## 59	Corn2017LeafObjective2Collection2T1R2FBG9	Corn	Leaf	7/5/17
## 60	Corn2017LeafObjective2Collection2T1R2FCH9	Corn	Leaf	7/5/17
## 61	Corn2017LeafObjective2Collection2T1R5CAH10	Corn	Leaf	7/5/17
## 62	Corn2017LeafObjective2Collection2T1R5CBA11	Corn	Leaf	7/5/17
## 63	Corn2017LeafObjective2Collection2T1R5CCC11	Corn	Leaf	7/5/17
## 64	Corn2017LeafObjective2Collection2T1R5FAE10	Corn	Leaf	7/5/17
## 65	Corn2017LeafObjective2Collection2T1R5FBF10	Corn	Leaf	7/5/17
## 66	Corn2017LeafObjective2Collection2T1R5FCG10	Corn	Leaf	7/5/17
## 67	Corn2017LeafObjective2Collection2T1R6CAB11	Corn	Leaf	7/5/17
## 68	Corn2017LeafObjective2Collection2T1R6CBG11	Corn	Leaf	7/5/17
## 69	Corn2017LeafObjective2Collection2T1R6CCH11	Corn	Leaf	7/5/17
## 70	Corn2017LeafObjective2Collection2T1R6FAD11	Corn	Leaf	7/5/17
## 71	Corn2017LeafObjective2Collection2T1R6FBE11	Corn	Leaf	7/5/17
## 72	Corn2017LeafObjective2Collection2T1R6FCF11	Corn	Leaf	7/5/17
## 73	Corn2017LeafObjective2Collection2T2R1CAD12	Corn	Leaf	7/5/17
## 74	Corn2017LeafObjective2Collection2T2R1CBE12	Corn	Leaf	7/5/17
## 75	Corn2017LeafObjective2Collection2T2R1CCF12	Corn	Leaf	7/5/17
## 76	Corn2017LeafObjective2Collection2T2R1FAA12	Corn	Leaf	7/5/17
## 77	Corn2017LeafObjective2Collection2T2R1FBB12	Corn	Leaf	7/5/17
## 78	Corn2017LeafObjective2Collection2T2R1FCC12	Corn	Leaf	7/5/17
## 79	Corn2017LeafObjective2Collection2T2R2CAB1	Corn	Leaf	7/5/17
## 80	Corn2017LeafObjective2Collection2T2R2CBC1	Corn	Leaf	7/5/17
## 81	Corn2017LeafObjective2Collection2T2R2CCD1	Corn	Leaf	7/5/17
## 82	Corn2017LeafObjective2Collection2T2R2FAG12	Corn	Leaf	7/5/17
## 83	Corn2017LeafObjective2Collection2T2R2FBH12	Corn	Leaf	7/5/17
## 84	Corn2017LeafObjective2Collection2T2R2FCA1	Corn	Leaf	7/5/17
## 85	Corn2017LeafObjective2Collection2T2R5CAH1	Corn	Leaf	7/5/17
## 86	Corn2017LeafObjective2Collection2T2R5CBA2	Corn	Leaf	7/5/17
## 87	Corn2017LeafObjective2Collection2T2R5CCB2	Corn	Leaf	7/5/17
## 88	Corn2017LeafObjective2Collection2T2R5FAE1	Corn	Leaf	7/5/17
## 89	Corn2017LeafObjective2Collection2T2R5FBF1	Corn	Leaf	7/5/17
## 90	Corn2017LeafObjective2Collection2T2R5FCG1	Corn	Leaf	7/5/17
## 91	Corn2017LeafObjective2Collection2T2R6CAF2	Corn	Leaf	7/5/17
## 92	Corn2017LeafObjective2Collection2T2R6CBG2	Corn	Leaf	7/5/17
## 93	Corn2017LeafObjective2Collection2T2R6CCH2	Corn	Leaf	7/5/17
## 94	Corn2017LeafObjective2Collection2T2R6FAC2	Corn	Leaf	7/5/17
## 95	Corn2017LeafObjective2Collection2T2R6FBD2	Corn	Leaf	7/5/17
## 96	Corn2017LeafObjective2Collection2T2R6FCE2	Corn	Leaf	7/5/17
## 97	Corn2017LeafObjective2Collection3T1R1CAA3	Corn	Leaf	7/31/17
## 98	Corn2017LeafObjective2Collection3T1R1CBB3	Corn	Leaf	7/31/17
## 99	Corn2017LeafObjective2Collection3T1R1CCC3	Corn	Leaf	7/31/17
## 100	Corn2017LeafObjective2Collection3T1R1FAD3	Corn	Leaf	7/31/17
## 101	Corn2017LeafObjective2Collection3T1R1FBE3	Corn	Leaf	7/31/17
## 102	Corn2017LeafObjective2Collection3T1R1FCF3	Corn	Leaf	7/31/17
## 103	Corn2017LeafObjective2Collection3T1R2CAG3	Corn	Leaf	7/31/17
## 104	Corn2017LeafObjective2Collection3T1R2CBH3	Corn	Leaf	7/31/17
## 105	Corn2017LeafObjective2Collection3T1R2CCA4	Corn	Leaf	7/31/17
## 106	Corn2017LeafObjective2Collection3T1R2FAB4	Corn	Leaf	7/31/17
## 107	Corn2017LeafObjective2Collection3T1R2FBC4	Corn	Leaf	7/31/17

## 108	Corn2017LeafObjective2Collection3T1R2FCD4	Corn	Leaf	7/31/17
## 109	Corn2017LeafObjective2Collection3T1R5CAE4	Corn	Leaf	7/31/17
## 110	Corn2017LeafObjective2Collection3T1R5CBF4	Corn	Leaf	7/31/17
## 111	Corn2017LeafObjective2Collection3T1R5CCG4	Corn	Leaf	7/31/17
## 112	Corn2017LeafObjective2Collection3T1R5FAH4	Corn	Leaf	7/31/17
## 113	Corn2017LeafObjective2Collection3T1R5FBA5	Corn	Leaf	7/31/17
## 114	Corn2017LeafObjective2Collection3T1R5FCB5	Corn	Leaf	7/31/17
## 115	Corn2017LeafObjective2Collection3T1R6CAC5	Corn	Leaf	7/31/17
## 116	Corn2017LeafObjective2Collection3T1R6CBD5	Corn	Leaf	7/31/17
## 117	Corn2017LeafObjective2Collection3T1R6CCE5	Corn	Leaf	7/31/17
## 118	Corn2017LeafObjective2Collection3T1R6FAF5	Corn	Leaf	7/31/17
## 119	Corn2017LeafObjective2Collection3T1R6FBG5	Corn	Leaf	7/31/17
## 120	Corn2017LeafObjective2Collection3T1R6FCH5	Corn	Leaf	7/31/17
## 121	Corn2017LeafObjective2Collection3T2R1CAB6	Corn	Leaf	7/31/17
## 122	Corn2017LeafObjective2Collection3T2R1CBC6	Corn	Leaf	7/31/17
## 123	Corn2017LeafObjective2Collection3T2R1CCD6	Corn	Leaf	7/31/17
## 124	Corn2017LeafObjective2Collection3T2R1FAE6	Corn	Leaf	7/31/17
## 125	Corn2017LeafObjective2Collection3T2R1FBF6	Corn	Leaf	7/31/17
## 126	Corn2017LeafObjective2Collection3T2R1FCG6	Corn	Leaf	7/31/17
## 127	Corn2017LeafObjective2Collection3T2R2CAH6	Corn	Leaf	7/31/17
## 128	Corn2017LeafObjective2Collection3T2R2CBA7	Corn	Leaf	7/31/17
## 129	Corn2017LeafObjective2Collection3T2R2CCB7	Corn	Leaf	7/31/17
## 130	Corn2017LeafObjective2Collection3T2R2FAC7	Corn	Leaf	7/31/17
## 131	Corn2017LeafObjective2Collection3T2R2FBD7	Corn	Leaf	7/31/17
## 132	Corn2017LeafObjective2Collection3T2R2FCE7	Corn	Leaf	7/31/17
## 133	Corn2017LeafObjective2Collection3T2R5CAF7	Corn	Leaf	7/31/17
## 134	Corn2017LeafObjective2Collection3T2R5CBG7	Corn	Leaf	7/31/17
## 135	Corn2017LeafObjective2Collection3T2R5CCH7	Corn	Leaf	7/31/17
## 136	Corn2017LeafObjective2Collection3T2R5FAA8	Corn	Leaf	7/31/17
## 137	Corn2017LeafObjective2Collection3T2R5FBB8	Corn	Leaf	7/31/17
## 138	Corn2017LeafObjective2Collection3T2R5FCC8	Corn	Leaf	7/31/17
## 139	Corn2017LeafObjective2Collection3T2R6CAD8	Corn	Leaf	7/31/17
## 140	Corn2017LeafObjective2Collection3T2R6CBE8	Corn	Leaf	7/31/17
## 141	Corn2017LeafObjective2Collection3T2R6CCF8	Corn	Leaf	7/31/17
## 142	Corn2017LeafObjective2Collection3T2R6FAG8	Corn	Leaf	7/31/17
## 143	Corn2017LeafObjective2Collection3T2R6FBH8	Corn	Leaf	7/31/17
## 144	Corn2017LeafObjective2Collection3T2R6FCA9	Corn	Leaf	7/31/17
## 145	T1R1AR4L	Soy	Leaf	8/16/18
## 146	T1R1BR4L	Soy	Leaf	8/16/18
## 147	T1R1CAR3L	Soy	Leaf	8/3/18
## 148	T1R1CAR6L	Soy	Leaf	8/27/18
## 149	T1R1CBR3L	Soy	Leaf	8/3/18
## 150	T1R1CBR6L	Soy	Leaf	8/27/18
## 151	T1R1CCR3L	Soy	Leaf	8/3/18
## 152	T1R1CCR6L	Soy	Leaf	8/27/18
## 153	T1R1CR4L	Soy	Leaf	8/16/18
## 154	T1R1FAR3L	Soy	Leaf	8/3/18
## 155	T1R1FAR4L	Soy	Leaf	8/16/18
## 156	T1R1FAR6L	Soy	Leaf	8/27/18
## 157	T1R1FBR3L	Soy	Leaf	8/3/18
## 158	T1R1FBR4L	Soy	Leaf	8/16/18
## 159	T1R1FBR6L	Soy	Leaf	8/27/18
## 160	T1R1FCR3L	Soy	Leaf	8/3/18
## 161	T1R1FCR4L	Soy	Leaf	8/16/18

## 162	T1R1FCR6L	Soy	Leaf	8/27/18
## 163	T1R2CAR3L	Soy	Leaf	8/3/18
## 164	T1R2CAR4L	Soy	Leaf	8/16/18
## 165	T1R2CAR6L	Soy	Leaf	8/27/18
## 166	T1R2CBR3L	Soy	Leaf	8/3/18
## 167	T1R2CBR4L	Soy	Leaf	8/16/18
## 168	T1R2CBR6L	Soy	Leaf	8/27/18
## 169	T1R2CCR3L	Soy	Leaf	8/3/18
## 170	T1R2CCR4L	Soy	Leaf	8/16/18
## 171	T1R2CCR6L	Soy	Leaf	8/27/18
## 172	T1R2FAR3L	Soy	Leaf	8/3/18
## 173	T1R2FAR4L	Soy	Leaf	8/16/18
## 174	T1R2FAR6L	Soy	Leaf	8/27/18
## 175	T1R2FBR3L	Soy	Leaf	8/3/18
## 176	T1R2FBR4L	Soy	Leaf	8/16/18
## 177	T1R2FBR6L	Soy	Leaf	8/27/18
## 178	T1R2FCR3L	Soy	Leaf	8/3/18
## 179	T1R2FCR4L	Soy	Leaf	8/16/18
## 180	T1R2FCR6L	Soy	Leaf	8/27/18
## 181	T1R5CAR3L	Soy	Leaf	8/3/18
## 182	T1R5CAR4L	Soy	Leaf	8/16/18
## 183	T1R5CAR6L	Soy	Leaf	8/27/18
## 184	T1R5CBR3L	Soy	Leaf	8/3/18
## 185	T1R5CBR4L	Soy	Leaf	8/16/18
## 186	T1R5CBR6L	Soy	Leaf	8/27/18
## 187	T1R5CCR3L	Soy	Leaf	8/3/18
## 188	T1R5CCR4L	Soy	Leaf	8/16/18
## 189	T1R5CCR6L	Soy	Leaf	8/27/18
## 190	T1R5FAR3L	Soy	Leaf	8/3/18
## 191	T1R5FAR4L	Soy	Leaf	8/16/18
## 192	T1R5FAR6L	Soy	Leaf	8/27/18
## 193	T1R5FBR3L	Soy	Leaf	8/3/18
## 194	T1R5FBR4L	Soy	Leaf	8/16/18
## 195	T1R5FBR6L	Soy	Leaf	8/27/18
## 196	T1R5FCR3L	Soy	Leaf	8/3/18
## 197	T1R5FCR4L	Soy	Leaf	8/16/18
## 198	T1R5FCR6L	Soy	Leaf	8/27/18
## 199	T1R6CAR3L	Soy	Leaf	8/3/18
## 200	T1R6CAR4L	Soy	Leaf	8/16/18
## 201	T1R6CAR6L	Soy	Leaf	8/27/18
## 202	T1R6CBR3L	Soy	Leaf	8/3/18
## 203	T1R6CBR4L	Soy	Leaf	8/16/18
## 204	T1R6CBR6L	Soy	Leaf	8/27/18
## 205	T1R6CCR3L	Soy	Leaf	8/3/18
## 206	T1R6CCR4L	Soy	Leaf	8/16/18
## 207	T1R6CCR6L	Soy	Leaf	8/27/18
## 208	T1R6FAR3L	Soy	Leaf	8/3/18
## 209	T1R6FAR4L	Soy	Leaf	8/16/18
## 210	T1R6FAR6L	Soy	Leaf	8/27/18
## 211	T1R6FBR3L	Soy	Leaf	8/3/18
## 212	T1R6FBR4L	Soy	Leaf	8/16/18
## 213	T1R6FBR6L	Soy	Leaf	8/27/18
## 214	T1R6FCR3L	Soy	Leaf	8/3/18
## 215	T1R6FCR4L	Soy	Leaf	8/16/18



## 216	T1R6FCR6L	Soy	Leaf	8/27/18
## 217	T2R1CAR3L	Soy	Leaf	8/3/18
## 218	T2R1CAR4L	Soy	Leaf	8/16/18
## 219	T2R1CAR6L	Soy	Leaf	8/27/18
## 220	T2R1CBR3L	Soy	Leaf	8/3/18
## 221	T2R1CBR4L	Soy	Leaf	8/16/18
## 222	T2R1CBR6L	Soy	Leaf	8/27/18
## 223	T2R1CCR3L	Soy	Leaf	8/3/18
## 224	T2R1CCR4L	Soy	Leaf	8/16/18
## 225	T2R1CCR6L	Soy	Leaf	8/27/18
## 226	T2R1FAR3L	Soy	Leaf	8/3/18
## 227	T2R1FAR4L	Soy	Leaf	8/16/18
## 228	T2R1FAR6L	Soy	Leaf	8/27/18
## 229	T2R1FBR3L	Soy	Leaf	8/3/18
## 230	T2R1FBR4L	Soy	Leaf	8/16/18
## 231	T2R1FBR6L	Soy	Leaf	8/27/18
## 232	T2R1FCR3L	Soy	Leaf	8/3/18
## 233	T2R1FCR4L	Soy	Leaf	8/16/18
## 234	T2R2CAR3L	Soy	Leaf	8/3/18
## 235	T2R2CAR4L	Soy	Leaf	8/16/18
## 236	T2R2CAR6L	Soy	Leaf	8/27/18
## 237	T2R2CBR3L	Soy	Leaf	8/3/18
## 238	T2R2CBR4L	Soy	Leaf	8/16/18
## 239	T2R2CBR6L	Soy	Leaf	8/27/18
## 240	T2R2CCR3L	Soy	Leaf	8/3/18
## 241	T2R2CCR4L	Soy	Leaf	8/16/18
## 242	T2R2CCR6L	Soy	Leaf	8/27/18
## 243	T2R2FAR3L	Soy	Leaf	8/3/18
## 244	T2R2FAR4L	Soy	Leaf	8/16/18
## 245	T2R2FAR6L	Soy	Leaf	8/27/18
## 246	T2R2FBR3L	Soy	Leaf	8/3/18
## 247	T2R2FBR4L	Soy	Leaf	8/16/18
## 248	T2R2FBR6L	Soy	Leaf	8/27/18
## 249	T2R2FCR3L	Soy	Leaf	8/3/18
## 250	T2R2FCR4L	Soy	Leaf	8/16/18
## 251	T2R2FCR6L	Soy	Leaf	8/27/18
## 252	T2R5CAR3L	Soy	Leaf	8/3/18
## 253	T2R5CAR4L	Soy	Leaf	8/16/18
## 254	T2R5CAR6L	Soy	Leaf	8/27/18
## 255	T2R5CBR3L	Soy	Leaf	8/3/18
## 256	T2R5CBR4L	Soy	Leaf	8/16/18
## 257	T2R5CBR6L	Soy	Leaf	8/27/18
## 258	T2R5CCR3L	Soy	Leaf	8/3/18
## 259	T2R5CCR4L	Soy	Leaf	8/16/18
## 260	T2R5CCR6L	Soy	Leaf	8/27/18
## 261	T2R5FAR3L	Soy	Leaf	8/3/18
## 262	T2R5FAR4L	Soy	Leaf	8/16/18
## 263	T2R5FAR6L	Soy	Leaf	8/27/18
## 264	T2R5FBR3L	Soy	Leaf	8/3/18
## 265	T2R5FBR4L	Soy	Leaf	8/16/18
## 266	T2R5FBR6L	Soy	Leaf	8/27/18
## 267	T2R5FCR3L	Soy	Leaf	8/3/18
## 268	T2R5FCR4L	Soy	Leaf	8/16/18
## 269	T2R5FCR6L	Soy	Leaf	8/27/18

## 270	T2R6CAR3L	Soy	Leaf	8/3/18
## 271	T2R6CAR4L	Soy	Leaf	8/16/18
## 272	T2R6CAR6L	Soy	Leaf	8/27/18
## 273	T2R6CBR3L	Soy	Leaf	8/3/18
## 274	T2R6CBR4L	Soy	Leaf	8/16/18
## 275	T2R6CBR6L	Soy	Leaf	8/27/18
## 276	T2R6CCR3L	Soy	Leaf	8/3/18
## 277	T2R6CCR4L	Soy	Leaf	8/16/18
## 278	T2R6CCR6L	Soy	Leaf	8/27/18
## 279	T2R6FAR3L	Soy	Leaf	8/3/18
## 280	T2R6FAR4L	Soy	Leaf	8/16/18
## 281	T2R6FAR6L	Soy	Leaf	8/27/18
## 282	T2R6FBR3L	Soy	Leaf	8/3/18
## 283	T2R6FBR4L	Soy	Leaf	8/16/18
## 284	T2R6FBR6L	Soy	Leaf	8/27/18
## 285	T2R6FCR3L	Soy	Leaf	8/3/18
## 286	T2R6FCR4L	Soy	Leaf	8/16/18
## 287	T2R6FCR6L	Soy	Leaf	8/27/18

##	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
## 7	V6	Conv.	R2	A	C	3
## 8	V6	Conv.	R2	B	C	8
## 9	V6	Conv.	R2	C	C	4
## 10	V6	Conv.	R2	A	F	4
## 11	V6	Conv.	R2	B	F	3
## 12	V6	Conv.	R2	C	F	5
## 13	V6	Conv.	R5	A	C	5
## 14	V6	Conv.	R5	B	C	4
## 15	V6	Conv.	R5	C	C	10
## 16	V6	Conv.	R5	A	F	4
## 17	V6	Conv.	R5	B	F	6
## 18	V6	Conv.	R5	C	F	6
## 19	V6	Conv.	R6	A	C	2
## 20	V6	Conv.	R6	B	C	1
## 21	V6	Conv.	R6	C	C	6
## 22	V6	Conv.	R6	A	F	1
## 23	V6	Conv.	R6	B	F	4
## 24	V6	Conv.	R6	C	F	2
## 25	V6	No-till	R1	A	C	6
## 26	V6	No-till	R1	B	C	3
## 27	V6	No-till	R1	C	C	4
## 28	V6	No-till	R1	A	F	15
## 29	V6	No-till	R1	B	F	5
## 30	V6	No-till	R1	C	F	9
## 31	V6	No-till	R2	A	C	5
## 32	V6	No-till	R2	B	C	5
## 33	V6	No-till	R2	C	C	6
## 34	V6	No-till	R2	A	F	15
## 35	V6	No-till	R2	B	F	3

## 36	V6	No-till	R2	C	F	2
## 37	V6	No-till	R5	A	C	9
## 38	V6	No-till	R5	B	C	9
## 39	V6	No-till	R5	C	C	3
## 40	V6	No-till	R5	A	F	8
## 41	V6	No-till	R5	B	F	1
## 42	V6	No-till	R5	C	F	12
## 43	V6	No-till	R6	A	C	11
## 44	V6	No-till	R6	B	C	7
## 45	V6	No-till	R6	C	C	7
## 46	V6	No-till	R6	A	F	6
## 47	V6	No-till	R6	B	F	6
## 48	V6	No-till	R6	C	F	3
## 49	V8	Conv.	R1	A	C	19
## 50	V8	Conv.	R1	B	C	11
## 51	V8	Conv.	R1	C	C	10
## 52	V8	Conv.	R1	A	F	4
## 53	V8	Conv.	R1	B	F	3
## 54	V8	Conv.	R1	C	F	10
## 55	V8	Conv.	R2	A	C	14
## 56	V8	Conv.	R2	B	C	7
## 57	V8	Conv.	R2	C	C	14
## 58	V8	Conv.	R2	A	F	3
## 59	V8	Conv.	R2	B	F	4
## 60	V8	Conv.	R2	C	F	2
## 61	V8	Conv.	R5	A	C	7
## 62	V8	Conv.	R5	B	C	17
## 63	V8	Conv.	R5	C	C	10
## 64	V8	Conv.	R5	A	F	4
## 65	V8	Conv.	R5	B	F	6
## 66	V8	Conv.	R5	C	F	3
## 67	V8	Conv.	R6	A	C	17
## 68	V8	Conv.	R6	B	C	5
## 69	V8	Conv.	R6	C	C	10
## 70	V8	Conv.	R6	A	F	2
## 71	V8	Conv.	R6	B	F	8
## 72	V8	Conv.	R6	C	F	6
## 73	V8	No-till	R1	A	C	10
## 74	V8	No-till	R1	B	C	19
## 75	V8	No-till	R1	C	C	19
## 76	V8	No-till	R1	A	F	4
## 77	V8	No-till	R1	B	F	7
## 78	V8	No-till	R1	C	F	6
## 79	V8	No-till	R2	A	C	18
## 80	V8	No-till	R2	B	C	11
## 81	V8	No-till	R2	C	C	11
## 82	V8	No-till	R2	A	F	6
## 83	V8	No-till	R2	B	F	8
## 84	V8	No-till	R2	C	F	10
## 85	V8	No-till	R5	A	C	17
## 86	V8	No-till	R5	B	C	13
## 87	V8	No-till	R5	C	C	15
## 88	V8	No-till	R5	A	F	11
## 89	V8	No-till	R5	B	F	8

## 90	V8	No-till	R5	C	F	6
## 91	V8	No-till	R6	A	C	6
## 92	V8	No-till	R6	B	C	13
## 93	V8	No-till	R6	C	C	21
## 94	V8	No-till	R6	A	F	10
## 95	V8	No-till	R6	B	F	7
## 96	V8	No-till	R6	C	F	6
## 97	V15	Conv.	R1	A	C	15
## 98	V15	Conv.	R1	B	C	16
## 99	V15	Conv.	R1	C	C	12
## 100	V15	Conv.	R1	A	F	15
## 101	V15	Conv.	R1	B	F	14
## 102	V15	Conv.	R1	C	F	10
## 103	V15	Conv.	R2	A	C	11
## 104	V15	Conv.	R2	B	C	12
## 105	V15	Conv.	R2	C	C	12
## 106	V15	Conv.	R2	A	F	17
## 107	V15	Conv.	R2	B	F	16
## 108	V15	Conv.	R2	C	F	8
## 109	V15	Conv.	R5	A	C	22
## 110	V15	Conv.	R5	B	C	26
## 111	V15	Conv.	R5	C	C	11
## 112	V15	Conv.	R5	A	F	23
## 113	V15	Conv.	R5	B	F	17
## 114	V15	Conv.	R5	C	F	5
## 115	V15	Conv.	R6	A	C	16
## 116	V15	Conv.	R6	B	C	10
## 117	V15	Conv.	R6	C	C	10
## 118	V15	Conv.	R6	A	F	8
## 119	V15	Conv.	R6	B	F	12
## 120	V15	Conv.	R6	C	F	17
## 121	V15	No-till	R1	A	C	8
## 122	V15	No-till	R1	B	C	14
## 123	V15	No-till	R1	C	C	7
## 124	V15	No-till	R1	A	F	15
## 125	V15	No-till	R1	B	F	11
## 126	V15	No-till	R1	C	F	19
## 127	V15	No-till	R2	A	C	15
## 128	V15	No-till	R2	B	C	13
## 129	V15	No-till	R2	C	C	16
## 130	V15	No-till	R2	A	F	20
## 131	V15	No-till	R2	B	F	32
## 132	V15	No-till	R2	C	F	31
## 133	V15	No-till	R5	A	C	25
## 134	V15	No-till	R5	B	C	18
## 135	V15	No-till	R5	C	C	20
## 136	V15	No-till	R5	A	F	33
## 137	V15	No-till	R5	B	F	33
## 138	V15	No-till	R5	C	F	14
## 139	V15	No-till	R6	A	C	12
## 140	V15	No-till	R6	B	C	22
## 141	V15	No-till	R6	C	C	21
## 142	V15	No-till	R6	A	F	36
## 143	V15	No-till	R6	B	F	18

## 144	V15	No-till	R6	C	F	29
## 145	R4	Conv.	R1	A	C	21
## 146	R4	Conv.	R1	B	C	12
## 147	R3	Conv.	R1	A	C	15
## 148	R6	Conv.	R1	A	C	22
## 149	R3	Conv.	R1	B	C	18
## 150	R6	Conv.	R1	B	C	20
## 151	R3	Conv.	R1	C	C	18
## 152	R6	Conv.	R1	C	C	21
## 153	R4	Conv.	R1	C	C	19
## 154	R3	Conv.	R1	A	F	15
## 155	R4	Conv.	R1	A	F	11
## 156	R6	Conv.	R1	A	F	10
## 157	R3	Conv.	R1	B	F	10
## 158	R4	Conv.	R1	B	F	7
## 159	R6	Conv.	R1	B	F	6
## 160	R3	Conv.	R1	C	F	16
## 161	R4	Conv.	R1	C	F	16
## 162	R6	Conv.	R1	C	F	15
## 163	R3	Conv.	R2	A	C	7
## 164	R4	Conv.	R2	A	C	28
## 165	R6	Conv.	R2	A	C	22
## 166	R3	Conv.	R2	B	C	9
## 167	R4	Conv.	R2	B	C	19
## 168	R6	Conv.	R2	B	C	15
## 169	R3	Conv.	R2	C	C	14
## 170	R4	Conv.	R2	C	C	21
## 171	R6	Conv.	R2	C	C	18
## 172	R3	Conv.	R2	A	F	13
## 173	R4	Conv.	R2	A	F	11
## 174	R6	Conv.	R2	A	F	12
## 175	R3	Conv.	R2	B	F	12
## 176	R4	Conv.	R2	B	F	8
## 177	R6	Conv.	R2	B	F	4
## 178	R3	Conv.	R2	C	F	15
## 179	R4	Conv.	R2	C	F	8
## 180	R6	Conv.	R2	C	F	10
## 181	R3	Conv.	R5	A	C	25
## 182	R4	Conv.	R5	A	C	18
## 183	R6	Conv.	R5	A	C	23
## 184	R3	Conv.	R5	B	C	18
## 185	R4	Conv.	R5	B	C	16
## 186	R6	Conv.	R5	B	C	22
## 187	R3	Conv.	R5	C	C	19
## 188	R4	Conv.	R5	C	C	14
## 189	R6	Conv.	R5	C	C	17
## 190	R3	Conv.	R5	A	F	22
## 191	R4	Conv.	R5	A	F	9
## 192	R6	Conv.	R5	A	F	7
## 193	R3	Conv.	R5	B	F	13
## 194	R4	Conv.	R5	B	F	14
## 195	R6	Conv.	R5	B	F	9
## 196	R3	Conv.	R5	C	F	23
## 197	R4	Conv.	R5	C	F	9

## 198	R6	Conv.	R5	C	F	6
## 199	R3	Conv.	R6	A	C	25
## 200	R4	Conv.	R6	A	C	22
## 201	R6	Conv.	R6	A	C	20
## 202	R3	Conv.	R6	B	C	27
## 203	R4	Conv.	R6	B	C	19
## 204	R6	Conv.	R6	B	C	15
## 205	R3	Conv.	R6	C	C	23
## 206	R4	Conv.	R6	C	C	22
## 207	R6	Conv.	R6	C	C	13
## 208	R3	Conv.	R6	A	F	18
## 209	R4	Conv.	R6	A	F	13
## 210	R6	Conv.	R6	A	F	17
## 211	R3	Conv.	R6	B	F	19
## 212	R4	Conv.	R6	B	F	10
## 213	R6	Conv.	R6	B	F	11
## 214	R3	Conv.	R6	C	F	17
## 215	R4	Conv.	R6	C	F	5
## 216	R6	Conv.	R6	C	F	16
## 217	R3	No-till	R1	A	C	20
## 218	R4	No-till	R1	A	C	25
## 219	R6	No-till	R1	A	C	18
## 220	R3	No-till	R1	B	C	21
## 221	R4	No-till	R1	B	C	17
## 222	R6	No-till	R1	B	C	15
## 223	R3	No-till	R1	C	C	22
## 224	R4	No-till	R1	C	C	27
## 225	R6	No-till	R1	C	C	20
## 226	R3	No-till	R1	A	F	25
## 227	R4	No-till	R1	A	F	11
## 228	R6	No-till	R1	A	F	12
## 229	R3	No-till	R1	B	F	39
## 230	R4	No-till	R1	B	F	12
## 231	R6	No-till	R1	B	F	9
## 232	R3	No-till	R1	C	F	19
## 233	R4	No-till	R1	C	F	7
## 234	R3	No-till	R2	A	C	18
## 235	R4	No-till	R2	A	C	24
## 236	R6	No-till	R2	A	C	16
## 237	R3	No-till	R2	B	C	18
## 238	R4	No-till	R2	B	C	17
## 239	R6	No-till	R2	B	C	16
## 240	R3	No-till	R2	C	C	14
## 241	R4	No-till	R2	C	C	22
## 242	R6	No-till	R2	C	C	25
## 243	R3	No-till	R2	A	F	22
## 244	R4	No-till	R2	A	F	10
## 245	R6	No-till	R2	A	F	13
## 246	R3	No-till	R2	B	F	13
## 247	R4	No-till	R2	B	F	8
## 248	R6	No-till	R2	B	F	13
## 249	R3	No-till	R2	C	F	15
## 250	R4	No-till	R2	C	F	10
## 251	R6	No-till	R2	C	F	10

## 252	R3	No-till	R5	A	C	25
## 253	R4	No-till	R5	A	C	19
## 254	R6	No-till	R5	A	C	17
## 255	R3	No-till	R5	B	C	13
## 256	R4	No-till	R5	B	C	16
## 257	R6	No-till	R5	B	C	19
## 258	R3	No-till	R5	C	C	15
## 259	R4	No-till	R5	C	C	9
## 260	R6	No-till	R5	C	C	19
## 261	R3	No-till	R5	A	F	15
## 262	R4	No-till	R5	A	F	5
## 263	R6	No-till	R5	A	F	12
## 264	R3	No-till	R5	B	F	14
## 265	R4	No-till	R5	B	F	5
## 266	R6	No-till	R5	B	F	17
## 267	R3	No-till	R5	C	F	11
## 268	R4	No-till	R5	C	F	6
## 269	R6	No-till	R5	C	F	28
## 270	R3	No-till	R6	A	C	18
## 271	R4	No-till	R6	A	C	15
## 272	R6	No-till	R6	A	C	19
## 273	R3	No-till	R6	B	C	15
## 274	R4	No-till	R6	B	C	14
## 275	R6	No-till	R6	B	C	20
## 276	R3	No-till	R6	C	C	14
## 277	R4	No-till	R6	C	C	23
## 278	R6	No-till	R6	C	C	24
## 279	R3	No-till	R6	A	F	11
## 280	R4	No-till	R6	A	F	8
## 281	R6	No-till	R6	A	F	7
## 282	R3	No-till	R6	B	F	11
## 283	R4	No-till	R6	B	F	7
## 284	R6	No-till	R6	B	F	14
## 285	R3	No-till	R6	C	F	21
## 286	R4	No-till	R6	C	F	9
## 287	R6	No-till	R6	C	F	14

```
microbiome.fungi %>% # Note: A syntax allowing the combination of an output to an input
  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
```

`summarise()` We can use the `summarise()` function to find things like means and standard deviations/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 within the conventional
```

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

We can also connect multiple summary statistics here. More powerful.

```
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
```

This is useful, but maybe we want to have summary statistics by group! We can also do this very easily using the `group_by()` function.

```
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
```

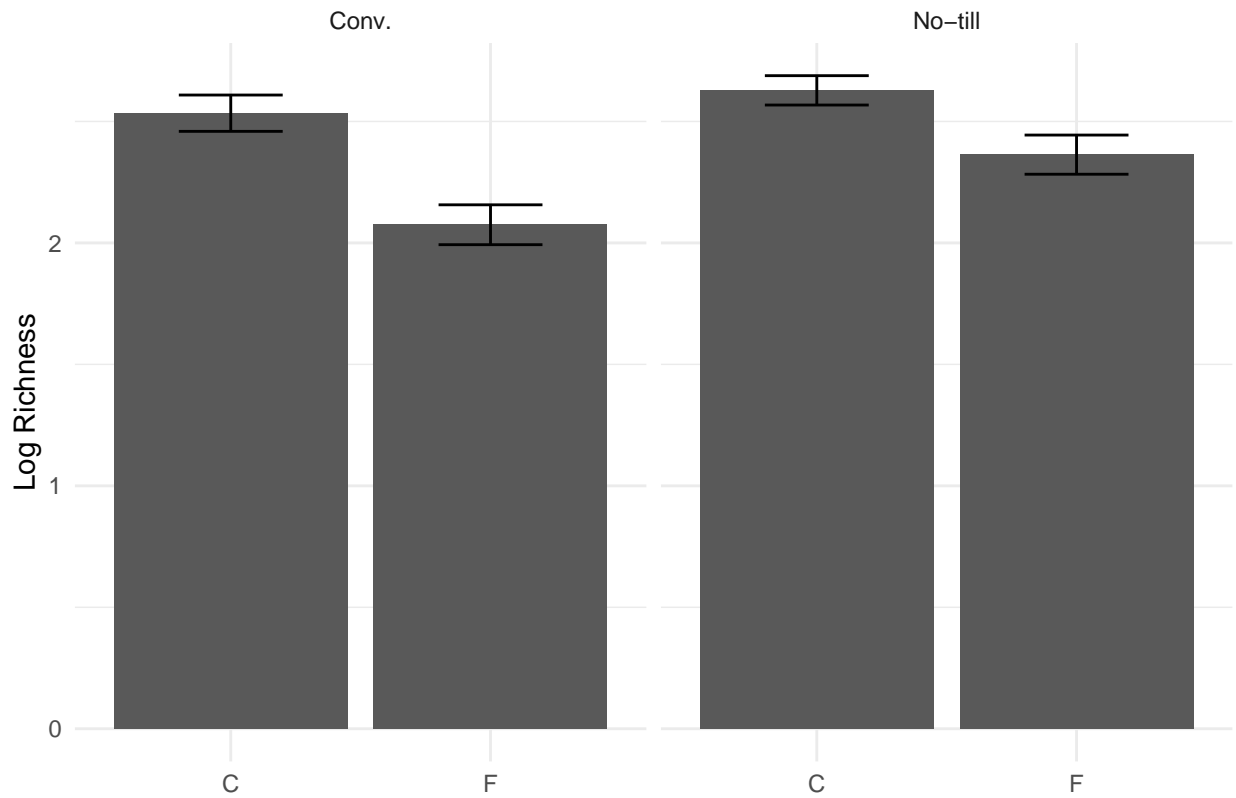


**Connecting to plotting** These groups of functions and packages also all work together very nicely. For example, direct input into ggplot is possible. In which case you would not have to enter the data statement, you just need to start inputting your aesthetics.

```
plot1 <- 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.

plot1



**Joining** The join group of functions are super useful. Have you ever tried to match up data by rows based on some criteria? Its almost impossible without messing up over 10-15 rows of data. Note: Allow the joining of multiple datasets based on a common column variable. For example, joining datasets back to a metadata file.

More info can be found here: <https://dplyr.tidyverse.org/reference/mutate-joins.html>

But we can easily do this with the joining functions. They include:

-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

To try these out lets split our data into separate sets including taxonomy and metadata.

Here we are also sampling 100 random rows of our dataset using the `sample_n()` function

```
# 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
```

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

```
##                               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
```

Now this is kind of a silly example because we already had the data set joined how we wanted it and split it apart. But you can imagine if you have two separate data sets with one column in common and you wanted to combine them into one, instead of taking days to do this by hand you could simply load into R and do it.

**Pivoting** Pivoting is also useful for converting from wide to long format and back again. We can do this with `pivot_longer()` and `pivot_wider()`

More info can be found here: [https://tidyr.tidyverse.org/reference/pivot\\_wider.html](https://tidyr.tidyverse.org/reference/pivot_wider.html)

I will demonstrate `pivot_wider()` assuming that most data is already formatted as long data. Lets explore turning our data set into a wide format, since its in long format.

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>%
  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
```

Wide format - sets the values within the fungicide column into column names

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>% # selecting columns
  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
```

Easily can take the difference between the fungicide and control now.

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>% # selecting columns filter(Class == "Soil")
  group_by(Treatment, Fungicide) %>% # grouping by treatment and fungicide to later calculate summary statistics
  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.
```

```
## '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
```

Now we can easily calculate the difference between fungicide and control and plot it.

```
microbiome.fungi %>%
  select(SampleID, Crop, Compartment:Fungicide, richness) %>% # selecting columns filter(Class == "Soil")
  group_by(Treatment, Fungicide) %>% # grouping by treatment and fungicide to later calculate summary statistics
  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.
```

