Tidyverse

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## Seemless data wrangeling

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.pakcages("tidyverse")

library(tidyverse)

## ── Attaching packages ─────────────────────────────────────── tidyverse 1.3.2 ──  
## ✔ ggplot2 3.4.1 ✔ purrr 0.3.5   
## ✔ tibble 3.1.8 ✔ dplyr 1.0.10  
## ✔ tidyr 1.2.1 ✔ stringr 1.5.0   
## ✔ readr 2.1.3 ✔ forcats 0.5.2   
## ── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ dplyr::lag() masks stats::lag()

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 & statistics

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("Microbiome.csv")

If we look at the structure of the data we can see that the dataset is 1,353,422 rows. This is too large for excel to handle. So we literally cannot use it in excel.

str(microbiome.fungi)

## 'data.frame': 1353422 obs. of 42 variables:  
## $ X : int 1242826 1320150 794589 1242688 1320170 1243099 1319917 1242871 1243075 1242973 ...  
## $ OTU : chr "FOTU\_7" "FOTU\_9" "FOTU\_44" "FOTU\_7" ...  
## $ Sample : chr "Corn2017RootObjective2Collection2T2R5BFE1" "Corn2017RootObjective2Collection1T1R1ACD10" "Corn2017RootObjective2Collection1T1R2BFC12" "Corn2017RootObjective2Collection2T2R6BFB4" ...  
## $ Abundance : num 0.997 0.996 0.993 0.989 0.984 ...  
## $ SampleID : chr "Corn2017RootObjective2Collection2T2R5BFE1" "Corn2017RootObjective2Collection1T1R1ACD10" "Corn2017RootObjective2Collection1T1R2BFC12" "Corn2017RootObjective2Collection2T2R6BFB4" ...  
## $ BarcodeSequence : chr "ATCGTCCGCG" "CAACGTGCTC" "CCTGTCCTAT" "ACTGCTATCG" ...  
## $ LinkerPrimerSequence: chr "CAAGCAGAAGACGGCATACGAGAT" "CAAGCAGAAGACGGCATACGAGAT" "CAAGCAGAAGACGGCATACGAGAT" "CAAGCAGAAGACGGCATACGAGAT" ...  
## $ Region : chr "ITS" "ITS" "ITS" "ITS" ...  
## $ BC\_plate : int 1 3 3 1 3 1 3 3 3 1 ...  
## $ BC\_name : chr "PCR\_R\_bc5" "PCR\_R\_bc268" "PCR\_R\_bc283" "PCR\_R\_bc26" ...  
## $ Crop : chr "Corn" "Corn" "Corn" "Corn" ...  
## $ Objective : chr "Objective 2" "Objective 2" "Objective 2" "Objective 2" ...  
## $ Collection : int 2 1 1 2 2 2 2 2 2 2 ...  
## $ Compartment : chr "Root" "Root" "Root" "Root" ...  
## $ DateSampled : chr "5-Jul-17" "26-Jun-17" "26-Jun-17" "5-Jul-17" ...  
## $ GrowthStage : chr "V8" "V6" "V6" "V8" ...  
## $ Treatment : chr "T2" "T1" "T1" "T2" ...  
## $ Rep : chr "R5" "R1" "R2" "R6" ...  
## $ sample\_Sample : chr "B" "A" "B" "B" ...  
## $ Fungicide : chr "F" "C" "F" "F" ...  
## $ Target\_organism : chr "Fungi" "Fungi" "Fungi" "Fungi" ...  
## $ Location : chr "Kellogg Biological Station" "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 ...  
## $ Phi2 : logi NA NA NA NA NA NA ...  
## $ PhiNO : logi NA NA NA NA NA NA ...  
## $ PhiNPQ : logi NA NA NA NA NA NA ...  
## $ Relative.Chlorophyll: logi NA NA NA NA NA NA ...  
## $ Sample\_or\_Control : chr "True Sample" "True Sample" "True Sample" "True Sample" ...  
## $ is.neg : logi FALSE FALSE FALSE FALSE FALSE FALSE ...  
## $ OTU\_ID : chr "FOTU\_7" "FOTU\_9" "FOTU\_44" "FOTU\_7" ...  
## $ Kingdom : chr "Fungi" "Fungi" "Fungi" "Fungi" ...  
## $ Phylum : chr "Ascomycota" "Ascomycota" "Ascomycota" "Ascomycota" ...  
## $ Class : chr "Sordariomycetes" "Dothideomycetes" "Dothideomycetes" "Sordariomycetes" ...  
## $ Order : chr "Sordariales" "Pleosporales" "Pleosporales" "Sordariales" ...  
## $ Family : chr "Chaetomiaceae" "Didymellaceae" "Sporormiaceae" "Chaetomiaceae" ...  
## $ Genus : chr NA "Didymella" "Preussia" NA ...  
## $ Species : chr NA "Didymella sp." "Preussia sp." NA ...  
## $ Isolate : chr NA NA NA NA ...  
## $ Isolate\_percent\_id : num 0 0 0 0 0 0 0 0 0 0 ...  
## $ BestMatch : chr "Chaetomiaceae" "Didymella sp." "Preussia sp." "Chaetomiaceae" ...  
## $ Taxonomy : chr "FOTU\_7-Chaetomiaceae" "FOTU\_9-Didymella sp." "FOTU\_44-Preussia sp." "FOTU\_7-Chaetomiaceae" ...

Lets start exploring the data.

the first thing we can do is select only the columns we need since it seems that there are lots of columns that we may not need.

#### select()

microbiome.fungi2 <- select(microbiome.fungi, OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy)

Note the syntax. I listed all the column headers I wanted, but at the end I used Kingdom:Taxonomy 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, Class == "Sordariomycetes"))

## OTU SampleID Abundance Crop Compartment  
## 1 FOTU\_7 Corn2017RootObjective2Collection2T2R5BFE1 0.9970508 Corn Root  
## 2 FOTU\_7 Corn2017RootObjective2Collection2T2R6BFB4 0.9886459 Corn Root  
## 3 FOTU\_7 Corn2017RootObjective2Collection2T2R5ACD11 0.9786059 Corn Root  
## 4 FOTU\_7 Corn2017RootObjective2Collection2T2R2BCA8 0.9634735 Corn Root  
## 5 FOTU\_7 Corn2017RootObjective2Collection2T2R1CFB6 0.9592154 Corn Root  
## 6 FOTU\_7 Corn2017RootObjective2Collection2T2R5CFD12 0.9567938 Corn Root  
## DateSampled GrowthStage Treatment Rep Fungicide Kingdom Phylum  
## 1 5-Jul-17 V8 T2 R5 F Fungi Ascomycota  
## 2 5-Jul-17 V8 T2 R6 F Fungi Ascomycota  
## 3 5-Jul-17 V8 T2 R5 C Fungi Ascomycota  
## 4 5-Jul-17 V8 T2 R2 C Fungi Ascomycota  
## 5 5-Jul-17 V8 T2 R1 F Fungi Ascomycota  
## 6 5-Jul-17 V8 T2 R5 F Fungi Ascomycota  
## Class Order Family Genus Species Isolate  
## 1 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 2 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 3 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 4 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 5 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 6 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## Isolate\_percent\_id BestMatch Taxonomy  
## 1 0 Chaetomiaceae FOTU\_7-Chaetomiaceae  
## 2 0 Chaetomiaceae FOTU\_7-Chaetomiaceae  
## 3 0 Chaetomiaceae FOTU\_7-Chaetomiaceae  
## 4 0 Chaetomiaceae FOTU\_7-Chaetomiaceae  
## 5 0 Chaetomiaceae FOTU\_7-Chaetomiaceae  
## 6 0 Chaetomiaceae FOTU\_7-Chaetomiaceae

#### mutate()

Mutate allows us to quickly create new columns. Say we wanted to transform the Abundance column into a percentage by multiplying by 100.

head(mutate(microbiome.fungi2, Percent = Abundance\*100))

## OTU SampleID Abundance Crop Compartment  
## 1 FOTU\_7 Corn2017RootObjective2Collection2T2R5BFE1 0.9970508 Corn Root  
## 2 FOTU\_9 Corn2017RootObjective2Collection1T1R1ACD10 0.9955440 Corn Root  
## 3 FOTU\_44 Corn2017RootObjective2Collection1T1R2BFC12 0.9927446 Corn Root  
## 4 FOTU\_7 Corn2017RootObjective2Collection2T2R6BFB4 0.9886459 Corn Root  
## 5 FOTU\_9 Corn2017RootObjective2Collection2T1R5BCC2 0.9835863 Corn Root  
## 6 FOTU\_7 Corn2017RootObjective2Collection2T2R5ACD11 0.9786059 Corn Root  
## DateSampled GrowthStage Treatment Rep Fungicide Kingdom Phylum  
## 1 5-Jul-17 V8 T2 R5 F Fungi Ascomycota  
## 2 26-Jun-17 V6 T1 R1 C Fungi Ascomycota  
## 3 26-Jun-17 V6 T1 R2 F Fungi Ascomycota  
## 4 5-Jul-17 V8 T2 R6 F Fungi Ascomycota  
## 5 5-Jul-17 V8 T1 R5 C Fungi Ascomycota  
## 6 5-Jul-17 V8 T2 R5 C Fungi Ascomycota  
## Class Order Family Genus Species Isolate  
## 1 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 2 Dothideomycetes Pleosporales Didymellaceae Didymella Didymella sp. <NA>  
## 3 Dothideomycetes Pleosporales Sporormiaceae Preussia Preussia sp. <NA>  
## 4 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 5 Dothideomycetes Pleosporales Didymellaceae Didymella Didymella sp. <NA>  
## 6 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## Isolate\_percent\_id BestMatch Taxonomy Percent  
## 1 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 99.70508  
## 2 0 Didymella sp. FOTU\_9-Didymella sp. 99.55440  
## 3 0 Preussia sp. FOTU\_44-Preussia sp. 99.27446  
## 4 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 98.86459  
## 5 0 Didymella sp. FOTU\_9-Didymella sp. 98.35863  
## 6 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 97.86059

#### 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.

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 transfered to the next step.

microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 mutate(Percent = Abundance\*100) %>%  
 head()

## OTU SampleID Abundance Crop Compartment  
## 1 FOTU\_7 Corn2017RootObjective2Collection2T2R5BFE1 0.9970508 Corn Root  
## 2 FOTU\_7 Corn2017RootObjective2Collection2T2R6BFB4 0.9886459 Corn Root  
## 3 FOTU\_7 Corn2017RootObjective2Collection2T2R5ACD11 0.9786059 Corn Root  
## 4 FOTU\_7 Corn2017RootObjective2Collection2T2R2BCA8 0.9634735 Corn Root  
## 5 FOTU\_7 Corn2017RootObjective2Collection2T2R1CFB6 0.9592154 Corn Root  
## 6 FOTU\_7 Corn2017RootObjective2Collection2T2R5CFD12 0.9567938 Corn Root  
## DateSampled GrowthStage Treatment Rep Fungicide Kingdom Phylum  
## 1 5-Jul-17 V8 T2 R5 F Fungi Ascomycota  
## 2 5-Jul-17 V8 T2 R6 F Fungi Ascomycota  
## 3 5-Jul-17 V8 T2 R5 C Fungi Ascomycota  
## 4 5-Jul-17 V8 T2 R2 C Fungi Ascomycota  
## 5 5-Jul-17 V8 T2 R1 F Fungi Ascomycota  
## 6 5-Jul-17 V8 T2 R5 F Fungi Ascomycota  
## Class Order Family Genus Species Isolate  
## 1 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 2 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 3 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 4 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 5 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## 6 Sordariomycetes Sordariales Chaetomiaceae <NA> <NA> <NA>  
## Isolate\_percent\_id BestMatch Taxonomy Percent  
## 1 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 99.70508  
## 2 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 98.86459  
## 3 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 97.86059  
## 4 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 96.34735  
## 5 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 95.92154  
## 6 0 Chaetomiaceae FOTU\_7-Chaetomiaceae 95.67938

#### summarise()

We can use the summarise() function to find things like means and standard deviations/errors.

microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent)) %>%  
 head()

## Mean  
## 1 0.02803439

So on average, Ascomycota makes up about 0.02% of the microbiome.

We can also connect multiple summary statistics here.

microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent),   
 n = n(),   
 sd.dev = sd(Percent)) %>%  
 mutate(std.err = sd.dev/sqrt(n))

## Mean n sd.dev std.err  
## 1 0.02803439 382260 0.854294 0.001381745

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(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent),   
 n = n(),   
 sd.dev = sd(Percent)) %>%  
 mutate(std.err = sd.dev/sqrt(n))

## # A tibble: 20 × 5  
## Order Mean n sd.dev std.err  
## <chr> <dbl> <int> <dbl> <dbl>  
## 1 Branch06 0.0295 6094 0.477 0.00611   
## 2 Chaetosphaeriales 0.0241 7756 0.445 0.00505   
## 3 Coniochaetales 0.00747 16620 0.375 0.00291   
## 4 Conioscyphales 0.00936 2770 0.257 0.00489   
## 5 Diaporthales 0.0293 40996 0.715 0.00353   
## 6 Glomerellales 0.00400 12742 0.0920 0.000815   
## 7 Hypocreales 0.0210 119110 0.524 0.00152   
## 8 Magnaporthales 0.0348 8864 0.808 0.00859   
## 9 Melanosporales 0.0339 1108 0.637 0.0191   
## 10 Microascales 0.0435 5540 1.19 0.0160   
## 11 Myrmecridiales 0.00562 3324 0.0722 0.00125   
## 12 Ophiostomatales 0.000563 1662 0.0133 0.000325   
## 13 Phomatosporales 0.0379 554 0.549 0.0233   
## 14 Phyllachorales 0.00350 1662 0.0222 0.000546   
## 15 Pleosporales 0.0000400 554 0.000942 0.0000400  
## 16 Pleurotheciales 0.000443 1108 0.0136 0.000409   
## 17 Sordariales 0.0543 73682 1.56 0.00573   
## 18 Trichosphaeriales 0.158 1108 0.609 0.0183   
## 19 Xylariales 0.0181 40442 0.417 0.00208   
## 20 <NA> 0.0248 36564 0.735 0.00384

We could also use the arrange() function to quickly sort our resultant data by a specific column

# arrange from least to most  
microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent),   
 n = n(),   
 sd.dev = sd(Percent)) %>%  
 mutate(std.err = sd.dev/sqrt(n)) %>%  
 arrange(Mean)

## # A tibble: 20 × 5  
## Order Mean n sd.dev std.err  
## <chr> <dbl> <int> <dbl> <dbl>  
## 1 Pleosporales 0.0000400 554 0.000942 0.0000400  
## 2 Pleurotheciales 0.000443 1108 0.0136 0.000409   
## 3 Ophiostomatales 0.000563 1662 0.0133 0.000325   
## 4 Phyllachorales 0.00350 1662 0.0222 0.000546   
## 5 Glomerellales 0.00400 12742 0.0920 0.000815   
## 6 Myrmecridiales 0.00562 3324 0.0722 0.00125   
## 7 Coniochaetales 0.00747 16620 0.375 0.00291   
## 8 Conioscyphales 0.00936 2770 0.257 0.00489   
## 9 Xylariales 0.0181 40442 0.417 0.00208   
## 10 Hypocreales 0.0210 119110 0.524 0.00152   
## 11 Chaetosphaeriales 0.0241 7756 0.445 0.00505   
## 12 <NA> 0.0248 36564 0.735 0.00384   
## 13 Diaporthales 0.0293 40996 0.715 0.00353   
## 14 Branch06 0.0295 6094 0.477 0.00611   
## 15 Melanosporales 0.0339 1108 0.637 0.0191   
## 16 Magnaporthales 0.0348 8864 0.808 0.00859   
## 17 Phomatosporales 0.0379 554 0.549 0.0233   
## 18 Microascales 0.0435 5540 1.19 0.0160   
## 19 Sordariales 0.0543 73682 1.56 0.00573   
## 20 Trichosphaeriales 0.158 1108 0.609 0.0183

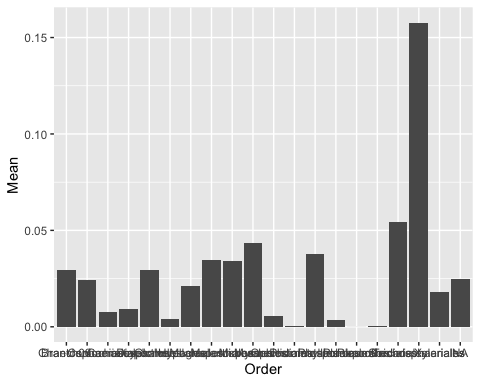
# arrange from most to least  
microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent),   
 n = n(),   
 sd.dev = sd(Percent)) %>%  
 mutate(std.err = sd.dev/sqrt(n)) %>%  
 arrange(-Mean)

## # A tibble: 20 × 5  
## Order Mean n sd.dev std.err  
## <chr> <dbl> <int> <dbl> <dbl>  
## 1 Trichosphaeriales 0.158 1108 0.609 0.0183   
## 2 Sordariales 0.0543 73682 1.56 0.00573   
## 3 Microascales 0.0435 5540 1.19 0.0160   
## 4 Phomatosporales 0.0379 554 0.549 0.0233   
## 5 Magnaporthales 0.0348 8864 0.808 0.00859   
## 6 Melanosporales 0.0339 1108 0.637 0.0191   
## 7 Branch06 0.0295 6094 0.477 0.00611   
## 8 Diaporthales 0.0293 40996 0.715 0.00353   
## 9 <NA> 0.0248 36564 0.735 0.00384   
## 10 Chaetosphaeriales 0.0241 7756 0.445 0.00505   
## 11 Hypocreales 0.0210 119110 0.524 0.00152   
## 12 Xylariales 0.0181 40442 0.417 0.00208   
## 13 Conioscyphales 0.00936 2770 0.257 0.00489   
## 14 Coniochaetales 0.00747 16620 0.375 0.00291   
## 15 Myrmecridiales 0.00562 3324 0.0722 0.00125   
## 16 Glomerellales 0.00400 12742 0.0920 0.000815   
## 17 Phyllachorales 0.00350 1662 0.0222 0.000546   
## 18 Ophiostomatales 0.000563 1662 0.0133 0.000325   
## 19 Pleurotheciales 0.000443 1108 0.0136 0.000409   
## 20 Pleosporales 0.0000400 554 0.000942 0.0000400

#### 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 inputing your aesthetics.

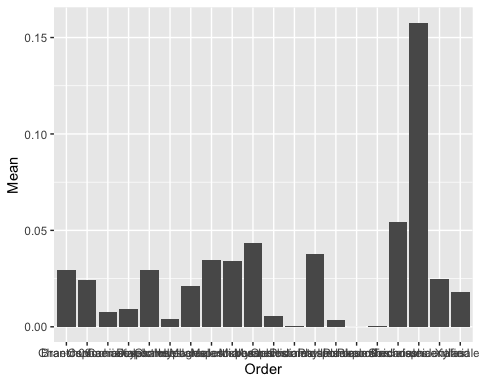
microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent),   
 n = n(),   
 sd.dev = sd(Percent)) %>%  
 mutate(std.err = sd.dev/sqrt(n)) %>%  
 ggplot(aes(x = Order, y = Mean)) +  
 geom\_bar(stat="identity")



#### Dealing with NA values

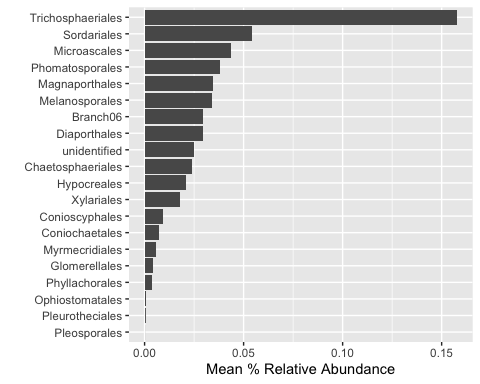
This dataset the NA value means an unidenfied fungus. So for plotting we would want to change that to unidentified. We can deal with NA values nicely within the tidyverse.

microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent),   
 n = n(),   
 sd.dev = sd(Percent)) %>%  
   
 mutate(std.err = sd.dev/sqrt(n)) %>%  
 replace\_na(list(Order = "unidentified")) %>%  
 ggplot(aes(x = Order, y = Mean)) +  
 geom\_bar(stat="identity")



Arrange for ggplot() using fct\_reorder()

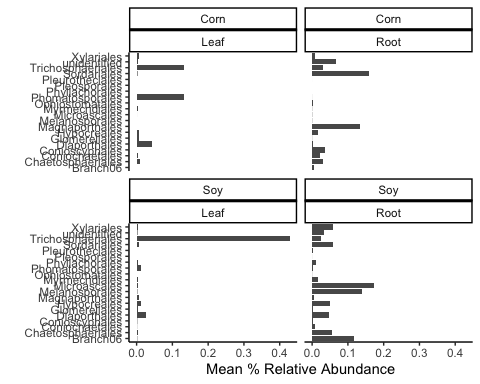
microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent),   
 n = n(),   
 sd.dev = sd(Percent)) %>%  
   
 mutate(std.err = sd.dev/sqrt(n)) %>%  
 replace\_na(list(Order = "unidentified")) %>%  
 mutate(Order2 = fct\_reorder(Order, desc(-Mean))) %>%  
 ggplot(aes(x = Mean, y = Order2)) +  
 geom\_bar(stat="identity") +   
 xlab("Mean % Relative Abundance") +  
 ylab("")



Making it really sofisticated now by separating by crop and compartment and faceting

microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order, Crop, Compartment) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent),   
 n = n(),   
 sd.dev = sd(Percent)) %>%  
 mutate(std.err = sd.dev/sqrt(n)) %>%  
 replace\_na(list(Order = "unidentified")) %>%  
 mutate(Order2 = fct\_reorder(Order, desc(-Mean))) %>%  
 ggplot(aes(x = Mean, y = Order2)) +  
 geom\_bar(stat="identity") +   
 xlab("Mean % Relative Abundance") +  
 ylab("") +   
 facet\_wrap(~Crop\*Compartment) +  
 theme\_classic()

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



#### 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.

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

taxonomy <- microbiome.fungi2 %>%  
 select(OTU, Kingdom:Taxonomy) %>%  
 sample\_n(size = 100)  
  
metadata <- microbiome.fungi2 %>%   
 select(OTU:Fungicide) %>%  
 sample\_n(size = 100)  
  
left\_join(taxonomy, metadata, by = "OTU") # notice the NAs in the metadata since some OTUs did not appear in the random sample.

## OTU Kingdom Phylum Class Order  
## 1 FOTU\_520 Fungi Ascomycota Leotiomycetes Helotiales  
## 2 FOTU\_279 Fungi Ascomycota Sordariomycetes Hypocreales  
## 3 FOTU\_3660 Fungi Ascomycota Eurotiomycetes Chaetothyriales  
## 4 FOTU\_1090 Fungi Ascomycota Dothideomycetes <NA>  
## 5 FOTU\_1088 Fungi Ascomycota Dothideomycetes Pleosporales  
## 6 FOTU\_6502 Fungi Ascomycota Dothideomycetes Pleosporales  
## 7 FOTU\_303 Fungi Ascomycota Dothideomycetes Capnodiales  
## 8 FOTU\_3982 Fungi Ascomycota Leotiomycetes Thelebolales  
## 9 FOTU\_4045 Fungi Ascomycota Dothideomycetes Pleosporales  
## 10 FOTU\_1361 Fungi Ascomycota <NA> <NA>  
## 11 FOTU\_128 Fungi Ascomycota Dothideomycetes Pleosporales  
## 12 FOTU\_4153 Fungi Ascomycota <NA> <NA>  
## 13 FOTU\_1586 Fungi Ascomycota Sordariomycetes Hypocreales  
## 14 FOTU\_1668 Fungi Ascomycota Dothideomycetes Capnodiales  
## 15 FOTU\_1390 Fungi Ascomycota Sordariomycetes Hypocreales  
## 16 FOTU\_4050 Fungi Ascomycota Saccharomycetes Saccharomycetales  
## 17 FOTU\_2532 Fungi Ascomycota <NA> <NA>  
## 18 FOTU\_189 Fungi Ascomycota Leotiomycetes Helotiales  
## 19 FOTU\_1446 Fungi Ascomycota Sordariomycetes <NA>  
## 20 FOTU\_5990 Fungi Ascomycota Dothideomycetes Pleosporales  
## 21 FOTU\_3307 Fungi Ascomycota Dothideomycetes Pleosporales  
## 22 FOTU\_4929 Fungi Ascomycota Sordariomycetes Hypocreales  
## 23 FOTU\_6048 Fungi Ascomycota Dothideomycetes Pleosporales  
## 24 FOTU\_6801 Fungi Ascomycota Sordariomycetes Sordariales  
## 25 FOTU\_1832 Fungi Ascomycota <NA> <NA>  
## 26 FOTU\_6838 Fungi Ascomycota Dothideomycetes Pleosporales  
## 27 FOTU\_5626 Fungi Ascomycota Dothideomycetes Capnodiales  
## 28 FOTU\_6645 Fungi Ascomycota Sordariomycetes Hypocreales  
## 29 FOTU\_5321 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 30 FOTU\_5621 Fungi Ascomycota Sordariomycetes Sordariales  
## 31 FOTU\_1118 Fungi Ascomycota Sordariomycetes Glomerellales  
## 32 FOTU\_3692 Fungi Ascomycota Dothideomycetes Pleosporales  
## 33 FOTU\_7139 Fungi Ascomycota Dothideomycetes Pleosporales  
## 34 FOTU\_320 Fungi Ascomycota Dothideomycetes Pleosporales  
## 35 FOTU\_450 Fungi Ascomycota Sordariomycetes Coniochaetales  
## 36 FOTU\_1584 Fungi Ascomycota Sordariomycetes Xylariales  
## 37 FOTU\_3439 Fungi Ascomycota Sordariomycetes Sordariales  
## 38 FOTU\_3407 Fungi Ascomycota Leotiomycetes Helotiales  
## 39 FOTU\_3331 Fungi Ascomycota Dothideomycetes Pleosporales  
## 40 FOTU\_248 Fungi Ascomycota Sordariomycetes Sordariales  
## 41 FOTU\_1332 Fungi Ascomycota Dothideomycetes Pleosporales  
## 42 FOTU\_6132 Fungi Ascomycota Dothideomycetes Pleosporales  
## 43 FOTU\_3787 Fungi Ascomycota Dothideomycetes Pleosporales  
## 44 FOTU\_456 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 45 FOTU\_5428 Fungi Ascomycota <NA> <NA>  
## 46 FOTU\_2440 Fungi Ascomycota Leotiomycetes Helotiales  
## 47 FOTU\_3733 Fungi Ascomycota Orbiliomycetes Orbiliales  
## 48 FOTU\_1083 Fungi Ascomycota Taphrinomycetes Taphrinales  
## 49 FOTU\_2594 Fungi Ascomycota Dothideomycetes <NA>  
## 50 FOTU\_234 Fungi Ascomycota Sordariomycetes Branch06  
## 51 FOTU\_524 Fungi Ascomycota Dothideomycetes Capnodiales  
## 52 FOTU\_268 Fungi Ascomycota Sordariomycetes Hypocreales  
## 53 FOTU\_4039 Fungi Ascomycota Sordariomycetes <NA>  
## 54 FOTU\_143 Fungi Ascomycota Sordariomycetes <NA>  
## 55 FOTU\_1607 Fungi Ascomycota Sordariomycetes Sordariales  
## 56 FOTU\_5888 Fungi Ascomycota Dothideomycetes Pleosporales  
## 57 FOTU\_3480 Fungi Ascomycota Dothideomycetes <NA>  
## 58 FOTU\_5802 Fungi Ascomycota Leotiomycetes Helotiales  
## 59 FOTU\_5647 Fungi Ascomycota Sordariomycetes Hypocreales  
## 60 FOTU\_5429 Fungi Ascomycota Dothideomycetes Pleosporales  
## 61 FOTU\_5543 Fungi Ascomycota Dothideomycetes Pleosporales  
## 62 FOTU\_3201 Fungi Ascomycota Dothideomycetes Pleosporales  
## 63 FOTU\_3097 Fungi Ascomycota <NA> <NA>  
## 64 FOTU\_6780 Fungi Ascomycota Sordariomycetes Magnaporthales  
## 65 FOTU\_5988 Fungi Ascomycota Dothideomycetes Pleosporales  
## 66 FOTU\_2011 Fungi Ascomycota Dothideomycetes Pleosporales  
## 67 FOTU\_1688 Fungi Ascomycota Sordariomycetes Diaporthales  
## 68 FOTU\_4682 Fungi Ascomycota <NA> <NA>  
## 69 FOTU\_5583 Fungi Ascomycota Sordariomycetes Pleosporales  
## 70 FOTU\_6834 Fungi Ascomycota Dothideomycetes Pleosporales  
## 71 FOTU\_4258 Fungi Ascomycota Dothideomycetes Pleosporales  
## 72 FOTU\_596 Fungi Ascomycota Sordariomycetes Hypocreales  
## 73 FOTU\_2979 Fungi Ascomycota Dothideomycetes Pleosporales  
## 74 FOTU\_1407 Fungi Ascomycota Sordariomycetes Sordariales  
## 75 FOTU\_4386 Fungi Ascomycota Sordariomycetes Hypocreales  
## 76 FOTU\_522 Fungi Ascomycota Sordariomycetes Xylariales  
## 77 FOTU\_531 Fungi Ascomycota Dothideomycetes <NA>  
## 78 FOTU\_3086 Fungi Ascomycota Sordariomycetes Diaporthales  
## 79 FOTU\_895 Fungi Ascomycota Leotiomycetes Helotiales  
## 80 FOTU\_3849 Fungi Ascomycota Sordariomycetes Ophiostomatales  
## 81 FOTU\_504 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 82 FOTU\_2530 Fungi Ascomycota Dothideomycetes <NA>  
## 83 FOTU\_1441 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 84 FOTU\_4944 Fungi Ascomycota Dothideomycetes Capnodiales  
## 85 FOTU\_5302 Fungi Ascomycota Saccharomycetes Saccharomycetales  
## 86 FOTU\_3115 Fungi Ascomycota Dothideomycetes Pleosporales  
## 87 FOTU\_561 Fungi Ascomycota Sordariomycetes Myrmecridiales  
## 88 FOTU\_6721 Fungi Ascomycota Sordariomycetes <NA>  
## 89 FOTU\_1568 Fungi Ascomycota Sordariomycetes <NA>  
## 90 FOTU\_11 Fungi Ascomycota Leotiomycetes Helotiales  
## 91 FOTU\_4725 Fungi Ascomycota Dothideomycetes Capnodiales  
## 92 FOTU\_5773 Fungi Ascomycota Laboulbeniomycetes Pyxidiophorales  
## 93 FOTU\_979 Fungi Ascomycota Leotiomycetes Helotiales  
## 94 FOTU\_1508 Fungi Ascomycota Sordariomycetes Hypocreales  
## 95 FOTU\_256 Fungi Ascomycota Sordariomycetes Diaporthales  
## 96 FOTU\_6732 Fungi Ascomycota Dothideomycetes Pleosporales  
## 97 FOTU\_2359 Fungi Ascomycota Dothideomycetes Pleosporales  
## 98 FOTU\_242 Fungi Ascomycota Leotiomycetes Helotiales  
## 99 FOTU\_4945 Fungi Ascomycota Leotiomycetes Erysiphales  
## 100 FOTU\_4971 Fungi Ascomycota Dothideomycetes Pleosporales  
## Family Genus Species  
## 1 Sclerotiniaceae Clarireedia Clarireedia sp.  
## 2 <NA> <NA> <NA>  
## 3 Herpotrichiellaceae Rhinocladiella Rhinocladiella sp.  
## 4 <NA> <NA> <NA>  
## 5 <NA> <NA> <NA>  
## 6 <NA> <NA> <NA>  
## 7 Dissoconiaceae Dissoconium Dissoconium sp.  
## 8 Pseudeurotiaceae Hyphozyma Hyphozyma sp.  
## 9 <NA> <NA> <NA>  
## 10 <NA> <NA> <NA>  
## 11 <NA> <NA> <NA>  
## 12 <NA> <NA> <NA>  
## 13 Ophiocordycipitaceae <NA> <NA>  
## 14 Mycosphaerellaceae Mycosphaerella Mycosphaerella sp.  
## 15 <NA> <NA> <NA>  
## 16 <NA> <NA> <NA>  
## 17 <NA> <NA> <NA>  
## 18 <NA> <NA> <NA>  
## 19 <NA> <NA> <NA>  
## 20 <NA> <NA> <NA>  
## 21 <NA> <NA> <NA>  
## 22 Bionectriaceae <NA> <NA>  
## 23 Didymellaceae <NA> <NA>  
## 24 Lasiosphaeriaceae Cladorrhinum Cladorrhinum sp.  
## 25 <NA> <NA> <NA>  
## 26 <NA> <NA> <NA>  
## 27 Mycosphaerellaceae Ramularia Ramularia sp.  
## 28 <NA> <NA> <NA>  
## 29 <NA> <NA> <NA>  
## 30 <NA> <NA> <NA>  
## 31 Glomerellaceae Colletotrichum Colletotrichum sp.  
## 32 Massariaceae Massaria Massaria sp.  
## 33 <NA> <NA> <NA>  
## 34 Amorosiaceae Angustimassarina Angustimassarina sp.  
## 35 Coniochaetaceae Lecythophora Lecythophora sp.  
## 36 Xylariaceae Hypoxylon Hypoxylon sp.  
## 37 Chaetomiaceae <NA> <NA>  
## 38 Helotiaceae <NA> <NA>  
## 39 Massarinaceae <NA> <NA>  
## 40 Lasiosphaeriaceae <NA> <NA>  
## 41 Lentitheciaceae Keissleriella Keissleriella sp.  
## 42 <NA> <NA> <NA>  
## 43 <NA> <NA> <NA>  
## 44 <NA> <NA> <NA>  
## 45 <NA> <NA> <NA>  
## 46 Hyaloscyphaceae Cistella Cistella sp.  
## 47 Orbiliaceae Dactylella Dactylella sp.  
## 48 Protomycetaceae Protomyces Protomyces sp.  
## 49 <NA> <NA> <NA>  
## 50 <NA> <NA> <NA>  
## 51 Dissoconiaceae Dissoconium Dissoconium sp.  
## 52 Hypocreaceae Monocillium Monocillium sp.  
## 53 <NA> <NA> <NA>  
## 54 <NA> <NA> <NA>  
## 55 Lasiosphaeriaceae <NA> <NA>  
## 56 <NA> <NA> <NA>  
## 57 <NA> <NA> <NA>  
## 58 <NA> <NA> <NA>  
## 59 Nectriaceae <NA> <NA>  
## 60 Lophiostomataceae <NA> <NA>  
## 61 <NA> <NA> <NA>  
## 62 <NA> <NA> <NA>  
## 63 <NA> <NA> <NA>  
## 64 Magnaporthaceae Gaeumannomyces Gaeumannomyces sp.  
## 65 <NA> <NA> <NA>  
## 66 <NA> <NA> <NA>  
## 67 Gnomoniaceae Ophiognomonia Ophiognomonia sp.  
## 68 <NA> <NA> <NA>  
## 69 <NA> <NA> <NA>  
## 70 <NA> <NA> <NA>  
## 71 <NA> <NA> <NA>  
## 72 Nectriaceae Fusarium Fusarium sp.  
## 73 Didymosphaeriaceae Paracamarosporium Paracamarosporium sp.  
## 74 <NA> <NA> <NA>  
## 75 Incertae\_sedis Acremonium Acremonium sp.  
## 76 Microdochiaceae Microdochium Microdochium sp.  
## 77 <NA> <NA> <NA>  
## 78 Incertae\_sedis Tubakia Tubakia sp.  
## 79 Helotiaceae Tricladium Tricladium sp.  
## 80 Ophiostomataceae Sporothrix Sporothrix sp.  
## 81 <NA> <NA> <NA>  
## 82 <NA> <NA> <NA>  
## 83 Aspergillaceae Penicillium Penicillium sp.  
## 84 Mycosphaerellaceae Cercospora Cercospora sp.  
## 85 Incertae\_sedis Candida Candida sp.  
## 86 Didymosphaeriaceae <NA> <NA>  
## 87 <NA> <NA> <NA>  
## 88 <NA> <NA> <NA>  
## 89 <NA> <NA> <NA>  
## 90 <NA> <NA> <NA>  
## 91 Mycosphaerellaceae Mycosphaerella Mycosphaerella sp.  
## 92 <NA> <NA> <NA>  
## 93 <NA> <NA> <NA>  
## 94 <NA> <NA> <NA>  
## 95 Valsaceae <NA> <NA>  
## 96 Amniculicolaceae Pseudomassariosphaeria Pseudomassariosphaeria sp.  
## 97 Didymosphaeriaceae Paraconiothyrium Paraconiothyrium sp.  
## 98 <NA> <NA> <NA>  
## 99 Erysiphaceae Pseudoidium Pseudoidium sp.  
## 100 <NA> <NA> <NA>  
## Isolate Isolate\_percent\_id BestMatch  
## 1 <NA> 0.000 Clarireedia sp.  
## 2 <NA> 0.000 Hypocreales  
## 3 <NA> 0.000 Rhinocladiella sp.  
## 4 <NA> 0.000 Dothideomycetes  
## 5 <NA> 0.000 Pleosporales  
## 6 <NA> 0.000 Pleosporales  
## 7 <NA> 0.000 Dissoconium sp.  
## 8 <NA> 0.000 Hyphozyma sp.  
## 9 <NA> 0.000 Pleosporales  
## 10 <NA> 0.000 Ascomycota  
## 11 <NA> 0.000 Pleosporales  
## 12 <NA> 0.000 Ascomycota  
## 13 JL82 76.303 Ophiocordycipitaceae  
## 14 <NA> 0.000 Mycosphaerella sp.  
## 15 JU-16 80.275 Hypocreales  
## 16 <NA> 0.000 Saccharomycetales  
## 17 <NA> 0.000 Ascomycota  
## 18 <NA> 0.000 Helotiales  
## 19 <NA> 0.000 Sordariomycetes  
## 20 <NA> 0.000 Pleosporales  
## 21 <NA> 0.000 Pleosporales  
## 22 Entomortierella\_parvispora 81.592 Bionectriaceae  
## 23 <NA> 0.000 Didymellaceae  
## 24 <NA> 0.000 Cladorrhinum sp.  
## 25 <NA> 0.000 Ascomycota  
## 26 <NA> 0.000 Pleosporales  
## 27 <NA> 0.000 Ramularia sp.  
## 28 <NA> 0.000 Hypocreales  
## 29 <NA> 0.000 Eurotiales  
## 30 <NA> 0.000 Sordariales  
## 31 <NA> 0.000 Colletotrichum sp.  
## 32 <NA> 0.000 Massaria sp.  
## 33 <NA> 0.000 Pleosporales  
## 34 <NA> 0.000 Angustimassarina sp.  
## 35 <NA> 0.000 Lecythophora sp.  
## 36 <NA> 0.000 Hypoxylon sp.  
## 37 <NA> 0.000 Chaetomiaceae  
## 38 <NA> 0.000 Helotiaceae  
## 39 V-MICO2\_3-2\_[len=506] 82.036 Massarinaceae  
## 40 <NA> 0.000 Lasiosphaeriaceae  
## 41 <NA> 0.000 Keissleriella sp.  
## 42 <NA> 0.000 Pleosporales  
## 43 <NA> 0.000 Pleosporales  
## 44 <NA> 0.000 Eurotiales  
## 45 <NA> 0.000 Ascomycota  
## 46 <NA> 0.000 Cistella sp.  
## 47 <NA> 0.000 Dactylella sp.  
## 48 <NA> 0.000 Protomyces sp.  
## 49 <NA> 0.000 Dothideomycetes  
## 50 <NA> 0.000 Branch06  
## 51 <NA> 0.000 Dissoconium sp.  
## 52 ABAK\_15 78.607 Monocillium sp.  
## 53 <NA> 0.000 Sordariomycetes  
## 54 <NA> 0.000 Sordariomycetes  
## 55 <NA> 0.000 Lasiosphaeriaceae  
## 56 <NA> 0.000 Pleosporales  
## 57 <NA> 0.000 Dothideomycetes  
## 58 <NA> 0.000 Helotiales  
## 59 Mortierella\_polycephala 91.542 Nectriaceae  
## 60 <NA> 0.000 Lophiostomataceae  
## 61 <NA> 0.000 Pleosporales  
## 62 <NA> 0.000 Pleosporales  
## 63 <NA> 0.000 Ascomycota  
## 64 <NA> 0.000 Gaeumannomyces sp.  
## 65 <NA> 0.000 Pleosporales  
## 66 <NA> 0.000 Pleosporales  
## 67 <NA> 0.000 Ophiognomonia sp.  
## 68 <NA> 0.000 Ascomycota  
## 69 <NA> 0.000 Pleosporales  
## 70 <NA> 0.000 Pleosporales  
## 71 <NA> 0.000 Pleosporales  
## 72 NVP27 91.038 Fusarium sp.  
## 73 <NA> 0.000 Paracamarosporium sp.  
## 74 <NA> 0.000 Sordariales  
## 75 C-ILSO2\_4-19\_[len=514] 86.634 Acremonium sp.  
## 76 <NA> 0.000 Microdochium sp.  
## 77 <NA> 0.000 Dothideomycetes  
## 78 <NA> 0.000 Tubakia sp.  
## 79 <NA> 0.000 Tricladium sp.  
## 80 <NA> 0.000 Sporothrix sp.  
## 81 <NA> 0.000 Eurotiales  
## 82 <NA> 0.000 Dothideomycetes  
## 83 Mortierella\_alpina 91.133 Penicillium sp.  
## 84 <NA> 0.000 Cercospora sp.  
## 85 <NA> 0.000 Candida sp.  
## 86 <NA> 0.000 Didymosphaeriaceae  
## 87 <NA> 0.000 Myrmecridiales  
## 88 <NA> 0.000 Sordariomycetes  
## 89 <NA> 0.000 Sordariomycetes  
## 90 <NA> 0.000 Helotiales  
## 91 <NA> 0.000 Mycosphaerella sp.  
## 92 <NA> 0.000 Pyxidiophorales  
## 93 <NA> 0.000 Helotiales  
## 94 JU-16 80.275 Hypocreales  
## 95 <NA> 0.000 Valsaceae  
## 96 <NA> 0.000 Pseudomassariosphaeria sp.  
## 97 <NA> 0.000 Paraconiothyrium sp.  
## 98 <NA> 0.000 Helotiales  
## 99 <NA> 0.000 Pseudoidium sp.  
## 100 V-MICO2\_3-2\_[len=506] 86.792 Pleosporales  
## Taxonomy  
## 1 FOTU\_520-Clarireedia sp.  
## 2 FOTU\_279-Hypocreales  
## 3 FOTU\_3660-Rhinocladiella sp.  
## 4 FOTU\_1090-Dothideomycetes  
## 5 FOTU\_1088-Pleosporales  
## 6 FOTU\_6502-Pleosporales  
## 7 FOTU\_303-Dissoconium sp.  
## 8 FOTU\_3982-Hyphozyma sp.  
## 9 FOTU\_4045-Pleosporales  
## 10 FOTU\_1361-Ascomycota  
## 11 FOTU\_128-Pleosporales  
## 12 FOTU\_4153-Ascomycota  
## 13 FOTU\_1586-Ophiocordycipitaceae  
## 14 FOTU\_1668-Mycosphaerella sp.  
## 15 FOTU\_1390-Hypocreales  
## 16 FOTU\_4050-Saccharomycetales  
## 17 FOTU\_2532-Ascomycota  
## 18 FOTU\_189-Helotiales  
## 19 FOTU\_1446-Sordariomycetes  
## 20 FOTU\_5990-Pleosporales  
## 21 FOTU\_3307-Pleosporales  
## 22 FOTU\_4929-Bionectriaceae  
## 23 FOTU\_6048-Didymellaceae  
## 24 FOTU\_6801-Cladorrhinum sp.  
## 25 FOTU\_1832-Ascomycota  
## 26 FOTU\_6838-Pleosporales  
## 27 FOTU\_5626-Ramularia sp.  
## 28 FOTU\_6645-Hypocreales  
## 29 FOTU\_5321-Eurotiales  
## 30 FOTU\_5621-Sordariales  
## 31 FOTU\_1118-Colletotrichum sp.  
## 32 FOTU\_3692-Massaria sp.  
## 33 FOTU\_7139-Pleosporales  
## 34 FOTU\_320-Angustimassarina sp.  
## 35 FOTU\_450-Lecythophora sp.  
## 36 FOTU\_1584-Hypoxylon sp.  
## 37 FOTU\_3439-Chaetomiaceae  
## 38 FOTU\_3407-Helotiaceae  
## 39 FOTU\_3331-Massarinaceae  
## 40 FOTU\_248-Lasiosphaeriaceae  
## 41 FOTU\_1332-Keissleriella sp.  
## 42 FOTU\_6132-Pleosporales  
## 43 FOTU\_3787-Pleosporales  
## 44 FOTU\_456-Eurotiales  
## 45 FOTU\_5428-Ascomycota  
## 46 FOTU\_2440-Cistella sp.  
## 47 FOTU\_3733-Dactylella sp.  
## 48 FOTU\_1083-Protomyces sp.  
## 49 FOTU\_2594-Dothideomycetes  
## 50 FOTU\_234-Branch06  
## 51 FOTU\_524-Dissoconium sp.  
## 52 FOTU\_268-Monocillium sp.  
## 53 FOTU\_4039-Sordariomycetes  
## 54 FOTU\_143-Sordariomycetes  
## 55 FOTU\_1607-Lasiosphaeriaceae  
## 56 FOTU\_5888-Pleosporales  
## 57 FOTU\_3480-Dothideomycetes  
## 58 FOTU\_5802-Helotiales  
## 59 FOTU\_5647-Nectriaceae  
## 60 FOTU\_5429-Lophiostomataceae  
## 61 FOTU\_5543-Pleosporales  
## 62 FOTU\_3201-Pleosporales  
## 63 FOTU\_3097-Ascomycota  
## 64 FOTU\_6780-Gaeumannomyces sp.  
## 65 FOTU\_5988-Pleosporales  
## 66 FOTU\_2011-Pleosporales  
## 67 FOTU\_1688-Ophiognomonia sp.  
## 68 FOTU\_4682-Ascomycota  
## 69 FOTU\_5583-Pleosporales  
## 70 FOTU\_6834-Pleosporales  
## 71 FOTU\_4258-Pleosporales  
## 72 FOTU\_596-Fusarium sp.  
## 73 FOTU\_2979-Paracamarosporium sp.  
## 74 FOTU\_1407-Sordariales  
## 75 FOTU\_4386-Acremonium sp.  
## 76 FOTU\_522-Microdochium sp.  
## 77 FOTU\_531-Dothideomycetes  
## 78 FOTU\_3086-Tubakia sp.  
## 79 FOTU\_895-Tricladium sp.  
## 80 FOTU\_3849-Sporothrix sp.  
## 81 FOTU\_504-Eurotiales  
## 82 FOTU\_2530-Dothideomycetes  
## 83 FOTU\_1441-Penicillium sp.  
## 84 FOTU\_4944-Cercospora sp.  
## 85 FOTU\_5302-Candida sp.  
## 86 FOTU\_3115-Didymosphaeriaceae  
## 87 FOTU\_561-Myrmecridiales  
## 88 FOTU\_6721-Sordariomycetes  
## 89 FOTU\_1568-Sordariomycetes  
## 90 FOTU\_11-Helotiales  
## 91 FOTU\_4725-Mycosphaerella sp.  
## 92 FOTU\_5773-Pyxidiophorales  
## 93 FOTU\_979-Helotiales  
## 94 FOTU\_1508-Hypocreales  
## 95 FOTU\_256-Valsaceae  
## 96 FOTU\_6732-Pseudomassariosphaeria sp.  
## 97 FOTU\_2359-Paraconiothyrium sp.  
## 98 FOTU\_242-Helotiales  
## 99 FOTU\_4945-Pseudoidium sp.  
## 100 FOTU\_4971-Pleosporales  
## SampleID Abundance Crop Compartment  
## 1 <NA> NA <NA> <NA>  
## 2 <NA> NA <NA> <NA>  
## 3 <NA> NA <NA> <NA>  
## 4 Corn2017RootObjective2Collection3T2R1AFG8 0 Corn Root  
## 5 <NA> NA <NA> <NA>  
## 6 <NA> NA <NA> <NA>  
## 7 <NA> NA <NA> <NA>  
## 8 <NA> NA <NA> <NA>  
## 9 <NA> NA <NA> <NA>  
## 10 <NA> NA <NA> <NA>  
## 11 <NA> NA <NA> <NA>  
## 12 <NA> NA <NA> <NA>  
## 13 <NA> NA <NA> <NA>  
## 14 <NA> NA <NA> <NA>  
## 15 <NA> NA <NA> <NA>  
## 16 <NA> NA <NA> <NA>  
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## 80 31-Jul-17 V15 T2 R5 C  
## 81 5-Jul-17 V8 T1 R1 F  
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# to take the common set of both datasets you can use inner\_join()  
inner\_join(taxonomy, metadata, by = "OTU")

## OTU Kingdom Phylum Class Order  
## 1 FOTU\_1090 Fungi Ascomycota Dothideomycetes <NA>  
## 2 FOTU\_320 Fungi Ascomycota Dothideomycetes Pleosporales  
## 3 FOTU\_3849 Fungi Ascomycota Sordariomycetes Ophiostomatales  
## 4 FOTU\_504 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 5 FOTU\_4944 Fungi Ascomycota Dothideomycetes Capnodiales  
## 6 FOTU\_256 Fungi Ascomycota Sordariomycetes Diaporthales  
## Family Genus Species Isolate  
## 1 <NA> <NA> <NA> <NA>  
## 2 Amorosiaceae Angustimassarina Angustimassarina sp. <NA>  
## 3 Ophiostomataceae Sporothrix Sporothrix sp. <NA>  
## 4 <NA> <NA> <NA> <NA>  
## 5 Mycosphaerellaceae Cercospora Cercospora sp. <NA>  
## 6 Valsaceae <NA> <NA> <NA>  
## Isolate\_percent\_id BestMatch Taxonomy  
## 1 0 Dothideomycetes FOTU\_1090-Dothideomycetes  
## 2 0 Angustimassarina sp. FOTU\_320-Angustimassarina sp.  
## 3 0 Sporothrix sp. FOTU\_3849-Sporothrix sp.  
## 4 0 Eurotiales FOTU\_504-Eurotiales  
## 5 0 Cercospora sp. FOTU\_4944-Cercospora sp.  
## 6 0 Valsaceae FOTU\_256-Valsaceae  
## SampleID Abundance Crop Compartment  
## 1 Corn2017RootObjective2Collection3T2R1AFG8 0 Corn Root  
## 2 T1R5CCR6R 0 Soy Root  
## 3 Corn2017LeafObjective2Collection3T2R5CBG7 0 Corn Leaf  
## 4 Corn2017LeafObjective2Collection2T1R1FBA9 0 Corn Leaf  
## 5 T2R6CCR3R 0 Soy Root  
## 6 T1R2CBR6R 0 Soy Root  
## DateSampled GrowthStage Treatment Rep Fungicide  
## 1 31-Jul-17 V15 T2 R1 F  
## 2 27-Aug-18 R6 T1 R5 C  
## 3 31-Jul-17 V15 T2 R5 C  
## 4 5-Jul-17 V8 T1 R1 F  
## 5 3-Aug-18 R3 T2 R6 C  
## 6 27-Aug-18 R6 T1 R2 C

# or full join to keep everything   
full\_join(taxonomy, metadata, by = "OTU")

## OTU Kingdom Phylum Class Order  
## 1 FOTU\_520 Fungi Ascomycota Leotiomycetes Helotiales  
## 2 FOTU\_279 Fungi Ascomycota Sordariomycetes Hypocreales  
## 3 FOTU\_3660 Fungi Ascomycota Eurotiomycetes Chaetothyriales  
## 4 FOTU\_1090 Fungi Ascomycota Dothideomycetes <NA>  
## 5 FOTU\_1088 Fungi Ascomycota Dothideomycetes Pleosporales  
## 6 FOTU\_6502 Fungi Ascomycota Dothideomycetes Pleosporales  
## 7 FOTU\_303 Fungi Ascomycota Dothideomycetes Capnodiales  
## 8 FOTU\_3982 Fungi Ascomycota Leotiomycetes Thelebolales  
## 9 FOTU\_4045 Fungi Ascomycota Dothideomycetes Pleosporales  
## 10 FOTU\_1361 Fungi Ascomycota <NA> <NA>  
## 11 FOTU\_128 Fungi Ascomycota Dothideomycetes Pleosporales  
## 12 FOTU\_4153 Fungi Ascomycota <NA> <NA>  
## 13 FOTU\_1586 Fungi Ascomycota Sordariomycetes Hypocreales  
## 14 FOTU\_1668 Fungi Ascomycota Dothideomycetes Capnodiales  
## 15 FOTU\_1390 Fungi Ascomycota Sordariomycetes Hypocreales  
## 16 FOTU\_4050 Fungi Ascomycota Saccharomycetes Saccharomycetales  
## 17 FOTU\_2532 Fungi Ascomycota <NA> <NA>  
## 18 FOTU\_189 Fungi Ascomycota Leotiomycetes Helotiales  
## 19 FOTU\_1446 Fungi Ascomycota Sordariomycetes <NA>  
## 20 FOTU\_5990 Fungi Ascomycota Dothideomycetes Pleosporales  
## 21 FOTU\_3307 Fungi Ascomycota Dothideomycetes Pleosporales  
## 22 FOTU\_4929 Fungi Ascomycota Sordariomycetes Hypocreales  
## 23 FOTU\_6048 Fungi Ascomycota Dothideomycetes Pleosporales  
## 24 FOTU\_6801 Fungi Ascomycota Sordariomycetes Sordariales  
## 25 FOTU\_1832 Fungi Ascomycota <NA> <NA>  
## 26 FOTU\_6838 Fungi Ascomycota Dothideomycetes Pleosporales  
## 27 FOTU\_5626 Fungi Ascomycota Dothideomycetes Capnodiales  
## 28 FOTU\_6645 Fungi Ascomycota Sordariomycetes Hypocreales  
## 29 FOTU\_5321 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 30 FOTU\_5621 Fungi Ascomycota Sordariomycetes Sordariales  
## 31 FOTU\_1118 Fungi Ascomycota Sordariomycetes Glomerellales  
## 32 FOTU\_3692 Fungi Ascomycota Dothideomycetes Pleosporales  
## 33 FOTU\_7139 Fungi Ascomycota Dothideomycetes Pleosporales  
## 34 FOTU\_320 Fungi Ascomycota Dothideomycetes Pleosporales  
## 35 FOTU\_450 Fungi Ascomycota Sordariomycetes Coniochaetales  
## 36 FOTU\_1584 Fungi Ascomycota Sordariomycetes Xylariales  
## 37 FOTU\_3439 Fungi Ascomycota Sordariomycetes Sordariales  
## 38 FOTU\_3407 Fungi Ascomycota Leotiomycetes Helotiales  
## 39 FOTU\_3331 Fungi Ascomycota Dothideomycetes Pleosporales  
## 40 FOTU\_248 Fungi Ascomycota Sordariomycetes Sordariales  
## 41 FOTU\_1332 Fungi Ascomycota Dothideomycetes Pleosporales  
## 42 FOTU\_6132 Fungi Ascomycota Dothideomycetes Pleosporales  
## 43 FOTU\_3787 Fungi Ascomycota Dothideomycetes Pleosporales  
## 44 FOTU\_456 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 45 FOTU\_5428 Fungi Ascomycota <NA> <NA>  
## 46 FOTU\_2440 Fungi Ascomycota Leotiomycetes Helotiales  
## 47 FOTU\_3733 Fungi Ascomycota Orbiliomycetes Orbiliales  
## 48 FOTU\_1083 Fungi Ascomycota Taphrinomycetes Taphrinales  
## 49 FOTU\_2594 Fungi Ascomycota Dothideomycetes <NA>  
## 50 FOTU\_234 Fungi Ascomycota Sordariomycetes Branch06  
## 51 FOTU\_524 Fungi Ascomycota Dothideomycetes Capnodiales  
## 52 FOTU\_268 Fungi Ascomycota Sordariomycetes Hypocreales  
## 53 FOTU\_4039 Fungi Ascomycota Sordariomycetes <NA>  
## 54 FOTU\_143 Fungi Ascomycota Sordariomycetes <NA>  
## 55 FOTU\_1607 Fungi Ascomycota Sordariomycetes Sordariales  
## 56 FOTU\_5888 Fungi Ascomycota Dothideomycetes Pleosporales  
## 57 FOTU\_3480 Fungi Ascomycota Dothideomycetes <NA>  
## 58 FOTU\_5802 Fungi Ascomycota Leotiomycetes Helotiales  
## 59 FOTU\_5647 Fungi Ascomycota Sordariomycetes Hypocreales  
## 60 FOTU\_5429 Fungi Ascomycota Dothideomycetes Pleosporales  
## 61 FOTU\_5543 Fungi Ascomycota Dothideomycetes Pleosporales  
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## 63 FOTU\_3097 Fungi Ascomycota <NA> <NA>  
## 64 FOTU\_6780 Fungi Ascomycota Sordariomycetes Magnaporthales  
## 65 FOTU\_5988 Fungi Ascomycota Dothideomycetes Pleosporales  
## 66 FOTU\_2011 Fungi Ascomycota Dothideomycetes Pleosporales  
## 67 FOTU\_1688 Fungi Ascomycota Sordariomycetes Diaporthales  
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## 69 FOTU\_5583 Fungi Ascomycota Sordariomycetes Pleosporales  
## 70 FOTU\_6834 Fungi Ascomycota Dothideomycetes Pleosporales  
## 71 FOTU\_4258 Fungi Ascomycota Dothideomycetes Pleosporales  
## 72 FOTU\_596 Fungi Ascomycota Sordariomycetes Hypocreales  
## 73 FOTU\_2979 Fungi Ascomycota Dothideomycetes Pleosporales  
## 74 FOTU\_1407 Fungi Ascomycota Sordariomycetes Sordariales  
## 75 FOTU\_4386 Fungi Ascomycota Sordariomycetes Hypocreales  
## 76 FOTU\_522 Fungi Ascomycota Sordariomycetes Xylariales  
## 77 FOTU\_531 Fungi Ascomycota Dothideomycetes <NA>  
## 78 FOTU\_3086 Fungi Ascomycota Sordariomycetes Diaporthales  
## 79 FOTU\_895 Fungi Ascomycota Leotiomycetes Helotiales  
## 80 FOTU\_3849 Fungi Ascomycota Sordariomycetes Ophiostomatales  
## 81 FOTU\_504 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 82 FOTU\_2530 Fungi Ascomycota Dothideomycetes <NA>  
## 83 FOTU\_1441 Fungi Ascomycota Eurotiomycetes Eurotiales  
## 84 FOTU\_4944 Fungi Ascomycota Dothideomycetes Capnodiales  
## 85 FOTU\_5302 Fungi Ascomycota Saccharomycetes Saccharomycetales  
## 86 FOTU\_3115 Fungi Ascomycota Dothideomycetes Pleosporales  
## 87 FOTU\_561 Fungi Ascomycota Sordariomycetes Myrmecridiales  
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## 90 FOTU\_11 Fungi Ascomycota Leotiomycetes Helotiales  
## 91 FOTU\_4725 Fungi Ascomycota Dothideomycetes Capnodiales  
## 92 FOTU\_5773 Fungi Ascomycota Laboulbeniomycetes Pyxidiophorales  
## 93 FOTU\_979 Fungi Ascomycota Leotiomycetes Helotiales  
## 94 FOTU\_1508 Fungi Ascomycota Sordariomycetes Hypocreales  
## 95 FOTU\_256 Fungi Ascomycota Sordariomycetes Diaporthales  
## 96 FOTU\_6732 Fungi Ascomycota Dothideomycetes Pleosporales  
## 97 FOTU\_2359 Fungi Ascomycota Dothideomycetes Pleosporales  
## 98 FOTU\_242 Fungi Ascomycota Leotiomycetes Helotiales  
## 99 FOTU\_4945 Fungi Ascomycota Leotiomycetes Erysiphales  
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## 27 Mycosphaerellaceae Ramularia Ramularia sp.  
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## 32 Massariaceae Massaria Massaria sp.  
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## 34 Amorosiaceae Angustimassarina Angustimassarina sp.  
## 35 Coniochaetaceae Lecythophora Lecythophora sp.  
## 36 Xylariaceae Hypoxylon Hypoxylon sp.  
## 37 Chaetomiaceae <NA> <NA>  
## 38 Helotiaceae <NA> <NA>  
## 39 Massarinaceae <NA> <NA>  
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## 47 Orbiliaceae Dactylella Dactylella sp.  
## 48 Protomycetaceae Protomyces Protomyces sp.  
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## 75 Incertae\_sedis Acremonium Acremonium sp.  
## 76 Microdochiaceae Microdochium Microdochium sp.  
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## 78 Incertae\_sedis Tubakia Tubakia sp.  
## 79 Helotiaceae Tricladium Tricladium sp.  
## 80 Ophiostomataceae Sporothrix Sporothrix sp.  
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## 84 Mycosphaerellaceae Cercospora Cercospora sp.  
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## 99 Erysiphaceae Pseudoidium Pseudoidium sp.  
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## Taxonomy  
## 1 FOTU\_520-Clarireedia sp.  
## 2 FOTU\_279-Hypocreales  
## 3 FOTU\_3660-Rhinocladiella sp.  
## 4 FOTU\_1090-Dothideomycetes  
## 5 FOTU\_1088-Pleosporales  
## 6 FOTU\_6502-Pleosporales  
## 7 FOTU\_303-Dissoconium sp.  
## 8 FOTU\_3982-Hyphozyma sp.  
## 9 FOTU\_4045-Pleosporales  
## 10 FOTU\_1361-Ascomycota  
## 11 FOTU\_128-Pleosporales  
## 12 FOTU\_4153-Ascomycota  
## 13 FOTU\_1586-Ophiocordycipitaceae  
## 14 FOTU\_1668-Mycosphaerella sp.  
## 15 FOTU\_1390-Hypocreales  
## 16 FOTU\_4050-Saccharomycetales  
## 17 FOTU\_2532-Ascomycota  
## 18 FOTU\_189-Helotiales  
## 19 FOTU\_1446-Sordariomycetes  
## 20 FOTU\_5990-Pleosporales  
## 21 FOTU\_3307-Pleosporales  
## 22 FOTU\_4929-Bionectriaceae  
## 23 FOTU\_6048-Didymellaceae  
## 24 FOTU\_6801-Cladorrhinum sp.  
## 25 FOTU\_1832-Ascomycota  
## 26 FOTU\_6838-Pleosporales  
## 27 FOTU\_5626-Ramularia sp.  
## 28 FOTU\_6645-Hypocreales  
## 29 FOTU\_5321-Eurotiales  
## 30 FOTU\_5621-Sordariales  
## 31 FOTU\_1118-Colletotrichum sp.  
## 32 FOTU\_3692-Massaria sp.  
## 33 FOTU\_7139-Pleosporales  
## 34 FOTU\_320-Angustimassarina sp.  
## 35 FOTU\_450-Lecythophora sp.  
## 36 FOTU\_1584-Hypoxylon sp.  
## 37 FOTU\_3439-Chaetomiaceae  
## 38 FOTU\_3407-Helotiaceae  
## 39 FOTU\_3331-Massarinaceae  
## 40 FOTU\_248-Lasiosphaeriaceae  
## 41 FOTU\_1332-Keissleriella sp.  
## 42 FOTU\_6132-Pleosporales  
## 43 FOTU\_3787-Pleosporales  
## 44 FOTU\_456-Eurotiales  
## 45 FOTU\_5428-Ascomycota  
## 46 FOTU\_2440-Cistella sp.  
## 47 FOTU\_3733-Dactylella sp.  
## 48 FOTU\_1083-Protomyces sp.  
## 49 FOTU\_2594-Dothideomycetes  
## 50 FOTU\_234-Branch06  
## 51 FOTU\_524-Dissoconium sp.  
## 52 FOTU\_268-Monocillium sp.  
## 53 FOTU\_4039-Sordariomycetes  
## 54 FOTU\_143-Sordariomycetes  
## 55 FOTU\_1607-Lasiosphaeriaceae  
## 56 FOTU\_5888-Pleosporales  
## 57 FOTU\_3480-Dothideomycetes  
## 58 FOTU\_5802-Helotiales  
## 59 FOTU\_5647-Nectriaceae  
## 60 FOTU\_5429-Lophiostomataceae  
## 61 FOTU\_5543-Pleosporales  
## 62 FOTU\_3201-Pleosporales  
## 63 FOTU\_3097-Ascomycota  
## 64 FOTU\_6780-Gaeumannomyces sp.  
## 65 FOTU\_5988-Pleosporales  
## 66 FOTU\_2011-Pleosporales  
## 67 FOTU\_1688-Ophiognomonia sp.  
## 68 FOTU\_4682-Ascomycota  
## 69 FOTU\_5583-Pleosporales  
## 70 FOTU\_6834-Pleosporales  
## 71 FOTU\_4258-Pleosporales  
## 72 FOTU\_596-Fusarium sp.  
## 73 FOTU\_2979-Paracamarosporium sp.  
## 74 FOTU\_1407-Sordariales  
## 75 FOTU\_4386-Acremonium sp.  
## 76 FOTU\_522-Microdochium sp.  
## 77 FOTU\_531-Dothideomycetes  
## 78 FOTU\_3086-Tubakia sp.  
## 79 FOTU\_895-Tricladium sp.  
## 80 FOTU\_3849-Sporothrix sp.  
## 81 FOTU\_504-Eurotiales  
## 82 FOTU\_2530-Dothideomycetes  
## 83 FOTU\_1441-Penicillium sp.  
## 84 FOTU\_4944-Cercospora sp.  
## 85 FOTU\_5302-Candida sp.  
## 86 FOTU\_3115-Didymosphaeriaceae  
## 87 FOTU\_561-Myrmecridiales  
## 88 FOTU\_6721-Sordariomycetes  
## 89 FOTU\_1568-Sordariomycetes  
## 90 FOTU\_11-Helotiales  
## 91 FOTU\_4725-Mycosphaerella sp.  
## 92 FOTU\_5773-Pyxidiophorales  
## 93 FOTU\_979-Helotiales  
## 94 FOTU\_1508-Hypocreales  
## 95 FOTU\_256-Valsaceae  
## 96 FOTU\_6732-Pseudomassariosphaeria sp.  
## 97 FOTU\_2359-Paraconiothyrium sp.  
## 98 FOTU\_242-Helotiales  
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## 125 Corn2017LeafObjective2Collection3T1R1CCC3 0.000000e+00 Corn Leaf  
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## 192 31-Jul-17 V15 T2 R1 C  
## 193 3-Aug-18 R3 T2 R5 C  
## 194 31-Jul-17 V15 T1 R6 F

Now this is kind of a silly example because we already had the dataset joined how we wanted it and split it appart. But you can immagine if you have two separate datasets 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>

I will demonstrate pivot\_wider() assuming that most data is already formatted as long data. Lets explore turning our dataset into a wide format, since its in long format.

microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order, Crop, Compartment, Fungicide) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent)) %>%  
 replace\_na(list(Order = "unidentified")) %>%  
 pivot\_wider(names\_from = Fungicide, values\_from = Mean) %>%  
 head()

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

## # A tibble: 6 × 5  
## # Groups: Order, Crop, Compartment [6]  
## Order Crop Compartment C F  
## <chr> <chr> <chr> <dbl> <dbl>  
## 1 Branch06 Corn Leaf 0 0   
## 2 Branch06 Corn Root 0.00368 0.00423  
## 3 Branch06 Soy Leaf 0.000744 0.00103  
## 4 Branch06 Soy Root 0.0717 0.166   
## 5 Chaetosphaeriales Corn Leaf 0.0109 0.00856  
## 6 Chaetosphaeriales Corn Root 0.0500 0.0111

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

microbiome.fungi %>%  
 select(OTU, SampleID, Abundance, Crop, Compartment, DateSampled, GrowthStage, Treatment, Rep, Fungicide, Kingdom:Taxonomy) %>%  
 filter(Class == "Sordariomycetes") %>%  
 group\_by(Order, Crop, Compartment, Fungicide) %>%  
 mutate(Percent = Abundance\*100) %>%  
 summarise(Mean = mean(Percent)) %>%  
 replace\_na(list(Order = "unidentified")) %>%  
 pivot\_wider(names\_from = Fungicide, values\_from = Mean, values\_fill = 0) %>%  
 mutate(diff = C - F) %>%  
 ggplot(aes(y = Order, x = diff)) +  
 geom\_point() +  
 facet\_wrap(~Crop\*Compartment)

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

