Funciones automatizadas para visualizar las barras de abundancia, diversidades alfa y beta; a diferentes niveles taxonomicos

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```
library("phyloseq")
library("ggplot2")
library("vegan")
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.6-4
```

```
library("RColorBrewer")
library("stringi")
```

Cargado de datos originales

```
setwd("/home/camila/GIT/Tesis_Maestria/Data/fresa_solena/Data1")
outpath = "/home/camila/GIT/Tesis_Maestria/Analisis_Comparativo/Fresa_Solena/Results_img"

fresa_kraken <- import_biom("fresa_kraken.biom")
colnames(fresa_kraken@tax_table@.Data) <- c("Kingdom", "Phylum", "Class", "Order", "Family", "Genus", "S
fresa_kraken@tax_table@.Data <- substr(fresa_kraken@tax_table@.Data,4,100)
colnames(fresa_kraken@otu_table@.Data) <- substr(colnames(fresa_kraken@otu_table@.Data),1,6)
metadata_fresa <- read.csv2("/home/camila/GIT/Tesis_Maestria/Data/fresa_solena/Data1/metadata.csv",head
fresa_kraken@sam_data <- sample_data(metadata_fresa)
fresa_kraken@sam_data$Sample<-row.names(fresa_kraken@sam_data)
colnames(fresa_kraken@sam_data)<-c('Treatment','Samples')
samples_to_remove <- c("MP2079","MP2080","MP2088","MP2109","MP2137")
fresa_kraken_fil <- prune_samples(!(sample_names(fresa_kraken) %in% samples_to_remove), fresa_kraken)
```

Subconjunto de "Eukaryota"

```
merge_Eukaryota<-subset_taxa(fresa_kraken_fil,Kingdom=="Eukaryota")
```

Subconjunto de "Bacteria"

```
merge_Bacteria<-subset_taxa(fresa_kraken_fil,Kingdom=="Bacteria")
```

Funciones

glomToGraph

Crea los subconjuntos de datos necesarios para más adelante

input phy <- es el objeto phyloseq base tax <- rango taxonomico al que queremos recortar output glom <- objeto phyloseq ya recortado percentages <- objeto phyloseq de porcentages sobre el glom percentages_df <- data frame de porcentages sobre el glom

```
glomToGraph<-function(phy,tax){
  ## creamos el subconjunto dependiendo del linaje taxonomico deseado
  glom <- tax_glom(phy, taxrank = tax)
  ## sacamos los porcentajes
  percentages <- transform_sample_counts(glom, function(x) x*100 / sum(x) )
  percentages_df <- psmelt(percentages)
  return(list(glom,percentages,percentages_df))
}
```

Graficar abundancias (stackbar)

```
Abundance_barras <- function(phy,tax,attribute,abundance_percentage){
  ##llamar funcion de datos
  Data <- glomToGraph(phy,tax)
  glom <- Data[[1]] #phyloseq
  percentages <- Data[[2]] #phyloseq
  percentages_df <- Data[[3]] # dataframe
  ## Graficamos para cada subconjunto las barras de abundancia
  plot_barras <- ggplot(data=percentages_df, aes_string(x='Sample', y='Abundance', fill=tax ,color=attri
    scale_colour_manual(values=c('white','black')) +
    geom_bar(aes(), stat="identity", position="stack") +
    labs(title = "Abundance", x='Sample', y='Abundance', color = tax) +
    theme(legend.key.size = unit(0.2, "cm"),
          legend.key.width = unit(0.25,"cm"),
          legend.position = "bottom",
          legend.direction = "horizontal",
          legend.title=element_text(size=8, face = "bold"),
          legend.text=element_text(size=6),
          text = element_text(size=12),
          axis.text.x = element_text(angle=90, size=5, hjust=1, vjust=0.5))
  percentages_df$tax<-percentages_df[,ncol(percentages_df)]
  percentages_df$tax[percentages_df$Abundance < abundance_percentage] <- "Others"
  percentages_df$tax <- as.factor(percentages_df$tax)
  plot_percentages <- ggplot(data=percentages_df, aes_string(x='Sample', y='Abundance', fill='tax' ,col
    scale_colour_manual(values=c('white','black')) +
```

```
    geom_bar(aes(), stat="identity", position="stack") +
    labs(title = "Abundance", x='Sample', y='Abundance', color = tax) +
    theme(legend.key.size = unit(0.3, "cm"),
          legend.key.width = unit(0.5,"cm"),
          legend.position = "bottom",
          legend.direction = "horizontal",
          legend.title=element_text(size=10, face = "bold"),
          legend.text=element_text(size=8),
          text = element_text(size=12),
          axis.text.x = element_text(angle=90, size=5, hjust=1, vjust=0.5))
  return(list(plot_barras,plot_percentages))
}
```

Graficar diversidad beta

```
Beta_diversity <- function(phy,tax,attribute,distance){
  Data <- glomToGraph(phy,tax)
  glom <- Data[[1]]
  #CREAR UN GLOM AL 10%
  percentages <- Data[[2]]
  percentages_df <- Data[[3]]
  ## Beta diversidad
  meta_ord <- ordinate(physeq = percentages, method = "NMDS", distance = distance)
  plot_beta <- plot_ordination(physeq = percentages, ordination = meta_ord, color = attribute) +
    geom_text(mapping = aes(label = colnames(phy@otu_table@.Data)), size = 3, vjust = 1.5)
  return(plot_beta)
}
```

Graficar diversidad alfa

```
Alpha_diversity <- function(phy,tax,attribute){
  ## llamamos la funcion que crea los dataset
  Data <- glomToGraph(phy,tax)
  glom <- Data[[1]]

  percentages <- Data[[2]]
  percentages_df <- Data[[3]]
  ## Alfa diversidad
  plot_alpha <- plot_richness(physeq = glom, measures = c("Observed","Chao1","Shannon","simpson"),x = a
  return(plot_alpha)
}
```

Graficas

Graficamos las barras de abundancia, las barras de abundancia aglomerando el 10% menos abundantes, alfa y beta diversidad para los siguientes niveles taxonomicos.

##———Eukarya by Phylum

```
Barras_Phylum <- Abundance_barras(merge_Eukaryota,'Phylum' , 'Treatment', 10.0)
```

```
## Warning: 'aes_string()' was deprecated in ggplot2 3.0.0.
## i Please use tidy evaluation idioms with 'aes()'.
## i See also 'vignette("ggplot2-in-packages")' for more information.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```
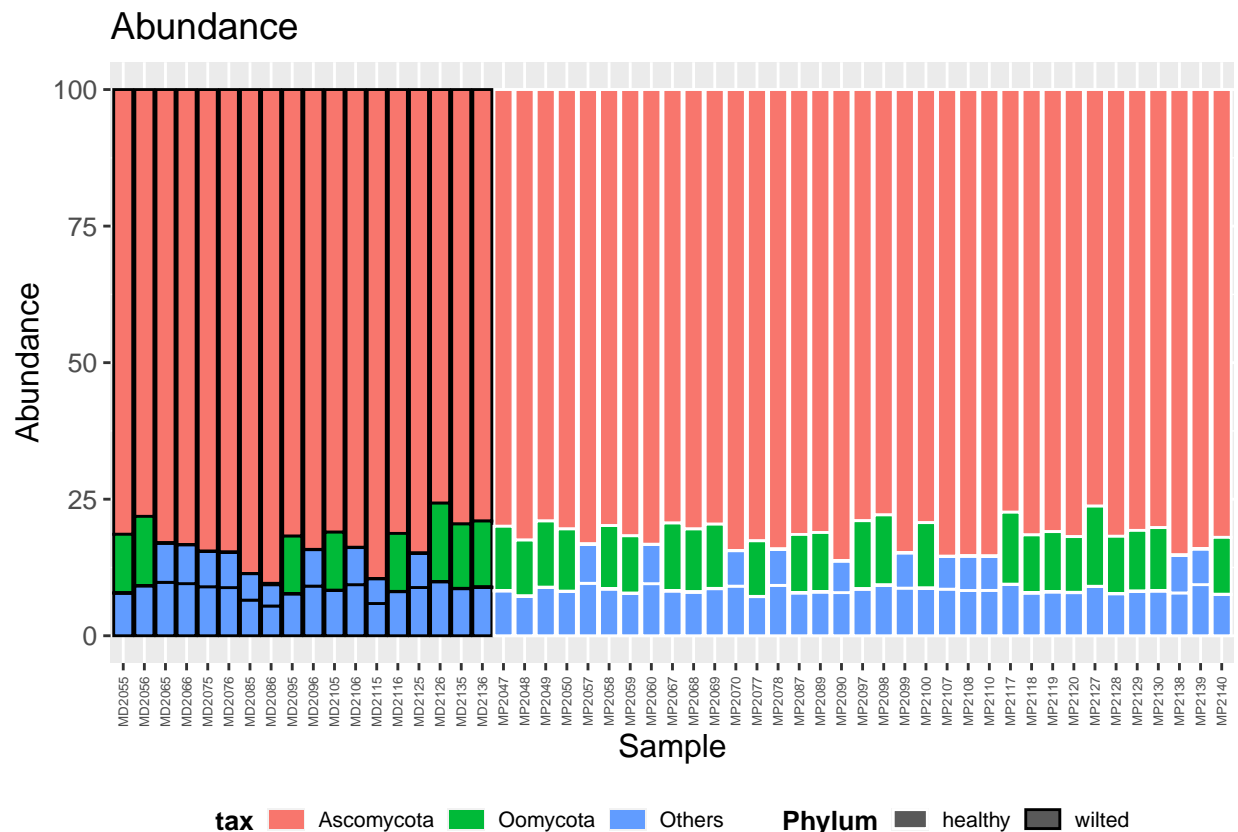
```
Barras_Phylum[1] # normal
```

```
## [[1]]
```
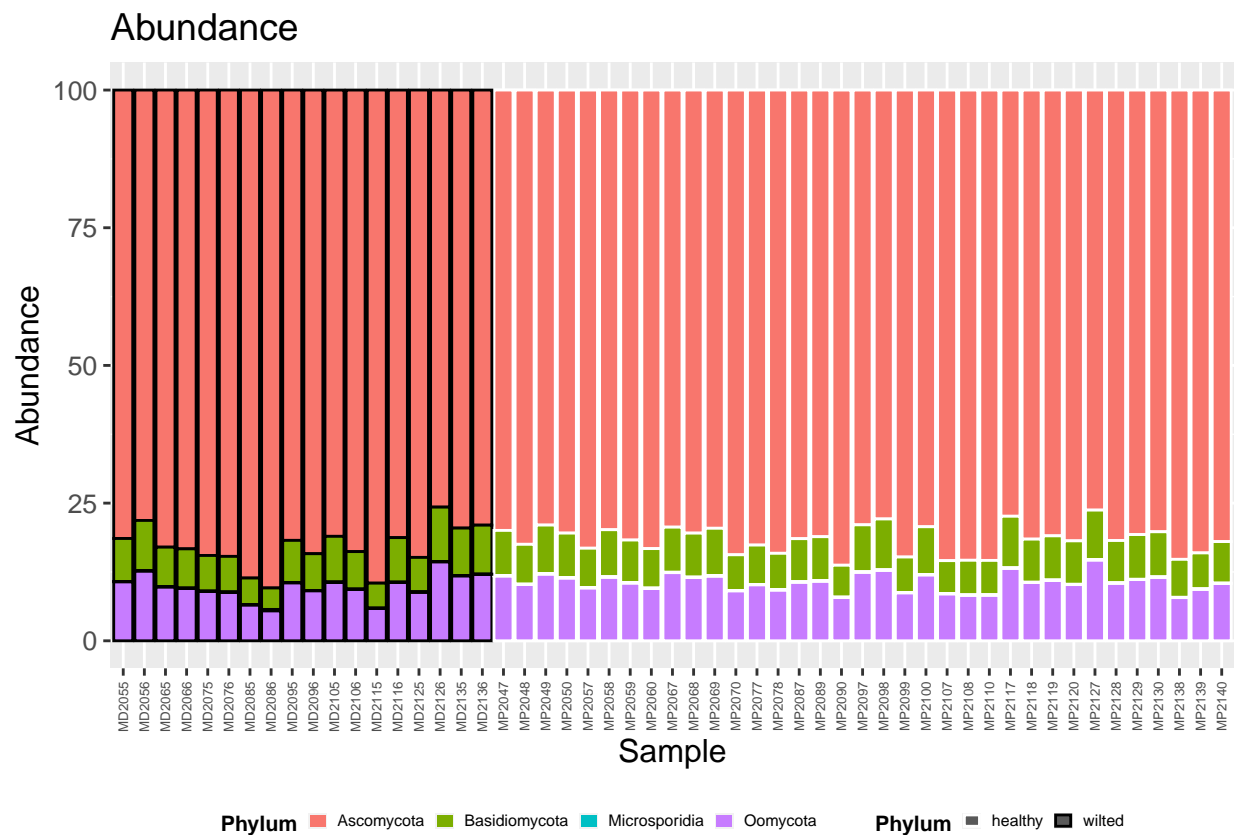


```
Barras_Phylum[2]
```

```
## [[1]]
```

Abundance

```
Beta_diversity(merge_Eukaryota , 'Phylum' , 'Treatment', 'bray')
```

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.01148681
## Run 1 stress 0.0001012286
## ... New best solution
## ... Procrustes: rmse 0.03438264  max resid 0.09018208
## Run 2 stress 8.080954e-05
## ... New best solution
## ... Procrustes: rmse 0.0002593369  max resid 0.0006111869
## ... Similar to previous best
## Run 3 stress 9.943482e-05
## ... Procrustes: rmse 0.0001287111  max resid 0.0003746192
## ... Similar to previous best
## Run 4 stress 5.946927e-05
## ... New best solution
## ... Procrustes: rmse 9.047211e-05  max resid 0.0002198202
## ... Similar to previous best
## Run 5 stress 9.885507e-05
## ... Procrustes: rmse 0.0001702104  max resid 0.0004297977
## ... Similar to previous best
## Run 6 stress 9.544256e-05
## ... Procrustes: rmse 0.000104487  max resid 0.0002663839
## ... Similar to previous best
```

```
## Run 7 stress 9.956639e-05
## ... Procrustes: rmse 8.390127e-05  max resid 0.0002437379
## ... Similar to previous best
## Run 8 stress 9.896738e-05
## ... Procrustes: rmse 0.0002583407  max resid 0.0006581007
## ... Similar to previous best
## Run 9 stress 7.056306e-05
## ... Procrustes: rmse 5.259222e-05  max resid 0.0001351559
## ... Similar to previous best
## Run 10 stress 9.479563e-05
## ... Procrustes: rmse 6.431556e-05  max resid 0.000134783
## ... Similar to previous best
## Run 11 stress 9.797854e-05
## ... Procrustes: rmse 0.0001674142  max resid 0.0004164753
## ... Similar to previous best
## Run 12 stress 0.0009492233
## Run 13 stress 0.0004211999
## ... Procrustes: rmse 0.0007288265  max resid 0.001932309
## ... Similar to previous best
## Run 14 stress 0.0001019576
## ... Procrustes: rmse 0.0002993734  max resid 0.000761613
## ... Similar to previous best
## Run 15 stress 9.067076e-05
## ... Procrustes: rmse 9.471571e-05  max resid 0.0002264973
## ... Similar to previous best
## Run 16 stress 9.6781e-05
## ... Procrustes: rmse 0.0001265178  max resid 0.0003112381
## ... Similar to previous best
## Run 17 stress 8.654003e-05
## ... Procrustes: rmse 0.0001074085  max resid 0.0002850164
## ... Similar to previous best
## Run 18 stress 6.269106e-05
## ... Procrustes: rmse 2.68101e-05  max resid 5.602508e-05
## ... Similar to previous best
## Run 19 stress 9.655239e-05
## ... Procrustes: rmse 0.0001244309  max resid 0.0003037819
## ... Similar to previous best
## Run 20 stress 0.0003162956
## ... Procrustes: rmse 0.0009368401  max resid 0.002436478
## ... Similar to previous best
## *** Best solution repeated 16 times


## Warning in metaMDS(veganifyOTU(physeq), distance, ...): stress is (nearly)
## zero: you may have insufficient data
```
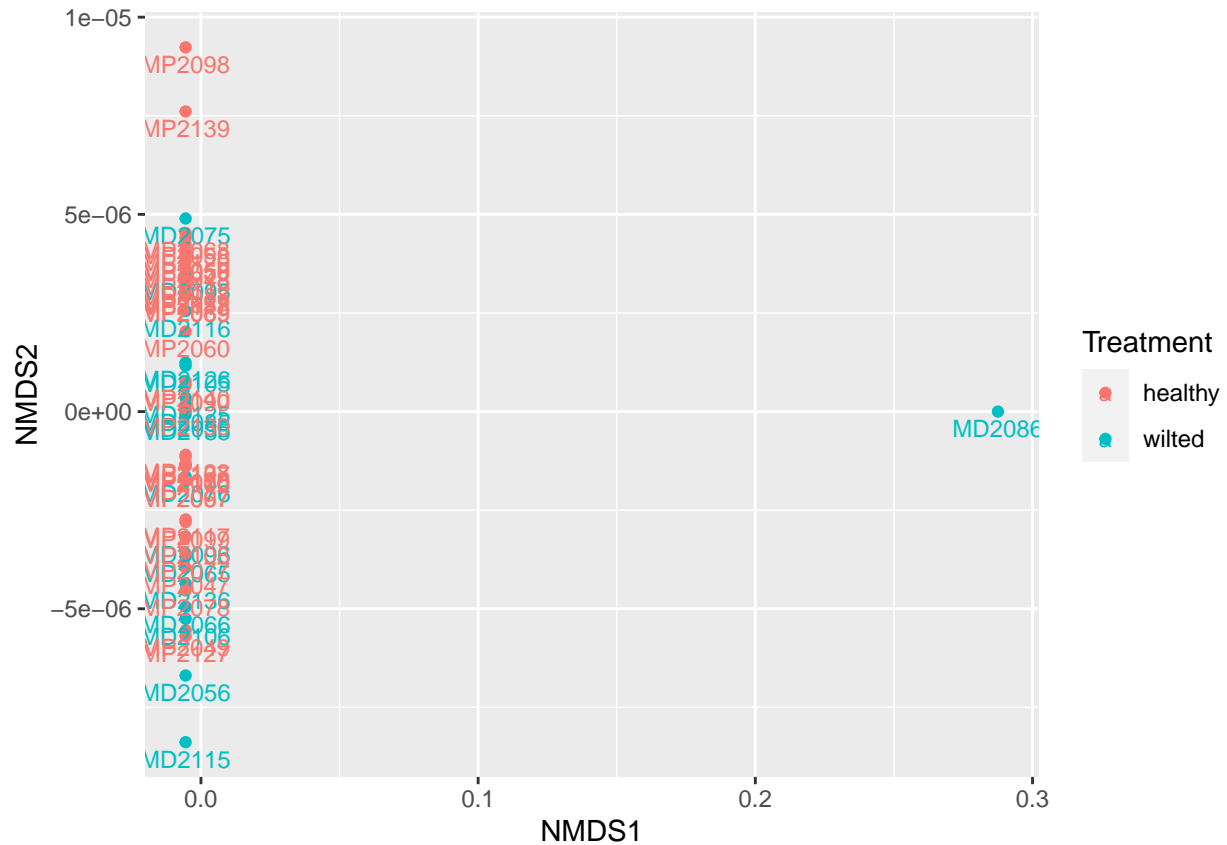
```
Alpha_diversity(merge_Eukaryota , 'Phylum' , 'Treatment')
```

```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```
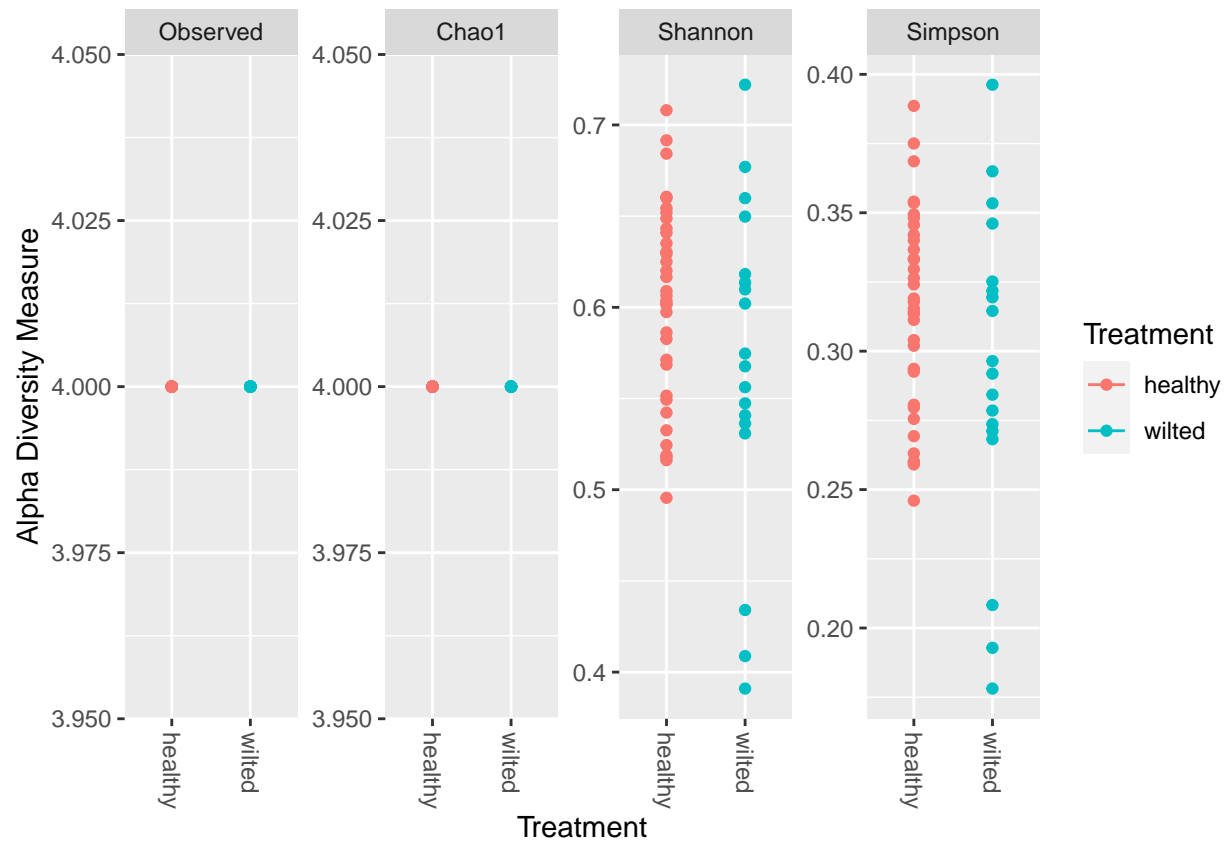
——————Eukarya by Family

```
Barras_Species <- Abundance_barras(merge_Eukaryota,'Family','Treatment',10.0)
Barras_Species[1]
```
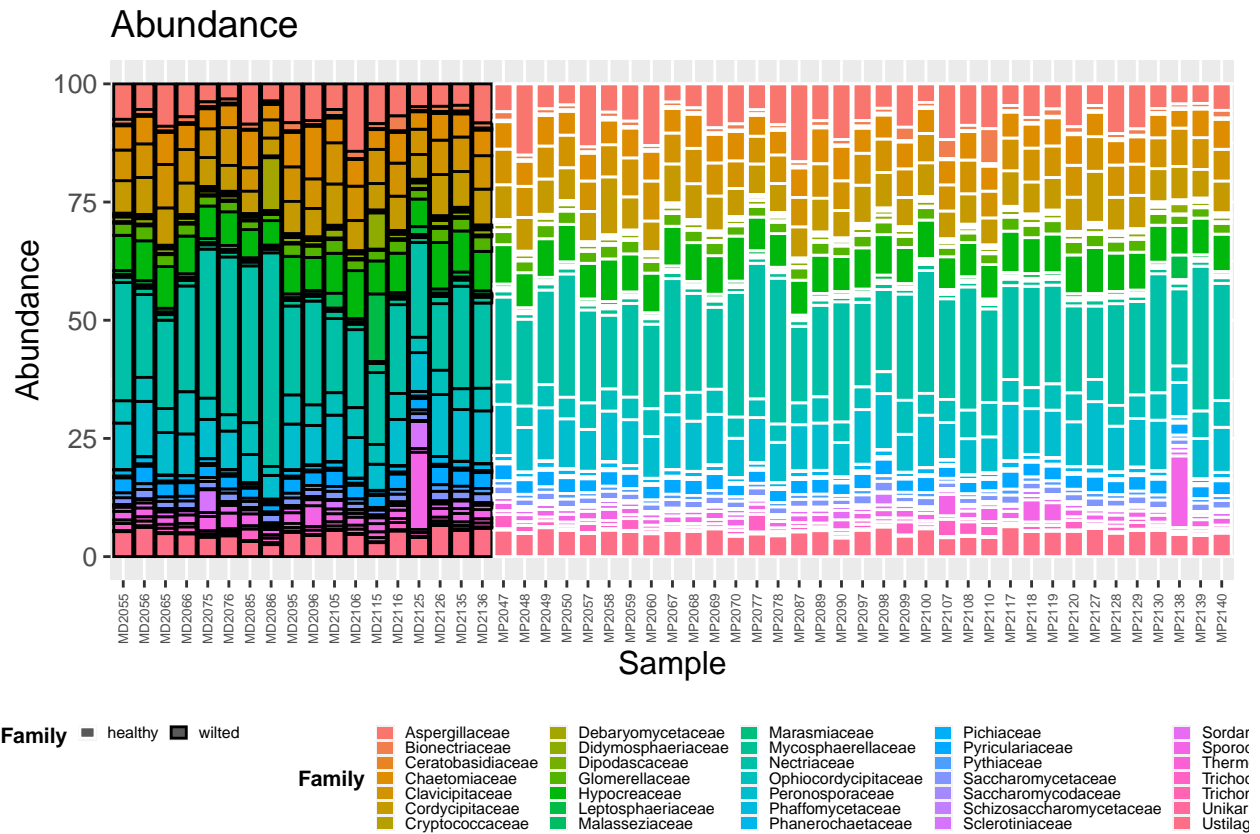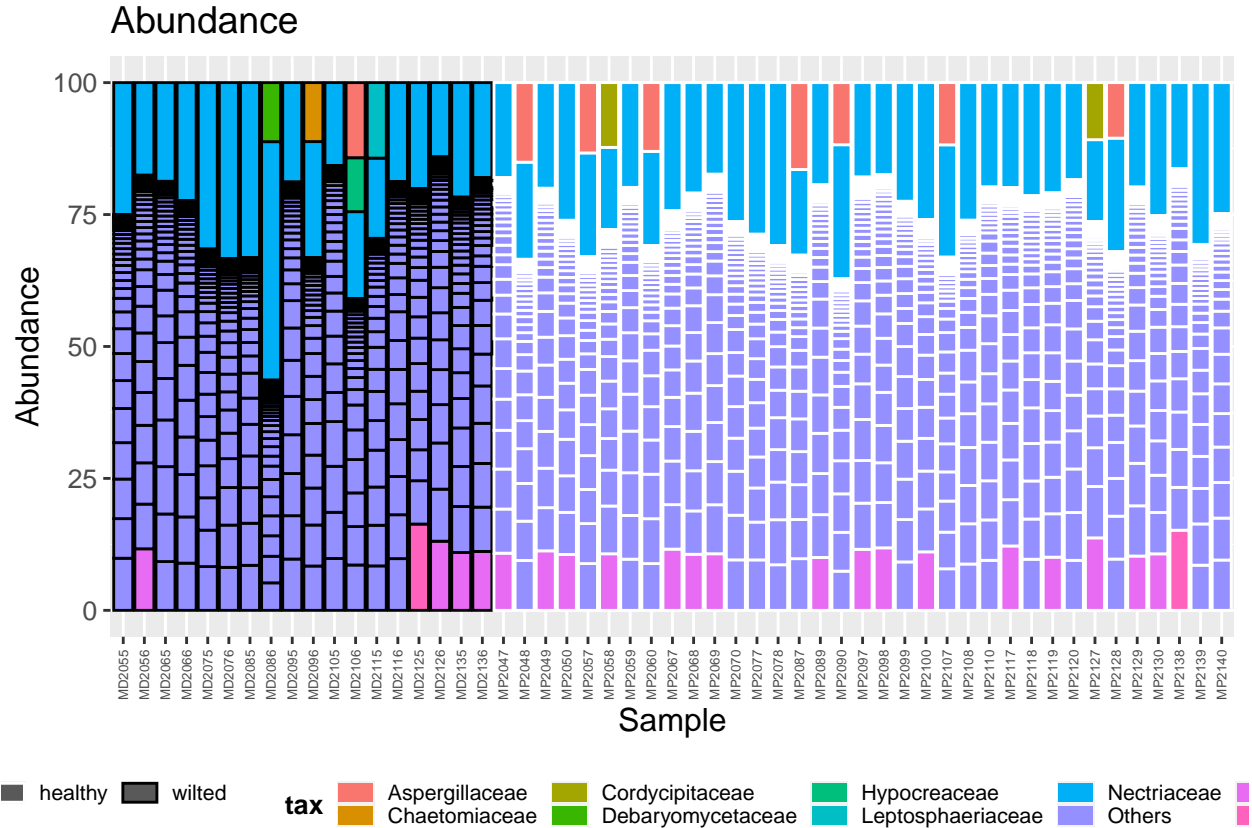
```
## [[1]]
```

Abundance

Abundance

```
Beta_diversity(merge_Eukaryota , 'Family' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1089081
## Run 1 stress 0.1088881
## ... New best solution
## ... Procrustes: rmse 0.00169424  max resid 0.009378103
## ... Similar to previous best
## Run 2 stress 0.1088884
## ... Procrustes: rmse 0.001265836  max resid 0.007170168
## ... Similar to previous best
## Run 3 stress 0.1089292
## ... Procrustes: rmse 0.008427579  max resid 0.05473371
## Run 4 stress 0.1089076
## ... Procrustes: rmse 0.001717778  max resid 0.009428019
## ... Similar to previous best
## Run 5 stress 0.1088922
## ... Procrustes: rmse 0.0007890617  max resid 0.004563198
## ... Similar to previous best
## Run 6 stress 0.1091132
## ... Procrustes: rmse 0.009868536  max resid 0.05417681
## Run 7 stress 0.1089292
## ... Procrustes: rmse 0.008430896  max resid 0.05472563
## Run 8 stress 0.1091137
## ... Procrustes: rmse 0.01001222  max resid 0.05396838
```

```
## Run 9 stress 0.1089299
## ... Procrustes: rmse 0.008416469  max resid 0.054788
## Run 10 stress 0.1089293
## ... Procrustes: rmse 0.008426162  max resid 0.05474377
## Run 11 stress 0.1089218
## ... Procrustes: rmse 0.000974449  max resid 0.005158194
## ... Similar to previous best
## Run 12 stress 0.1088884
## ... Procrustes: rmse 0.001341409  max resid 0.007533249
## ... Similar to previous best
## Run 13 stress 0.1089242
## ... Procrustes: rmse 0.002627083  max resid 0.0150801
## Run 14 stress 0.1088881
## ... Procrustes: rmse 5.634936e-06  max resid 2.393439e-05
## ... Similar to previous best
## Run 15 stress 0.1089298
## ... Procrustes: rmse 0.008417301  max resid 0.05478119
## Run 16 stress 0.1089185
## ... Procrustes: rmse 0.002321269  max resid 0.009035555
## ... Similar to previous best
## Run 17 stress 0.1088968
## ... Procrustes: rmse 0.002055205  max resid 0.009041251
## ... Similar to previous best
## Run 18 stress 0.1091401
## ... Procrustes: rmse 0.009638276  max resid 0.05345771
## Run 19 stress 0.108949
## ... Procrustes: rmse 0.00826652  max resid 0.05401651
## Run 20 stress 0.1089489
## ... Procrustes: rmse 0.008264563  max resid 0.05402098
## *** Best solution repeated 9 times
```
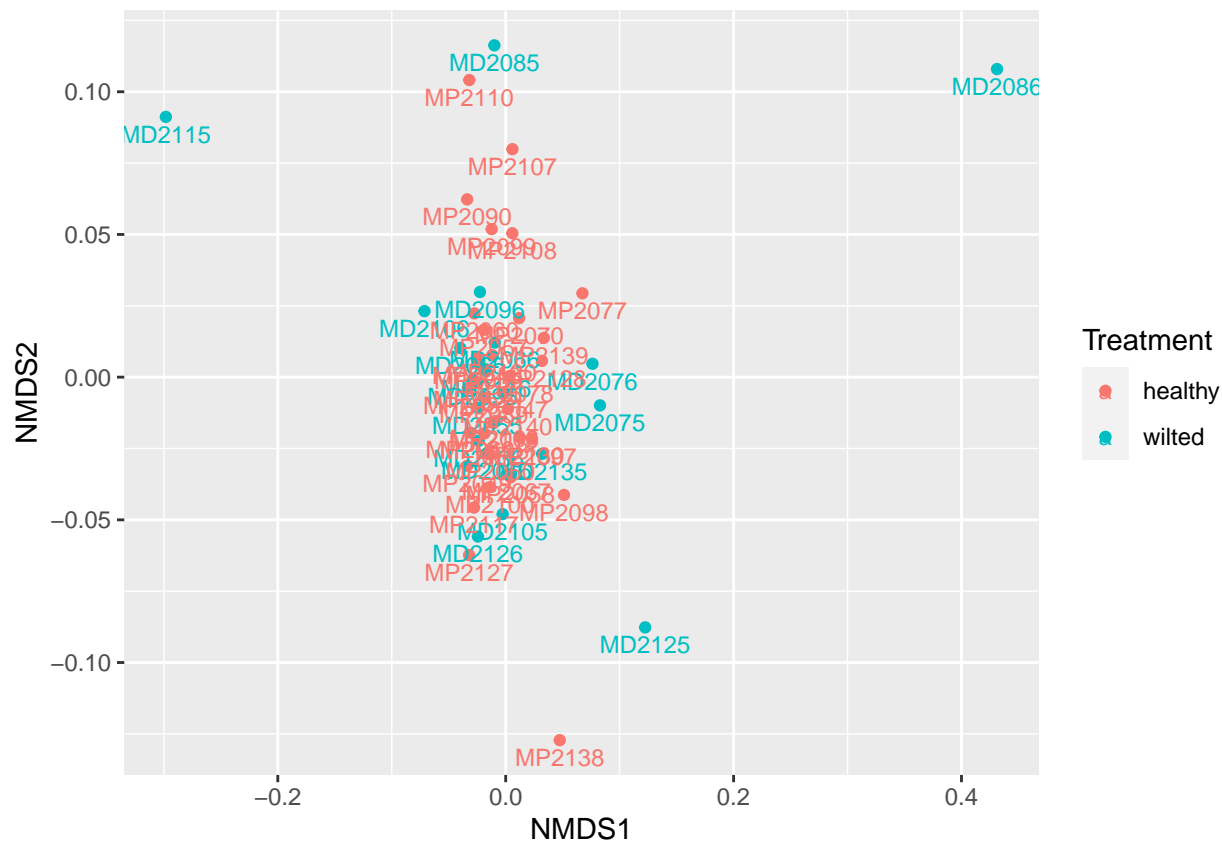
```
Alpha_diversity(merge_Eukaryota , 'Family' , 'Treatment')
```

```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```
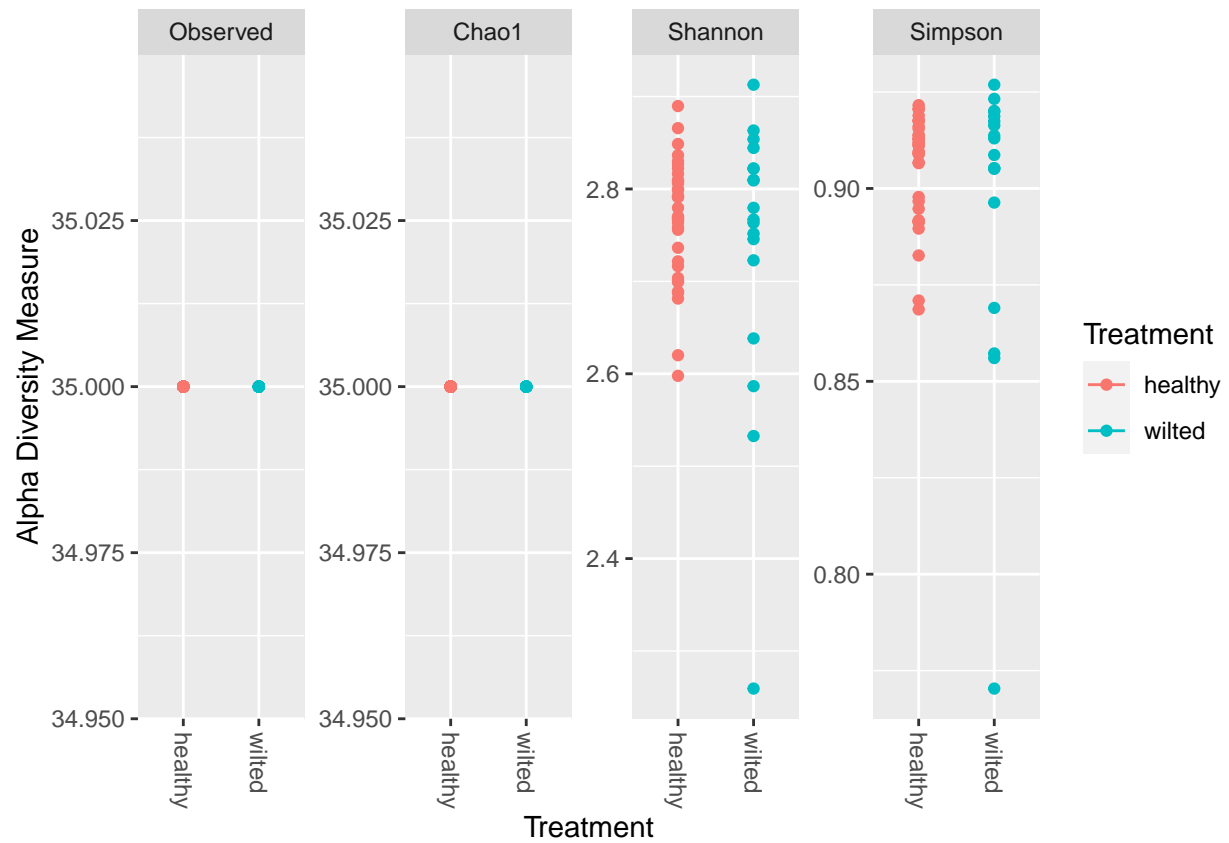
———Eukarya by Genero

```
Barras_Species <- Abundance_barras(merge_Eukaryota,'Genus','Treatment',10.0)
Barras_Species[1]
```

[[1]]

Abundance

Genus
Ampelomyces	Drechmeria	Naumovozyma	Purpureocillium	Thermothelomyces
Aspergillus	Encephalitozoon	Neopestalotiopsis	Pyricularia	Thermothielavioides
Beauveria	Eremothecium	Neurospora	Pythium	Torulaspora
Botrytis	Fusarium	Ogataea	Rhizoctonia	Trichoderma
Brettanomyces	Kazachstania	Paecilomyces	Saccharomyces	Ustilaginoidea
Candida	Kluyveromyces	Paraphaeosphaeria	Saccharomycodes	Ustilago
Cercospora	Komagataella	Penicillium	Scheffersomyces	Yarrowia
Clonostachys	Lachancea	Phlebiopsis	Schizosaccharomyces	Zygosaccharomyces
Colletotrichum	Malassezia	Phytophthora	Sporisorium	Zygotorulaspora
Cordyceps	Marasmius	Pichia	Sugiyamaella	Zymoseptoria
Cryptococcus	Metarhizium	Pochonia	Talaromyces	
Debaryomyces	Nakaseomyces	Pseudozyma	Tetrapisispora	

Genus ■ healthy ■

```
Barras_Species[2]
```

```
## [[1]]
```

```
Beta_diversity(merge_Eukaryota , 'Genus' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.110709
## Run 1 stress 0.1107087
## ... New best solution
## ... Procrustes: rmse 0.0007840091  max resid 0.004488343
## ... Similar to previous best
## Run 2 stress 0.1223849
## Run 3 stress 0.4035873
## Run 4 stress 0.1223838
## Run 5 stress 0.1107094
## ... Procrustes: rmse 0.0003365426  max resid 0.00192326
## ... Similar to previous best
## Run 6 stress 0.1107089
## ... Procrustes: rmse 0.000132357  max resid 0.0007613431
## ... Similar to previous best
## Run 7 stress 0.1223844
## Run 8 stress 0.1107097
## ... Procrustes: rmse 0.0004018827  max resid 0.002457857
## ... Similar to previous best
## Run 9 stress 0.1107095
## ... Procrustes: rmse 0.000934129  max resid 0.005321928
## ... Similar to previous best
## Run 10 stress 0.110709
```

```
## ... Procrustes: rmse 0.0007549733  max resid 0.004577962
## ... Similar to previous best
## Run 11 stress 0.1222476
## Run 12 stress 0.1119788
## Run 13 stress 0.1107095
## ... Procrustes: rmse 0.00092422  max resid 0.00527512
## ... Similar to previous best
## Run 14 stress 0.1239323
## Run 15 stress 0.1235015
## Run 16 stress 0.1321013
## Run 17 stress 0.1107098
## ... Procrustes: rmse 0.000447972  max resid 0.002563714
## ... Similar to previous best
## Run 18 stress 0.1315666
## Run 19 stress 0.1107096
## ... Procrustes: rmse 0.0003398341  max resid 0.001937171
## ... Similar to previous best
## Run 20 stress 0.1308436
## *** Best solution repeated 9 times
```



```
Alpha_diversity(merge_Eukaryota , 'Genus' , 'Treatment')
```

```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
```

```
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```


##———Eukarya by Species

```
Barras_Species <- Abundance_barras(merge_Eukaryota,'Species','Treatment',10.0)
Barras_Species[1]
```
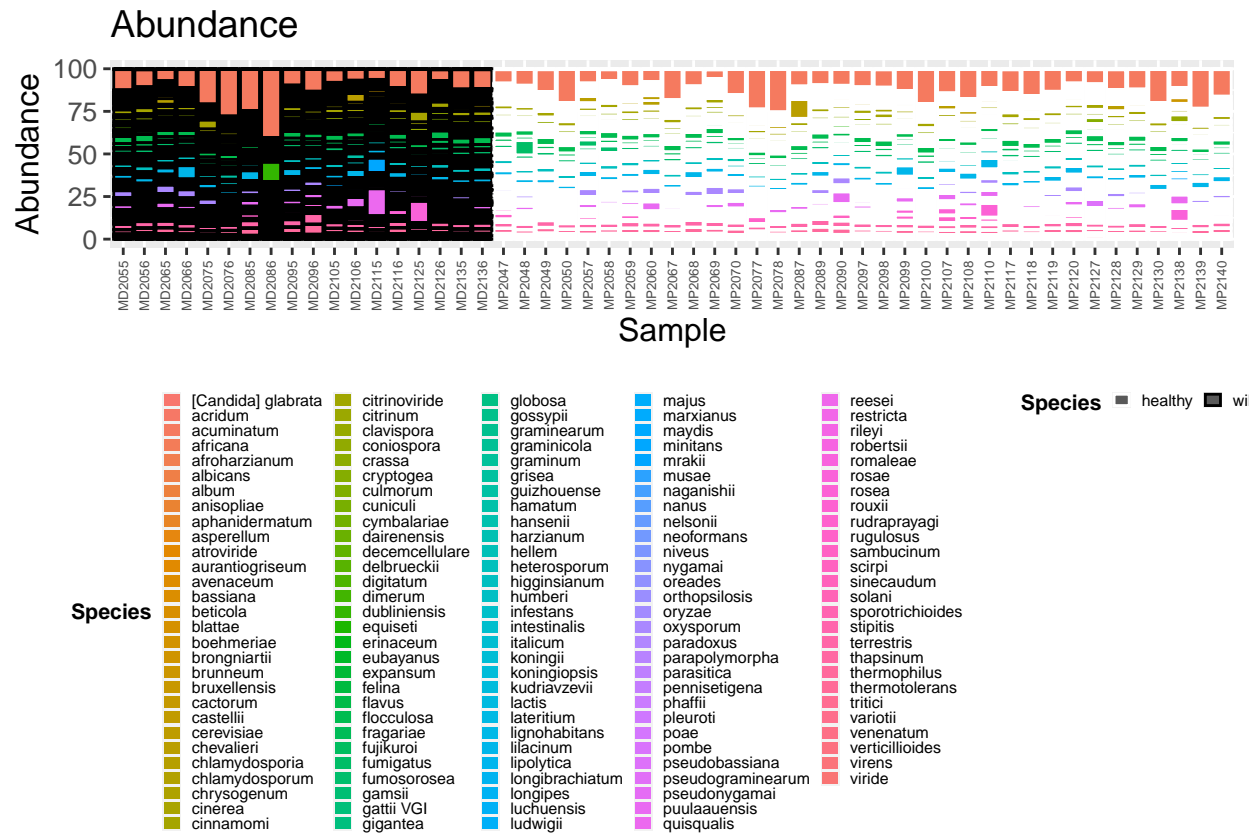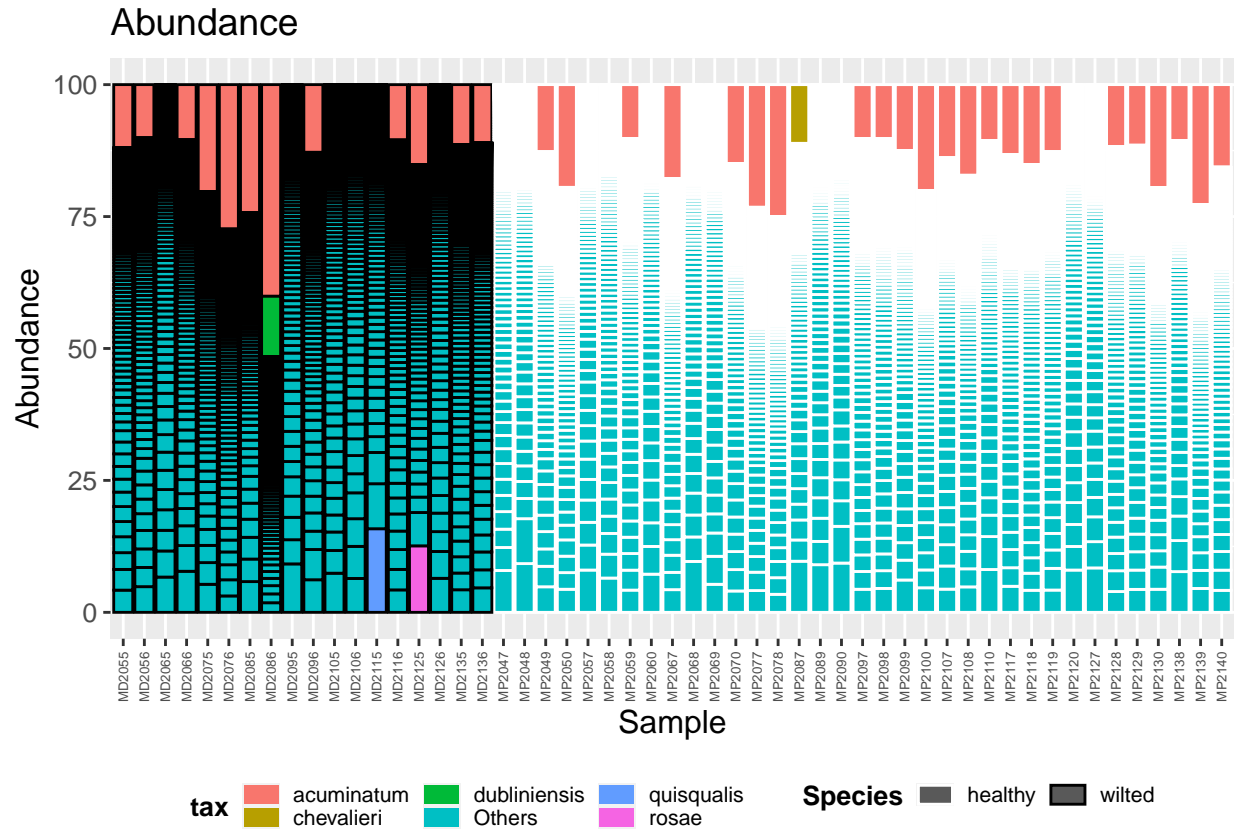
```
## [[1]]
```

Abundance

Barras_Species[2]

[[1]]

Abundance

tax
- acuminatum
- chevalieri
- dubliniensis
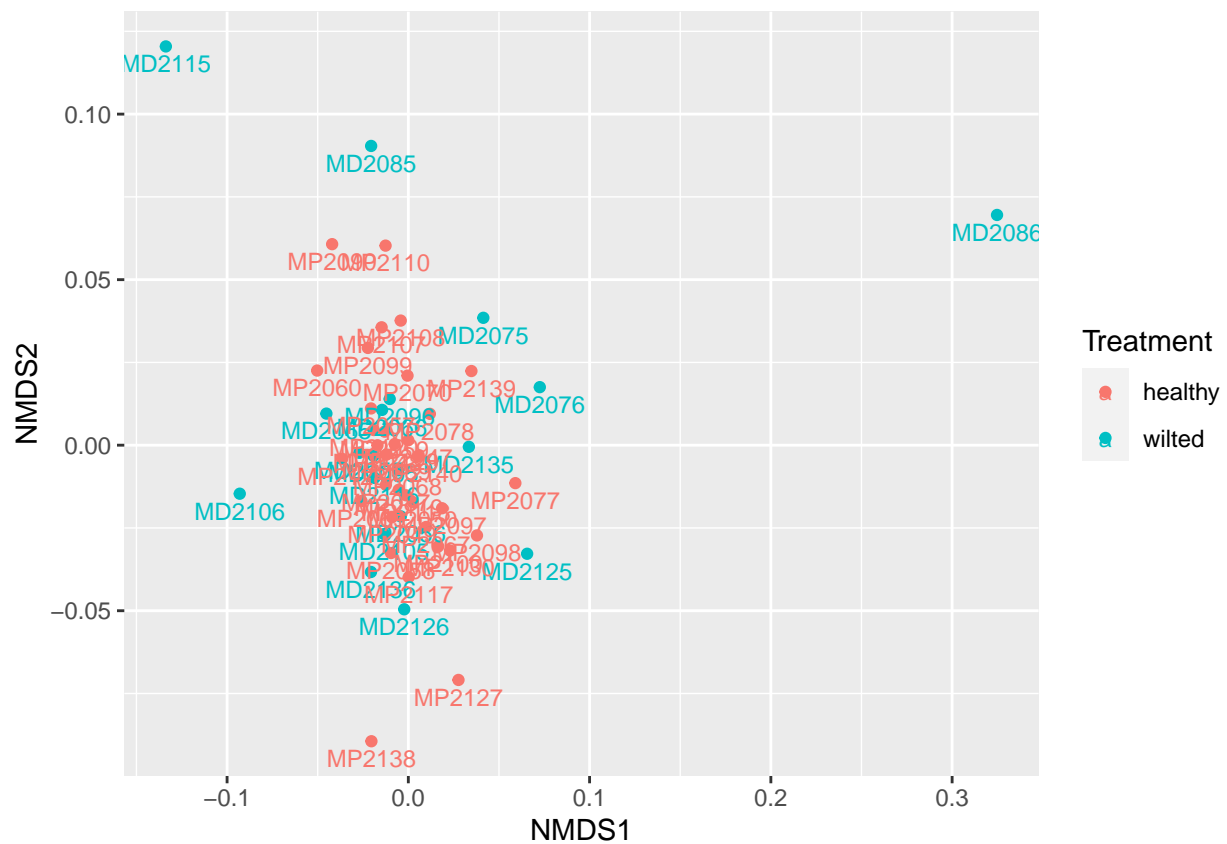- Others
- quisqualis
- rosae

Species healthy wilted

```
Beta_diversity(merge_Eukaryota , 'Species' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1226512
## Run 1 stress 0.1227531
## ... Procrustes: rmse 0.02315755  max resid 0.1274509
## Run 2 stress 0.1590668
## Run 3 stress 0.1272832
## Run 4 stress 0.1226511
## ... New best solution
## ... Procrustes: rmse 3.546733e-05  max resid 0.0001841906
## ... Similar to previous best
## Run 5 stress 0.1350911
## Run 6 stress 0.1226516
## ... Procrustes: rmse 0.0001415113  max resid 0.0007263343
## ... Similar to previous best
## Run 7 stress 0.1546168
## Run 8 stress 0.1345886
## Run 9 stress 0.135126
## Run 10 stress 0.1520428
## Run 11 stress 0.122651
## ... New best solution
## ... Procrustes: rmse 3.145075e-05  max resid 0.0001960645
## ... Similar to previous best
## Run 12 stress 0.1218544
```

```
## ... New best solution
## ... Procrustes: rmse 0.02016822   max resid 0.1286274
## Run 13 stress 0.1564026
## Run 14 stress 0.1226509
## Run 15 stress 0.1218542
## ... New best solution
## ... Procrustes: rmse 0.0001547836   max resid 0.0009934689
## ... Similar to previous best
## Run 16 stress 0.1226508
## Run 17 stress 0.1272834
## Run 18 stress 0.1550508
## Run 19 stress 0.1226508
## Run 20 stress 0.1541132
## *** Best solution repeated 1 times
```



```
Alpha_diversity(merge_Eukaryota , 'Species' , 'Treatment')
```
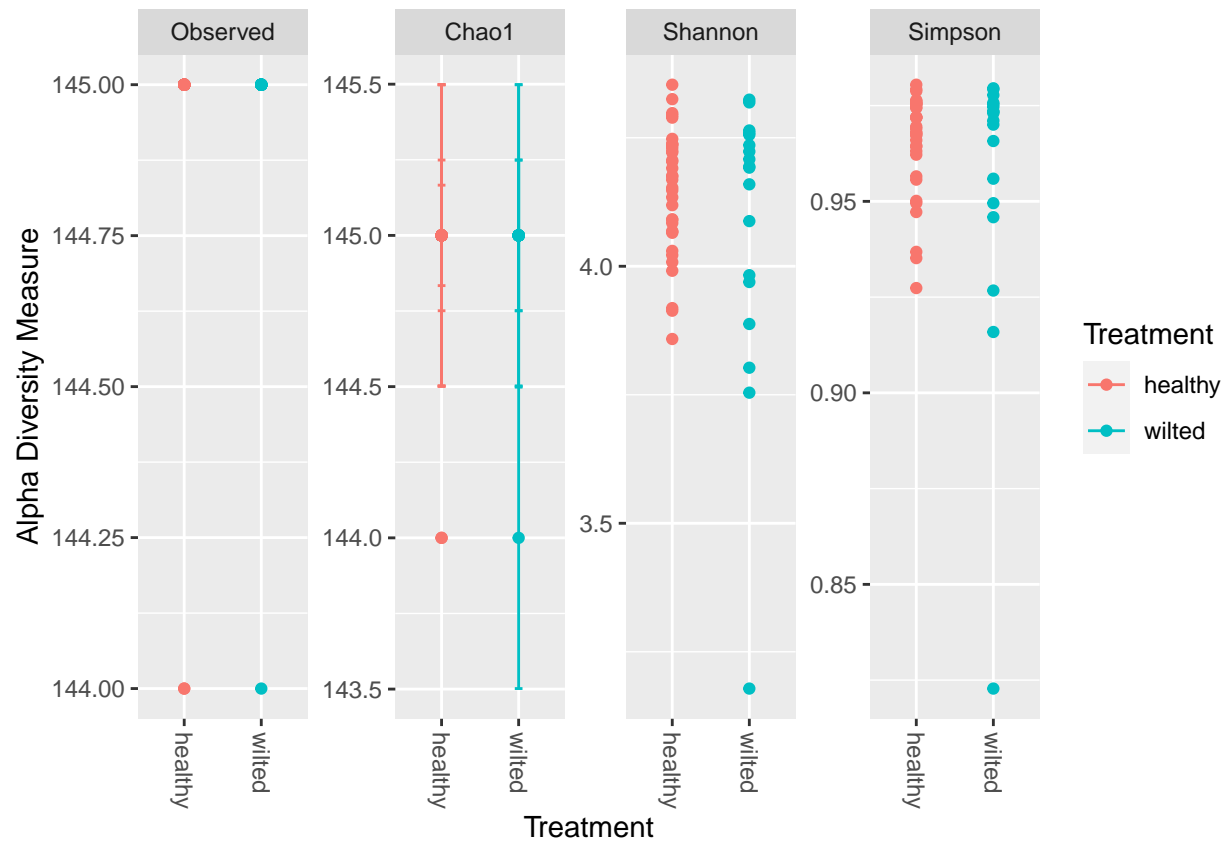
##———Bacteria by Phylum

```
Barras_Species <- Abundance_barras(merge_Bacteria,'Phylum','Treatment',10.0)
Barras_Species[1]
```

```
## [[1]]
```

Abundance

Phylum
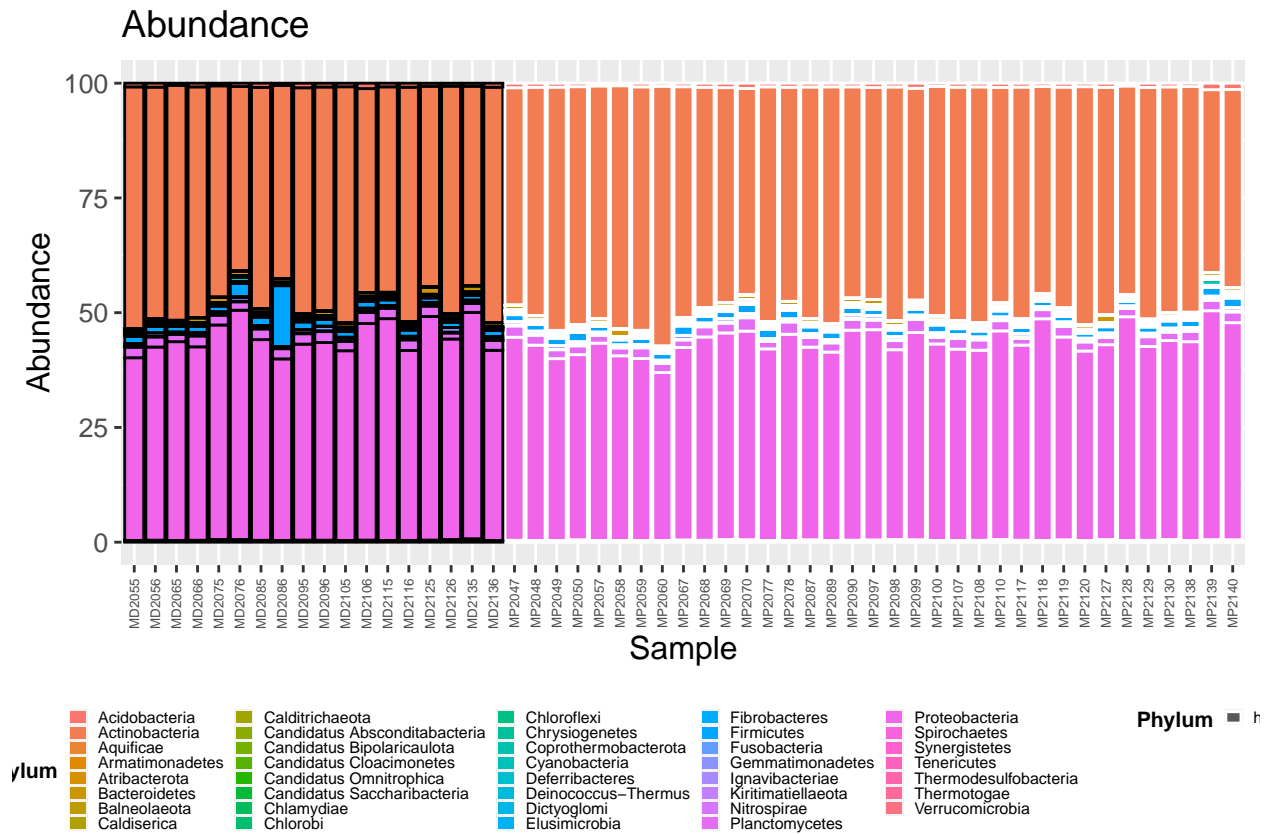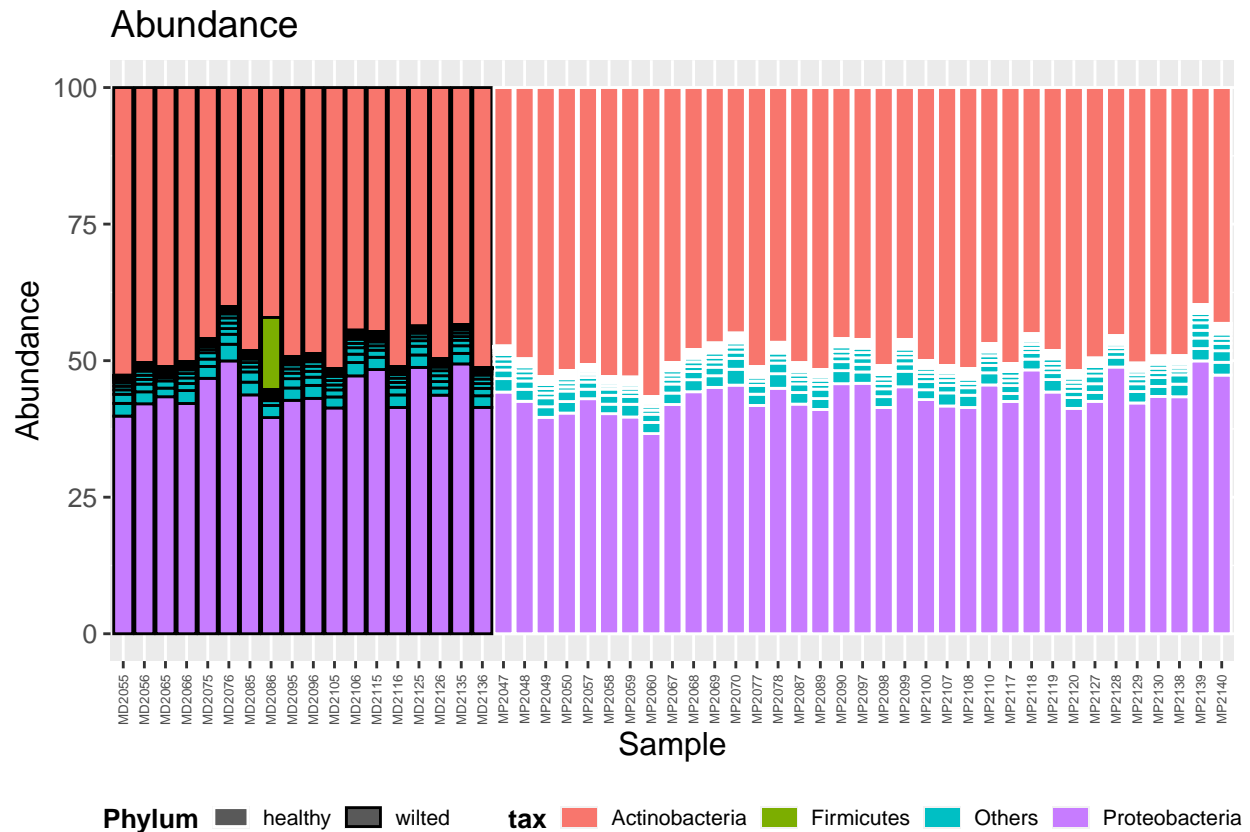- Acidobacteria
- Actinobacteria
- Aquificae
- Armatimonadetes
- Atribacterota
- Bacteroidetes
- Balneolaeota
- Caldiserica
- Calditrichaeota
- Candidatus Absconditabacteria
- Candidatus Bipolaricaulota
- Candidatus Cloacimonetes
- Candidatus Omnitrophica
- Candidatus Saccharibacteria
- Chlamydiae
- Chlorobi
- Chloroflexi
- Chrysiogenetes
- Coprothermobacterota
- Cyanobacteria
- Deferribacteres
- Deinococcus–Thermus
- Dictyoglomi
- Elusimicrobia
- Fibrobacteres
- Firmicutes
- Fusobacteria
- Gemmatimonadetes
- Ignavibacteriae
- Kiritimatiellaeota
- Nitrospirae
- Planctomycetes
- Proteobacteria
- Spirochaetes
- Synergistetes
- Tenericutes
- Thermodesulfobacteria
- Thermotogae
- Verrucomicrobia

Phylum

```
Barras_Species[2]
```

```
## [[1]]
```

Abundance

| Phylum | healthy | wilted | tax | ▮ Actinobacteria | ▮ Firmicutes | ▮ Others | ▮ Proteobacteria |

```
Beta_diversity(merge_Bacteria , 'Phylum' , 'Treatment', 'bray')
```

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.1520004
## Run 1 stress 0.1541159
## Run 2 stress 0.1719744
## Run 3 stress 0.1665614
## Run 4 stress 0.1676962
## Run 5 stress 0.1591786
## Run 6 stress 0.151391
## ... New best solution
## ... Procrustes: rmse 0.008729679  max resid 0.0517727
## Run 7 stress 0.1707262
## Run 8 stress 0.1602944
## Run 9 stress 0.1580849
## Run 10 stress 0.1711338
## Run 11 stress 0.152401
## Run 12 stress 0.1614016
## Run 13 stress 0.1601939
## Run 14 stress 0.1554219
## Run 15 stress 0.1648666
## Run 16 stress 0.1554203
## Run 17 stress 0.1696002
## Run 18 stress 0.1624861
```

```
## Run 19 stress 0.1554219
## Run 20 stress 0.1641734
## *** Best solution was not repeated -- monoMDS stopping criteria:
##      20: stress ratio > sratmax
```
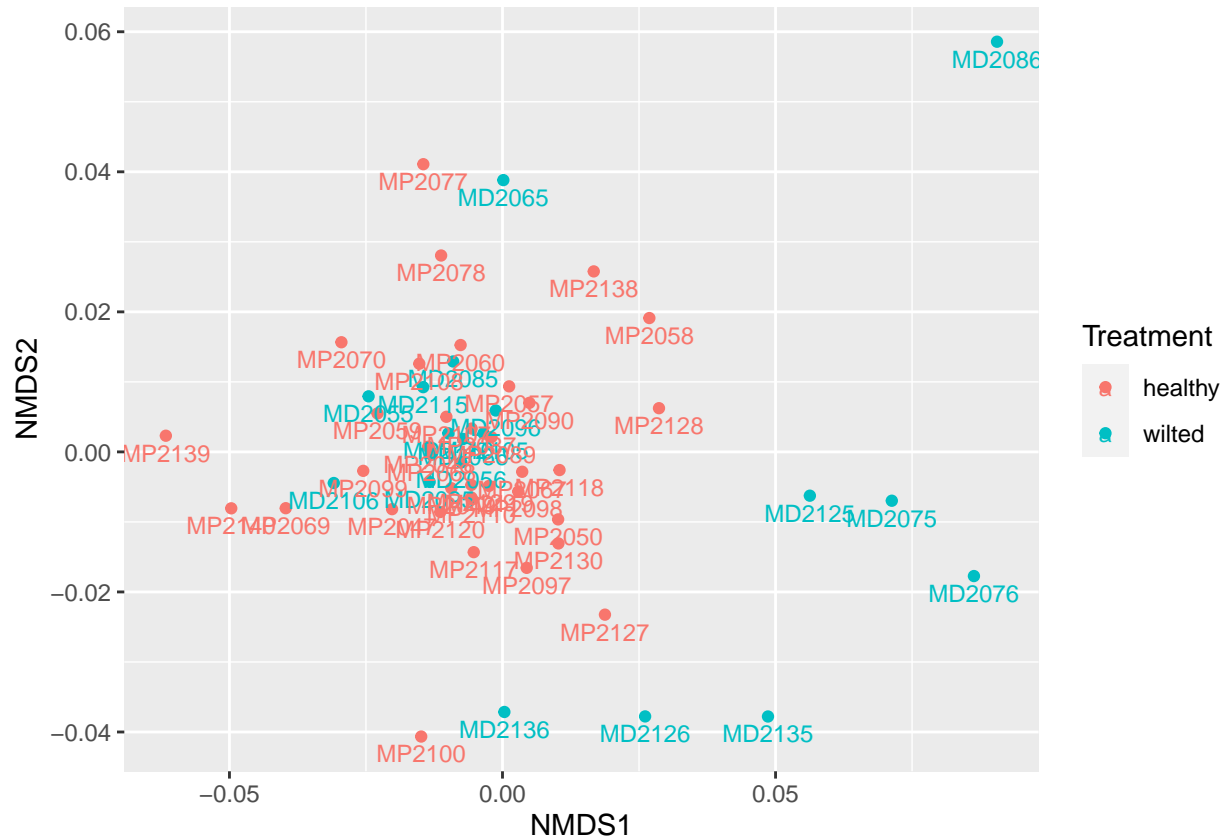


```
Alpha_diversity(merge_Bacteria , 'Phylum' , 'Treatment')
```

```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```
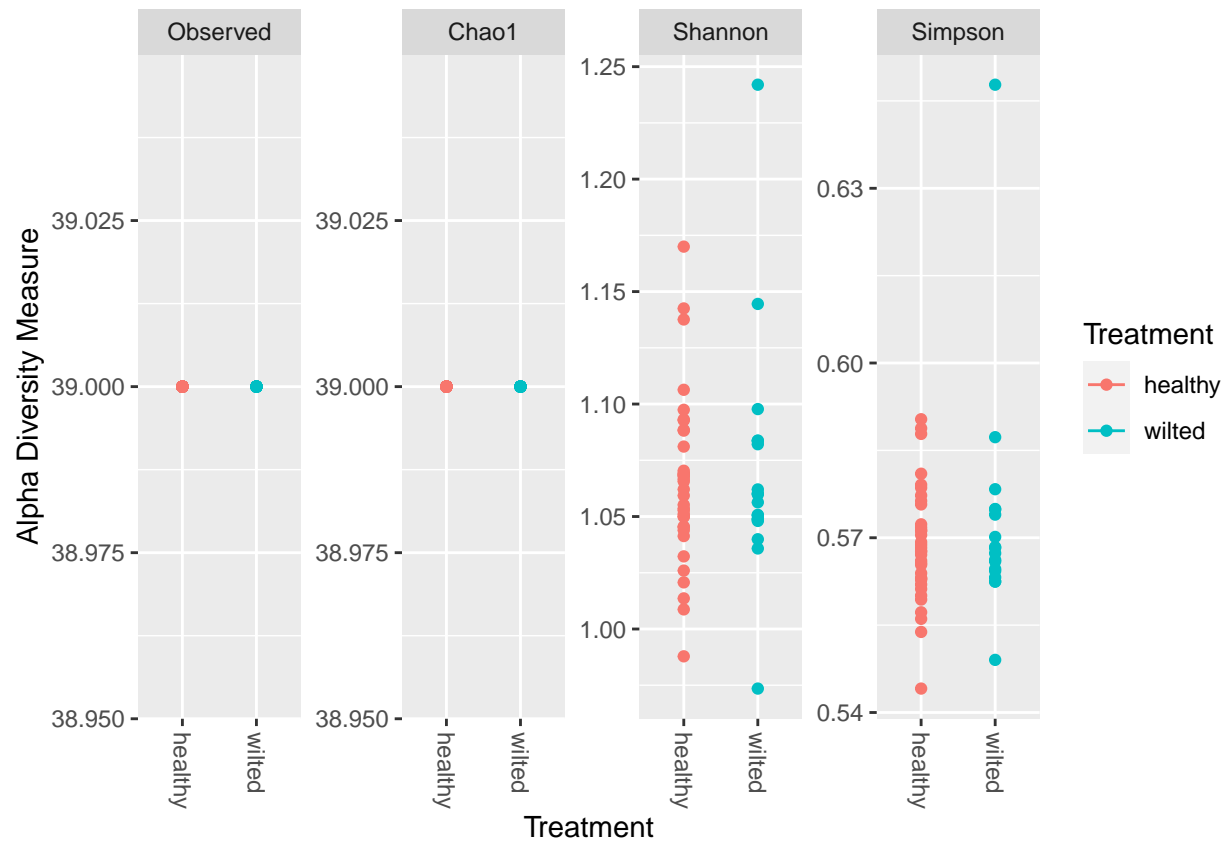
##———Bacteria by Familia

```
Barras_Species <- Abundance_barras(merge_Bacteria,'Family','Treatment',10.0)
Barras_Species[1]
```
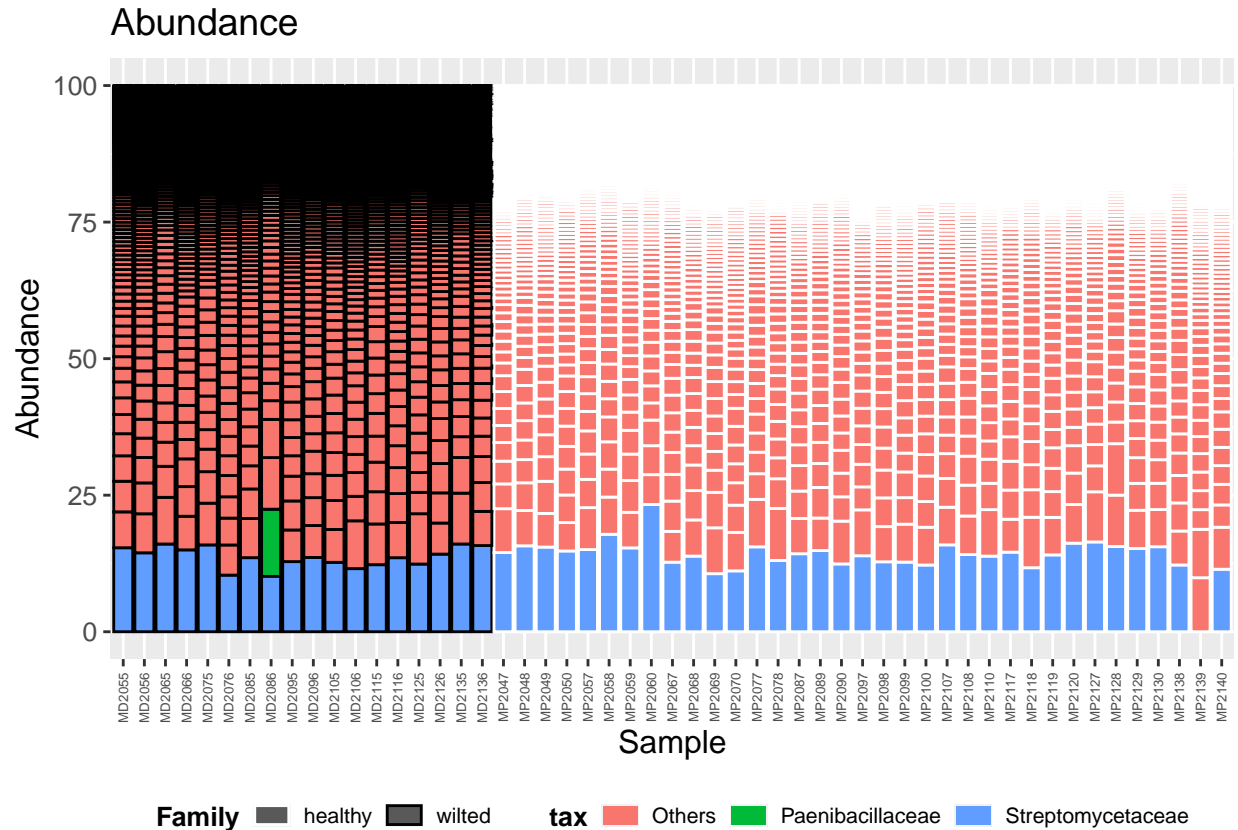
```
## [[1]]
```

Family

Actinomycetaceae
Actinopolymorphaceae
Actinopolysporaceae
Aerococcaceae
Aeromonadaceae
Akkermansiaceae
Alcaligenaceae
Alcanivoracaceae
Alicyclobacillaceae
Alteromonadaceae
Amoebophilaceae
Amorphaceae
Anaerohalosphaeraceae
Anaerolineaceae
Anaeromyxobacteraceae
Anaplasmataceae
Aphanizomenonaceae
Aphanothecaceae
Aquificaceae
Archangiaceae
Arcobacteraceae
Ardenticatenaceae
Atopobiaceae
Atribacteraceae
Aurantimonadaceae
Azonexaceae
Azospirillaceae
Bacillaceae
Bacteriovoracaceae
Bacteroidaceae
Baekduiaceae
Barnesiellaceae
Bartonellaceae
Bdellovibrionaceae
Beijerinckiaceae
Bernardetiaceae
Beutenbergiaceae
Bifidobacteriaceae
Blastochloridaceae
Blattabacteriaceae
Bogoriellaceae
Borreliaceae
Boseaceae
Brachyspiraceae
Bradymonadaceae
Bradyrhizobiaceae
Breoghaniaceae
Brevibacteriaceae
Brucellaceae
Bruguierivoracaceae
Bryobacteraceae
Budviciaceae
Burkholderiaceae
Caedimonadaceae
Caldilineaceae
Caldisericaceae
Calditrichaceae
Calotrichaceae

Chthonomonadaceae
Clostridiaceae
Clostridiales Family XVI. Incertae Sedis
Clostridiales Family XVII. Incertae Sedis
Cohaesibacteraceae
Coleofasciculaceae
Colwelliaceae
Comamonadaceae
Conexibacteraceae
Coprothermobacteraceae
Coriobacteriaceae
Corynebacteriaceae
Coxiellaceae
Crocinitomicaceae
Cyclobacteriaceae
Cytophagaceae
Deferribacteraceae
Dehalococcoidaceae
Deinococcaceae
Demequinaceae
Dermabacteraceae
Dermacoccaceae
Dermatophilaceae
Dermocarpellaceae
Desulfallaceae
Desulfarculaceae
Desulfitobacteriaceae
Desulfobacteraceae
Desulfobulbaceae
Desulfocapsaceae
Desulfohalobiaceae
Desulfomicrobiaceae
Desulfosudaceae
Desulfotomaculaceae
Desulfovibrionaceae
Desulfurellaceae
Desulfurobacteriaceae
Desulfuromonadaceae
Devosiaceae
Dictyoglomaceae
Dietziaceae
Dissulfurispiraceae
Dysgonomonadaceae
Ectothiorhodospiraceae
Eggerthellaceae
Egibacteraceae
Egicoccaceae
Elioraeaceae
Elusimicrobiaceae
Emcibacteraceae
Endomicrobiaceae
Endozoicomonadaceae
Enterobacteriaceae
Enterococcaceae
Entomoplasmataceae
Erwiniaceae
Erysipelotrichaceae
Erythrobacteraceae

Halobacteriovoraceae
Halobacteroidaceae
Halomonadaceae
Halothiobacillaceae
Hapalosiphonaceae
Helicobacteraceae
Heliobacteriaceae
Holosporaceae
Hydrogenimonaceae
Hydrogenophilaceae
Hydrogenothermaceae
Hyellaceae
Hymenobacteraceae
Hyphomicrobiaceae
Hyphomonadaceae
Iamiaceae
Ichthyobacteriaceae
Idiomarinaceae
Ignavibacteriaceae
Ilumatobacteraceae
Immundisolibacteraceae
Intrasporangiaceae
Isosphaeraceae
Jatrophihabitantaceae
Jiangellaceae
Jonesiaceae
Kaistiaceae
Kangiellaceae
Kineosporiaceae
Kiritimatiellaceae
Kofleriaceae
Koleobacteraceae
Kordiimonadaceae
Kosmotogaceae
Kribbellaceae
Ktedonosporobacteraceae
Kytococcaceae
Labilitrichaceae
Lachnospiraceae
Lacipirellulaceae
Lactobacillaceae
Lawsonellaceae
Legionellaceae
Leptolyngbyaceae
Leptospiraceae
Leptotrichiaceae
Lichenihabitantaceae
Limnochordaceae
Listeriaceae
Litoricolaceae
Magnetococcaceae
Mangrovivirgaceae
Maricaulaceae
Marinifilaceae
Marinilabiliaceae
Marinobacteraceae
Mariprofundaceae
Marivirgaceae

Nocardiaceae
Nocardioidaceae
Nocardiopsaceae
Nostocaceae
Oceanospirillaceae
Oculatellaceae
Odoribacteraceae
Oleiphilaceae
Opitutaceae
Orbaceae
Ornithinimicrobiaceae
Oscillatoriaceae
Oscillospiraceae
Oxalobacteraceae
Paenibacillaceae
Paludibacteraceae
Parachlamydiaceae
Parvibaculaceae
Parvularculaceae
Pasteurellaceae
Pectobacteriaceae
Pelagibacteraceae
Peptococcaceae
Peptoniphilaceae
Peptostreptococcaceae
Petrotogaceae
Phototrophicaceae
Phreatobacteraceae
Phycisphaeraceae
Phyllobacteriaceae
Pirellulaceae
Piscirickettsiaceae
Planctomycetaceae
Planococcaceae
Pleomorphomonadaceae
Polyangiaceae
Porphyromonadaceae
Prevotellaceae
Prochlorococcaceae
Prochlorotrichaceae
Prolixibacteraceae
Promicromonosporaceae
Propionibacteriaceae
Proteinivoraceae
Pseudanabaenaceae
Pseudoalteromonadaceae
Pseudomonadaceae
Pseudonocardiaceae
Psychromonadaceae
Puniceicoccaceae
Rhabdochlamydiaceae
Rhizobiaceae
Rhodanobacteraceae
Rhodobacteraceae
Rhodocyclaceae
Rhodospirillaceae
Rhodothermaceae
Rickettsiaceae

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`Barras_Species[2]`

`## [[1]]`

Abundance

**Family** — healthy — wilted **tax** ■ Others ■ Paenibacillaceae ■ Streptomycetaceae

```
Beta_diversity(merge_Bacteria , 'Family' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1412073
## Run 1 stress 0.1374745
## ... New best solution
## ... Procrustes: rmse 0.06404146  max resid 0.362518
## Run 2 stress 0.1405164
## Run 3 stress 0.1792916
## Run 4 stress 0.1401022
## Run 5 stress 0.1729145
## Run 6 stress 0.1370379
## ... New best solution
## ... Procrustes: rmse 0.01572709  max resid 0.05915357
## Run 7 stress 0.1391838
## Run 8 stress 0.1390465
## Run 9 stress 0.1721853
## Run 10 stress 0.1400264
## Run 11 stress 0.1412067
## Run 12 stress 0.1374452
## ... Procrustes: rmse 0.01063197  max resid 0.04902825
## Run 13 stress 0.1570078
## Run 14 stress 0.1401021
## Run 15 stress 0.14556
## Run 16 stress 0.137194
```

```
## ... Procrustes: rmse 0.01158332  max resid 0.05694715
## Run 17 stress 0.1704098
## Run 18 stress 0.1441743
## Run 19 stress 0.1371941
## ... Procrustes: rmse 0.01162238  max resid 0.0569763
## Run 20 stress 0.1517993
## *** Best solution was not repeated -- monoMDS stopping criteria:
##     20: stress ratio > sratmax
```
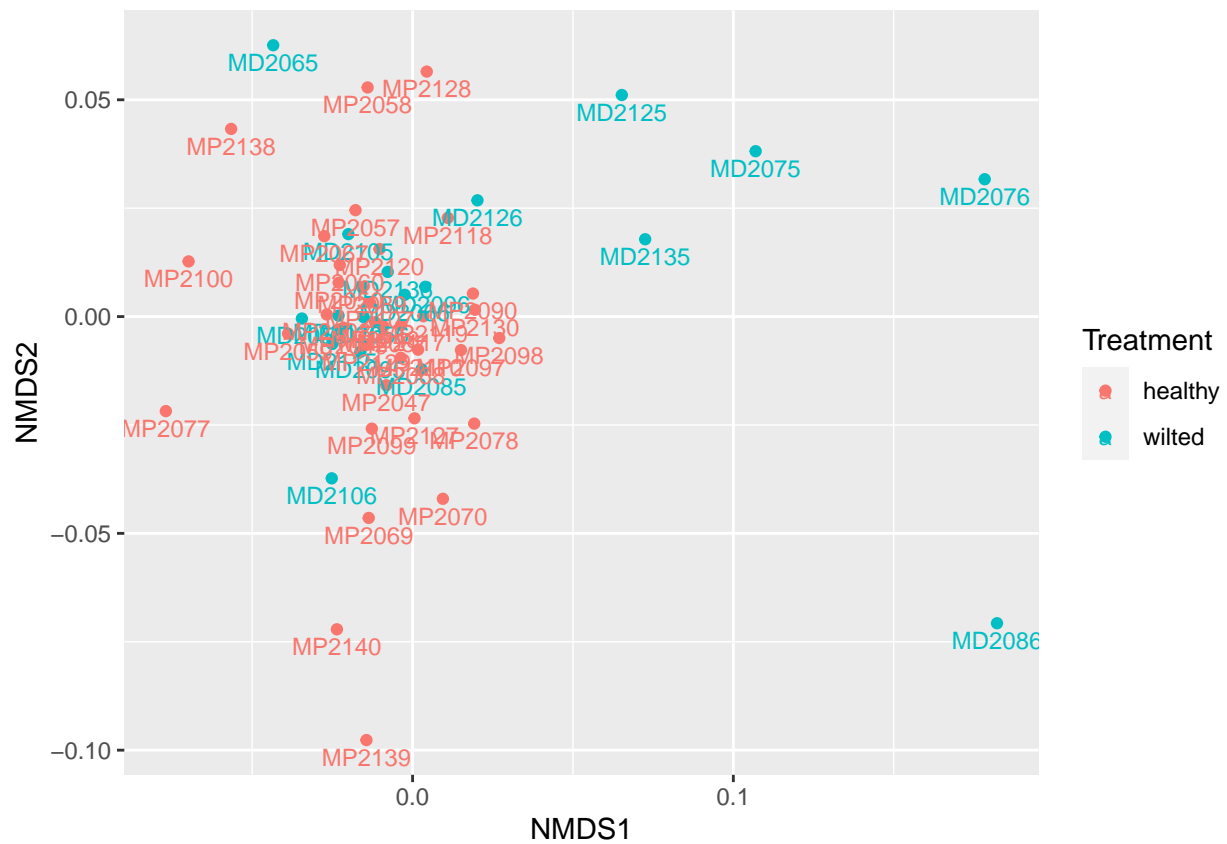


```
Alpha_diversity(merge_Bacteria , 'Family' , 'Treatment')
```
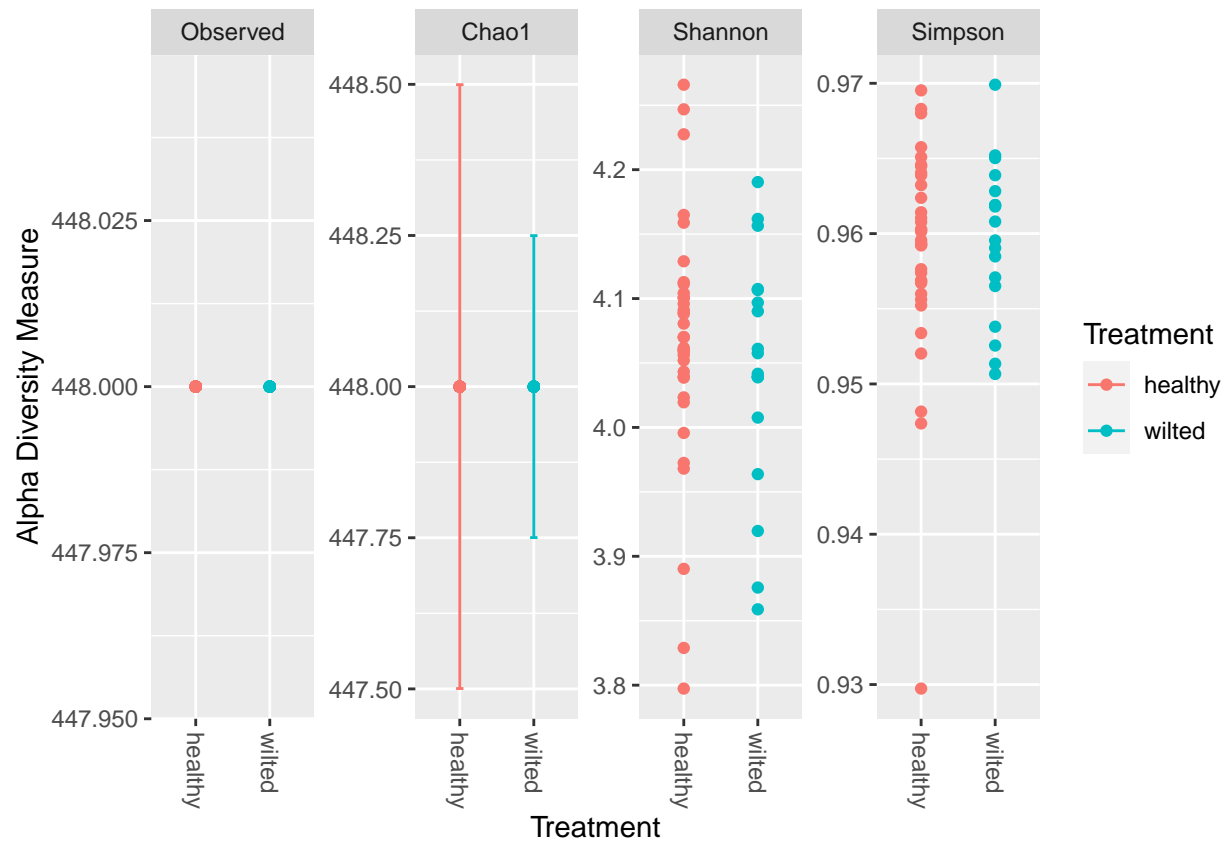
##———Bacteria by Genero

```
Barras_Species <- Abundance_barras(merge_Bacteria,'Genus','Treatment',10.0)
Barras_Species[1]
```

[[1]]

lex	Desulfarculus	Labrenzia	Paremcibacter	Subtercola
flexum	Desulfatibacillum	Labrys	Paroceanicella	Succinivibrio
habitans	Desulfitobacterium	Laceyella	Parolsenella	Suicoccus
luna	Desulfobacca	Lachnoanaerobaculum	Parvibaculum	Sulfidibacter
marina	Desulfobacter	Lachnoclostridium	Parvimonas	Sulfitobacter
ncola	Desulfobacula	Lachnospira	Parvularcula	Sulfuricaulis
rhabdus	Desulfobulbus	Lacibacter	Pasteurella	Sulfuricella
rufa	Desulfocapsa	Lacimicrobium	Paucibacter	Sulfuricurvum
salimonas	Desulfococcus	Lacinutrix	Paucilactobacillus	Sulfuriferula
salinus	Desulfocurvibacter	Lacipirellula	Pauljensenia	Sulfuriflexus
sediminimonas	Desulfofarcimen	Lacrimispora	Pectinatus	Sulfurifustis
sphaera	Desulfoglaeba	Lacticaseibacillus	Pectobacterium	Sulfurihydrogenibium
talea	Desulfohalobium	Lactiplantibacillus	Pediococcus	Sulfurimicrobium
iibacter	Desulfoluna	Lactobacillus	Pedobacter	Sulfurimonas
hidicoccus	Desulfolutivibrio	Lactococcus	Pedococcus	Sulfuriroseicoccus
hnia	Desulfomarina	Lacunisphaera	Pelagerythrobacter	Sulfuritalea
nobacterium	Desulfomicrobium	Lancefieldella	Pelagibacterium	Sulfuritortus
angium	Desulfomonile	Lapidilactobacillus	Pelagovum	Sulfurivermis
bacter	Desulfonema	Laribacter	Pelistega	Sulfurospirillum
cibacterium	Desulforamulus	Larkinella	Pelobacter	Sulfurovum
ibacter	Desulforapulum	Latilactobacillus	Pelodictyon	Sutcliffiella
imonas	Desulfosarcina	Lautropia	Pelolinea	Sutterella
natoleum	Desulfoscipio	Lawsonella	Pelosinus	Suttonella
nicicoccus	Desulfosediminicola	Lawsonia	Pengzhenrongella	Swingsia
nophonus	Desulfosporosinus	Leadbetterella	Peptacetobacter	Symbiobacterium
obacter	Desulfosudis	Leclercia	Peptoclostridium	Symmachiella
a	Desulfotalea	Lederbergia	Peptoniphilus	Synechococcus
ccacaulis	Desulfotomaculum	Leeuwenhoekiella	Peribacillus	Synechocystis
lassotoga	Desulfovibrio	Legionella	Periweissella	Syntrophobacter
ntibacter	Desulfurispirillum	Leifsonia	Permianibacter	Syntrophobotulus
obium	Desulfurivibrio	Leisingera	Persephonella	Syntrophomonas
acter	Desulfurobacterium	Lelliottia	Persicimonas	Syntrophotalea
ntiacibacter	Desulfuromonas	Leminorella	Peteryoungia	Syntrophothermus
ntimicrobium	Devosia	Lentibacillus	Petrimonas	Syntrophus
ntimonas	Devriesea	Lentilactobacillus	Petrocella	Tabrizicola
ticoccus	Dialister	Lentilitoribacter	Petrotoga	Tamlana
imonas	Diaminobutyricimonas	Lentzea	Phaeobacter	Tannerella
liella	Diaphorobacter	Leptodesmis	Phascolarctobacterium	Tardibacter
idibacter	Dichelobacter	Leptolyngbya	Phenylobacterium	Tardiphaga
wickia	Dickeya	Leptospira	Phnomibacter	Tateyamaria
acterium	Dictyoglomus	Leptospirillum	Phocaeicola	Tatlockia
rcus	Dietzia	Leptothermofonsia	Phoenicibacter	Tatumella
hizobium	Dinoroseobacter	Leptothrix	Photobacterium	Tautonia
pira	Dissulfurimicrobium	Leptotrichia	Photorhabdus	Taylorella
pirillum	Dissulfurispira	Leucobacter	Phototrophicus	Telmatocola
obacter	Dokdonella	Leuconostoc	Phreatobacter	Tenacibaculum
llus	Dokdonia	Levilactobacillus	Phycicoccus	Tenuifilum
erioplanes	Dolichospermum	Liberibacter	Phycisphaera	Tepidanaerobacter
eriovorax	Dolosigranulum	Lichenicola	Phyllobacterium	Tepidibacter
eroides	Dongshaea	Lichenihabitans	Phytobacter	Tepidiforma
cduia	Dorea	Ligilactobacillus	Phytohabitans	Tepidimonas
esiella	Draconibacterium	Lignipirellula	Pigmentiphaga	Tepiditoga
onella	Duganella	Limihaloglobus	Pikeienuella	Terasakiella
ia	Duncaniella	Limnobacter	Pimelobacter	Teredinibacter
lea	Dyadobacter	Limnobaculum	Pirellula	Terribacillus
lovibrio	Dyella	Limnochorda	Pirellulimonas	Terricaulis
giatoa	Dysgonomonas	Limnoglobus	Piscirickettsia	Terriglobus
urinckia	Dysosmobacter	Limnohabitans	Pistricoccus	Terrihabitans

Barras_Species[2]

[[1]]
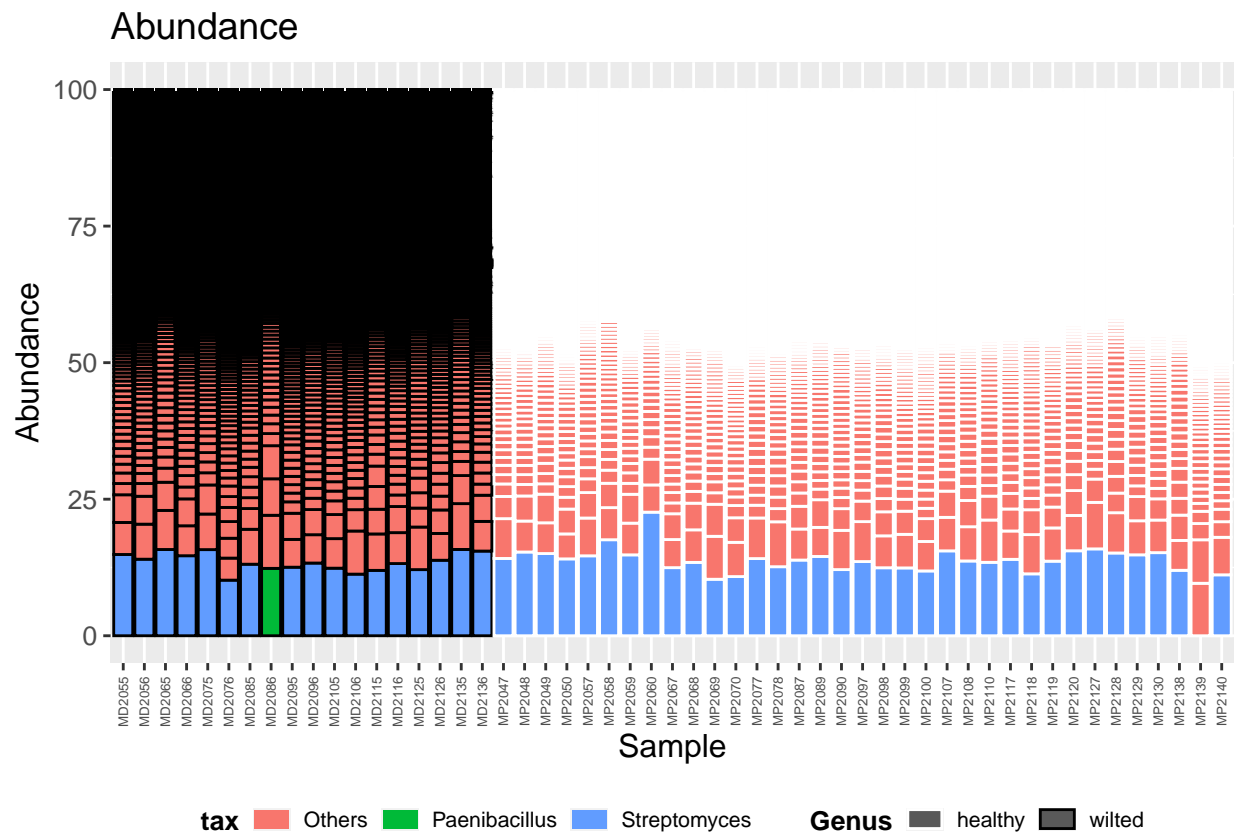
Abundance

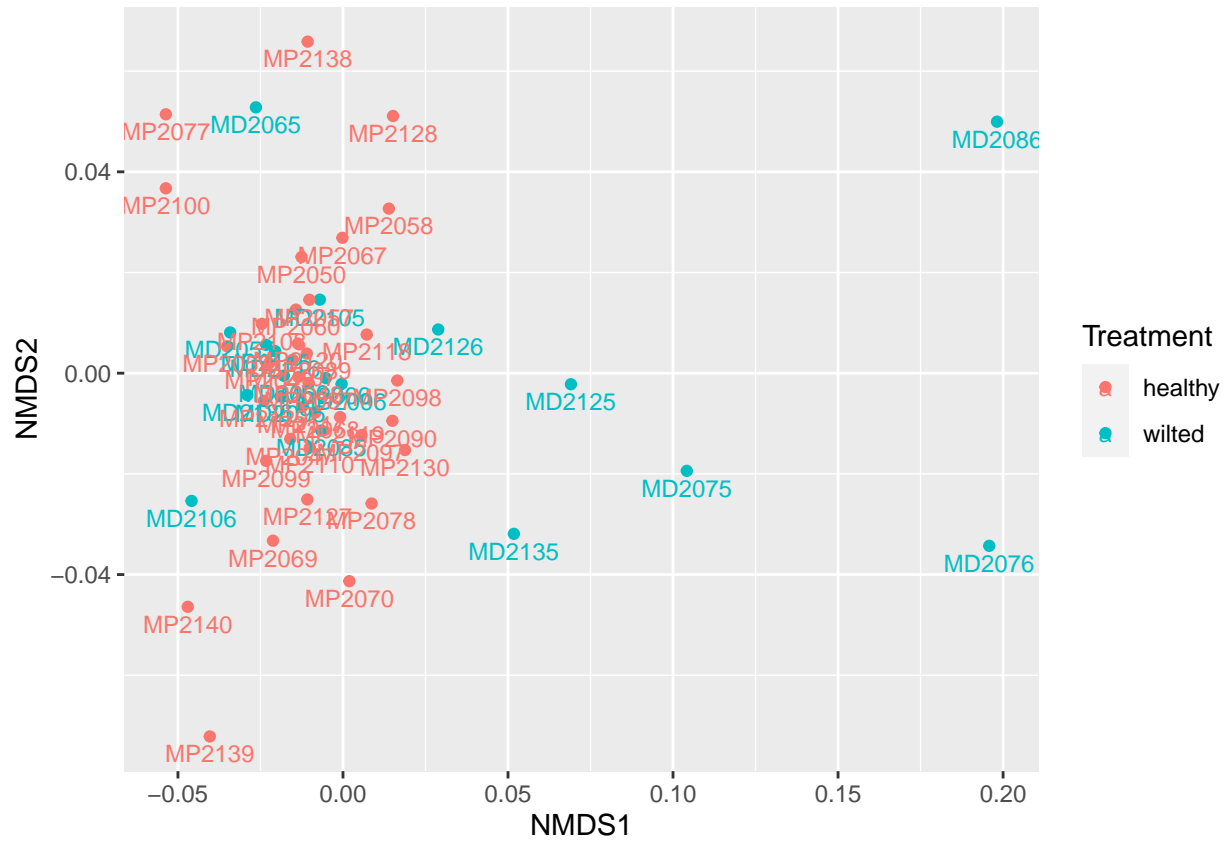| tax | ▮ Others ▮ Paenibacillus ▮ Streptomyces | **Genus** ▮ healthy ▮ wilted |

```
Beta_diversity(merge_Bacteria , 'Genus' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1467945
## Run 1 stress 0.1432835
## ... New best solution
## ... Procrustes: rmse 0.08892711  max resid 0.3292679
## Run 2 stress 0.1624125
## Run 3 stress 0.1452004
## Run 4 stress 0.1476409
## Run 5 stress 0.1490739
## Run 6 stress 0.1438418
## Run 7 stress 0.1481202
## Run 8 stress 0.1437861
## Run 9 stress 0.1480106
## Run 10 stress 0.1490668
## Run 11 stress 0.1476747
## Run 12 stress 0.1511661
## Run 13 stress 0.1432842
## ... Procrustes: rmse 0.0008987919  max resid 0.003811659
## ... Similar to previous best
## Run 14 stress 0.1638381
## Run 15 stress 0.1519965
## Run 16 stress 0.1476188
## Run 17 stress 0.1469869
```

```
## Run 18 stress 0.1578524
## Run 19 stress 0.1547472
## Run 20 stress 0.1500188
## *** Best solution repeated 1 times
```
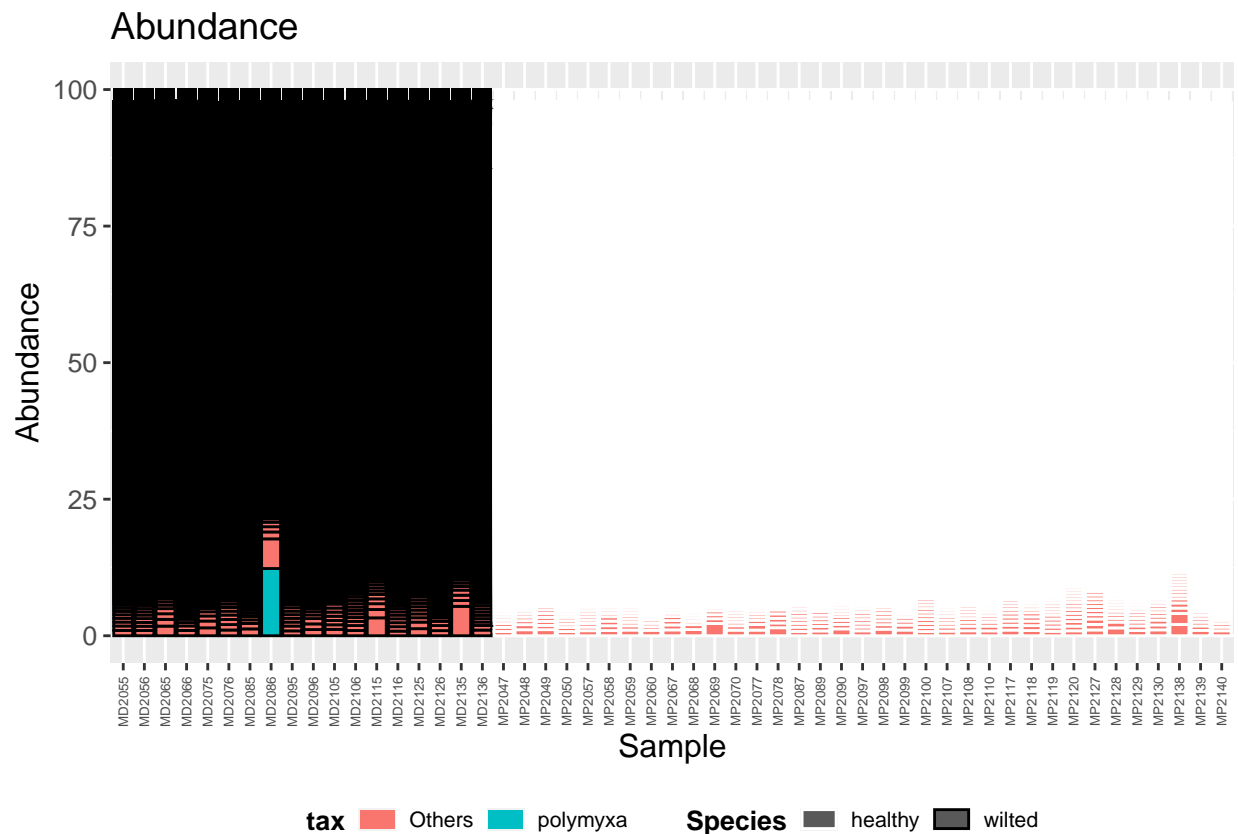


```
Alpha_diversity(merge_Bacteria , 'Genus' , 'Treatment')
```

———Bacteria by Species

```
Barras_Species <- Abundance_barras(merge_Bacteria,'Species','Treatment',10.0)
Barras_Species[1]
```

```
## [[1]]
```

e

lactamica	sp. 'Soap Lake #7'	sp. KSB–15	sp. X
lactarius	sp. (Blaberus giganteus)	sp. KSM–R2A25	sp. X
lactatifermentans	sp. (Blatta orientalis)	sp. KSM–R2A30	sp. X
lactatiformans	sp. (Blattella germanica)	sp. KT 15	sp. X
lactis	sp. (Cryptocercus kyebangensis)	sp. KT25b	sp. X
lactucae	sp. (Cryptocercus punctulatus) str. Cpu	sp. KTR9	sp. X
lacunae	sp. (ex Adelges kitamiensis)	sp. KUDC0405	sp. X
lacus	sp. (ex Biomphalaria glabrata)	sp. KUDC0406	sp. X
lacuslunae	sp. (Mastotermes darwiniensis)	sp. KUDC1026	sp. x
lacustris	sp. (Nauphoeta cinerea)	sp. KUDC1714	sp. X
laguerreae	sp. (Periplaneta americana)	sp. KUIN–1	sp. X
laidlawii	sp. 001	sp. Kuro–4	sp. X
laixinhei	sp. 007	sp. KW1	sp. X
lalkuanensis	sp. 008	sp. KX20019	sp. X
laminatus	sp. 02C 26	sp. KY–GH–1	sp. X
lanienae	sp. 09C 129	sp. KY–YJ–3	sp. X
lanii	sp. 09RB8471	sp. KY3	sp. Y
lansingensis	sp. 09RB8910	sp. KY5	sp. Y
lanthieri	sp. 1_2014MBL_MicDiv	sp. KY70	sp. Y
lapagei	sp. 1_2015MBL_MicDiv	sp. KY75	sp. Y
lapidicaptus	sp. 1–1C	sp. L–07	sp. Y
lapsinanis	sp. 1.5R	sp. L–2–11	sp. Y
lari	sp. 1(2017)	sp. L–8–10	sp. Y
lariciata	sp. 103DPR2	sp. L–8–3	sp. Y
larrymoorei	sp. 1063	sp. L–A4	sp. Y
larvae	sp. 107–1	sp. L12M9	sp. Y
lata	sp. 1070	sp. L1A13	sp. Y
latens	sp. 10FS3–1	sp. L1A34	sp. Y
laterosporus	sp. 10M–3C3	sp. L1A9	sp. Y
laumondii	sp. 10RB9215	sp. L1I39	sp. Y
lautus	sp. 11–1–2	sp. L1SW	sp. Y
lavamentivorans	sp. 11–B–312	sp. L2A1	sp. Y
lavendulae	sp. 113–1–2	sp. L2A11	sp. Y
leachii	sp. 113–3–3	sp. L3–i22	sp. Y
leadbetteri	sp. 113–3–9	sp. L3–i23	sp. Y
leeuwenhoekii	sp. 1137	sp. L3A3	sp. Y
leguminosarum	sp. 113P3	sp. L3A6	sp. Y
lehensis	sp. 114	sp. L3A8	sp. Y
lekithochrous	sp. 11515TR	sp. L5	sp. Y
lemovicicum	sp. 116–D4	sp. L51/94	sp. Y
lemurum	sp. 119287	sp. L5B5	sp. Y
lenghuensis	sp. 11B	sp. L6–1	sp. Y
lenta	sp. 11kri321	sp. L9–4	sp. Y
lentiflavum	sp. 12200R–103	sp. LA–2–3–30–S1–D2	sp. Y
lentis	sp. 13–15	sp. LA112445	sp. Y
lentocellum	sp. 131	sp. LA31	sp. Y
lentus	sp. 131–2–1	sp. LAB–08	sp. Y
leopoldii	sp. 131–2–5	sp. LADL05–105	sp. Y
leprae	sp. 131–3–5	sp. LAS2	sp. Y
lepromatosis	sp. 13159349	sp. LB1	sp. Y
leptomitoformis	sp. 135	sp. LBG001	sp. Y
lettingae	sp. 140616W15	sp. LBUM 1475	sp. Y
liangguodongii	sp. 14171R–50	sp. LBUM 1480	sp. Y
liangshanensis	sp. 14181154	sp. LBUM 1482	sp. Y
liaowanqingii	sp. 143–21	sp. LBUM920	sp. Y
libanensis	sp. 144S4	sp. LC2018020214	sp. Y
licheniformis	sp. 15–184	sp. LC6	sp. Y

andiella
ibbosus
ifera

Barras_Species[2]

[[1]]

Abundance

tax ■ Others ■ polymyxa **Species** ■ healthy ■ wilted

```
Beta_diversity(merge_Bacteria , 'Species' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1597841
## Run 1 stress 0.1603297
## Run 2 stress 0.1601333
## ... Procrustes: rmse 0.05751254  max resid 0.2742671
## Run 3 stress 0.1746425
## Run 4 stress 0.1682795
## Run 5 stress 0.1745846
## Run 6 stress 0.1595746
## ... New best solution
## ... Procrustes: rmse 0.06179215  max resid 0.2864908
## Run 7 stress 0.1667257
## Run 8 stress 0.1622331
## Run 9 stress 0.1853643
## Run 10 stress 0.1892493
## Run 11 stress 0.1632423
## Run 12 stress 0.1899387
## Run 13 stress 0.1618986
## Run 14 stress 0.1826662
## Run 15 stress 0.1604222
## Run 16 stress 0.1734581
## Run 17 stress 0.1590693
## ... New best solution
```

```
## ... Procrustes: rmse 0.03809861   max resid 0.1539445
## Run 18 stress 0.1680945
## Run 19 stress 0.1596331
## Run 20 stress 0.1586473
## ... New best solution
## ... Procrustes: rmse 0.04184967   max resid 0.1834734
## *** Best solution was not repeated -- monoMDS stopping criteria:
##      3: no. of iterations >= maxit
##     17: stress ratio > sratmax
```



```
Alpha_diversity(merge_Bacteria , 'Species' , 'Treatment')
```