230306_Reporte1Exploracion

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2023-04-03

```
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)
percentages_fil <- transform_sample_counts(fresa_kraken_fil, function(x) x*100 / sum(x) )
percentages_df <- psmelt(percentages_fil)
```

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

Crea los subconjuntos de datos input phy phyliseq total tax rango al que queremos recortar output

```
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

input entra el percentages_df

```
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=attr
    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$Abundance < abundance_percentage] <- "abundance_percentage"
  percentages_df$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 betadiversity

```
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 alphadiversity

```
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)
}
```
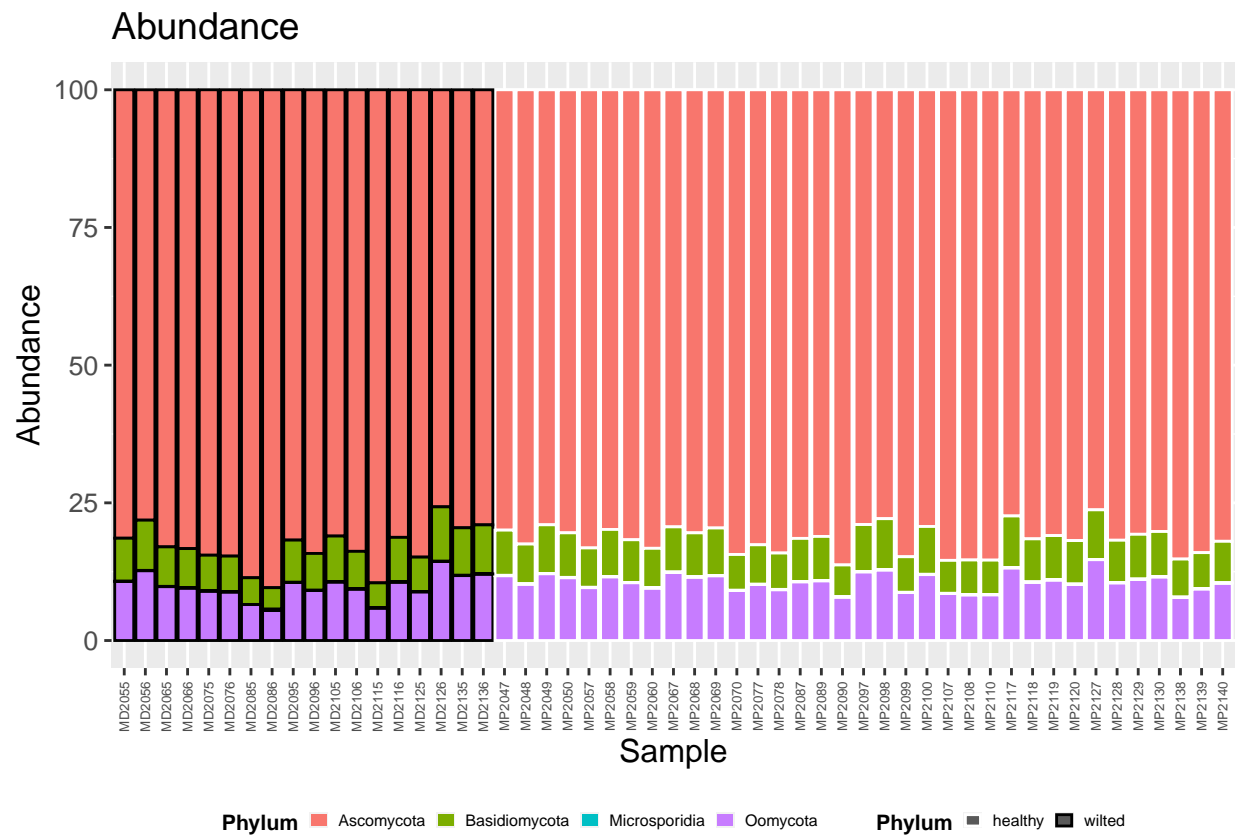
#———Eukarya by Phylum

```
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 ideoms with 'aes()'
```
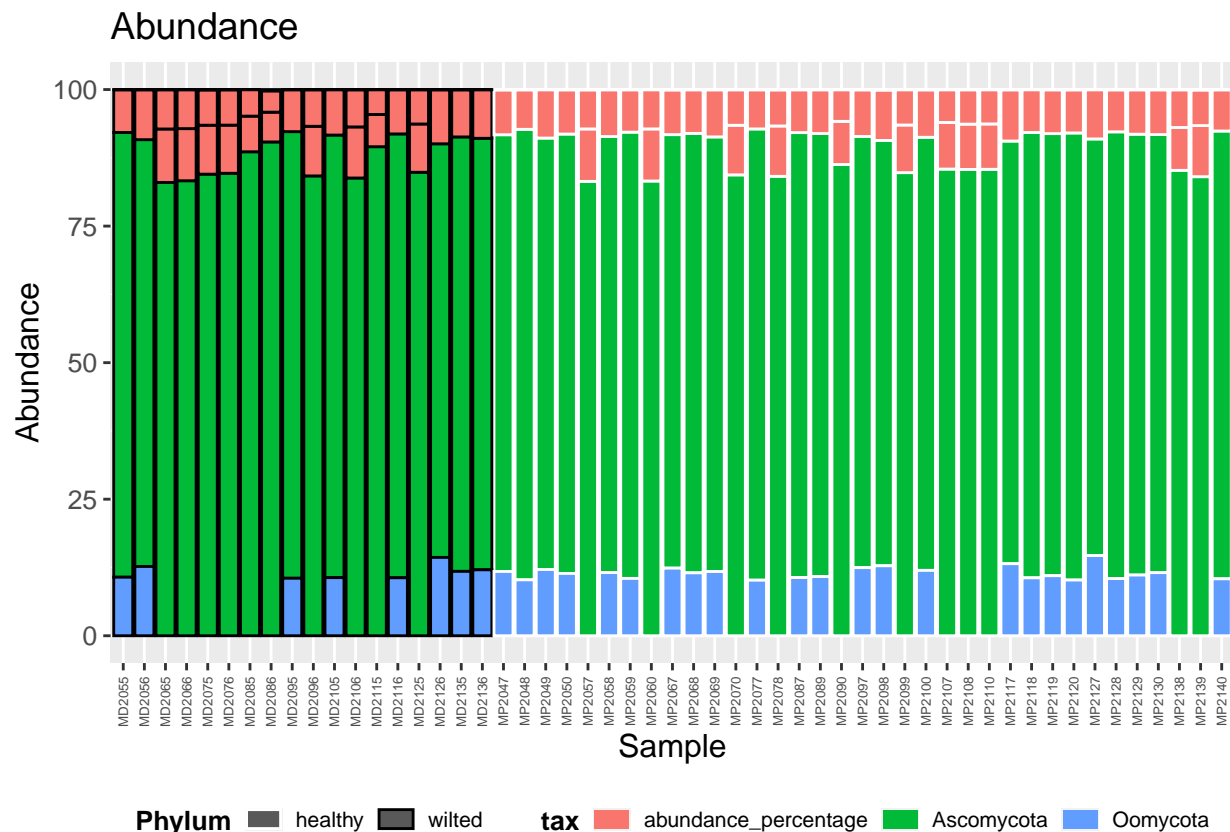
```
Barras_Phylum[1] # normal
```

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

Abundance

```
Barras_Phylum[2]
```

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

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

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.01148681
## Run 1 stress 9.641699e-05
## ... New best solution
## ... Procrustes: rmse 0.03460127  max resid 0.09064286
## Run 2 stress 9.692958e-05
## ... Procrustes: rmse 0.0001280624  max resid 0.0004094851
## ... Similar to previous best
## Run 3 stress 0.0009993135
## Run 4 stress 2.875625e-05
## ... New best solution
## ... Procrustes: rmse 0.0001075607  max resid 0.0002893054
## ... Similar to previous best
## Run 5 stress 7.419065e-05
## ... Procrustes: rmse 4.598373e-05  max resid 0.0001193756
## ... Similar to previous best
## Run 6 stress 7.803609e-05
## ... Procrustes: rmse 2.872485e-05  max resid 6.902742e-05
## ... Similar to previous best
## Run 7 stress 9.725895e-05
## ... Procrustes: rmse 0.0002168401  max resid 0.0005770855
## ... Similar to previous best
```

```
## Run 8 stress 8.900437e-05
## ... Procrustes: rmse 8.648394e-05  max resid 0.0002263783
## ... Similar to previous best
## Run 9 stress 9.712047e-05
## ... Procrustes: rmse 0.0001019901  max resid 0.0002717338
## ... Similar to previous best
## Run 10 stress 9.473721e-05
## ... Procrustes: rmse 0.0001079967  max resid 0.0002832011
## ... Similar to previous best
## Run 11 stress 9.169436e-05
## ... Procrustes: rmse 6.777917e-05  max resid 0.0001896028
## ... Similar to previous best
## Run 12 stress 0.0001125098
## ... Procrustes: rmse 0.000332578  max resid 0.0008723591
## ... Similar to previous best
## Run 13 stress 9.913374e-05
## ... Procrustes: rmse 0.000169905  max resid 0.0004530579
## ... Similar to previous best
## Run 14 stress 9.120442e-05
## ... Procrustes: rmse 2.554051e-05  max resid 0.0001256882
## ... Similar to previous best
## Run 15 stress 9.384635e-05
## ... Procrustes: rmse 7.33919e-05  max resid 0.0001795472
## ... Similar to previous best
## Run 16 stress 6.475988e-05
## ... Procrustes: rmse 3.209143e-05  max resid 7.189593e-05
## ... Similar to previous best
## Run 17 stress 0.0007519899
## Run 18 stress 0.0001067793
## ... Procrustes: rmse 0.0003143495  max resid 0.0008254772
## ... Similar to previous best
## Run 19 stress 9.906154e-05
## ... Procrustes: rmse 0.0001095915  max resid 0.0002853942
## ... Similar to previous best
## Run 20 stress 9.462542e-05
## ... Procrustes: rmse 0.0001393057  max resid 0.0003633612
## ... Similar to previous best
## *** Best solution repeated 16 times


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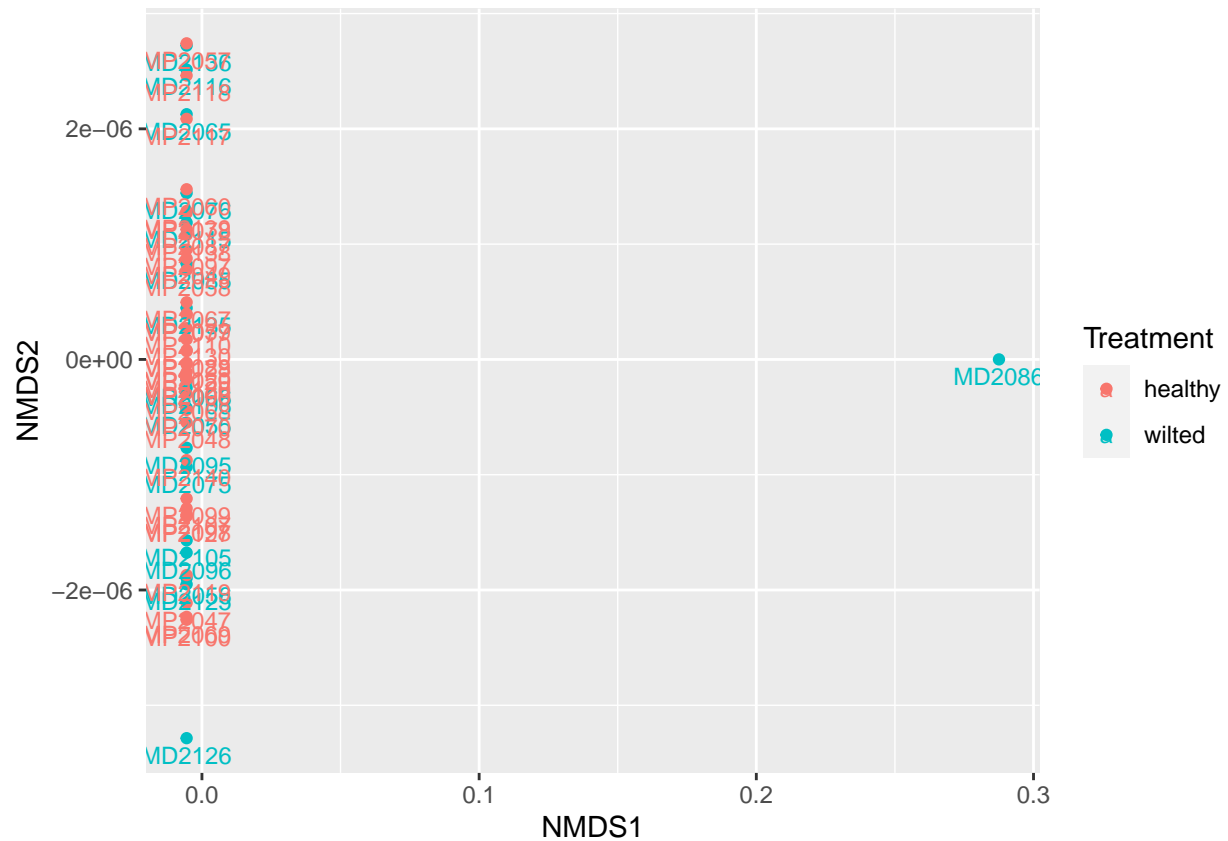
```
Alpha_diversity(merge_Eukaryota , 'Phylum' , 'Treatment')
```

```
## 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.
```
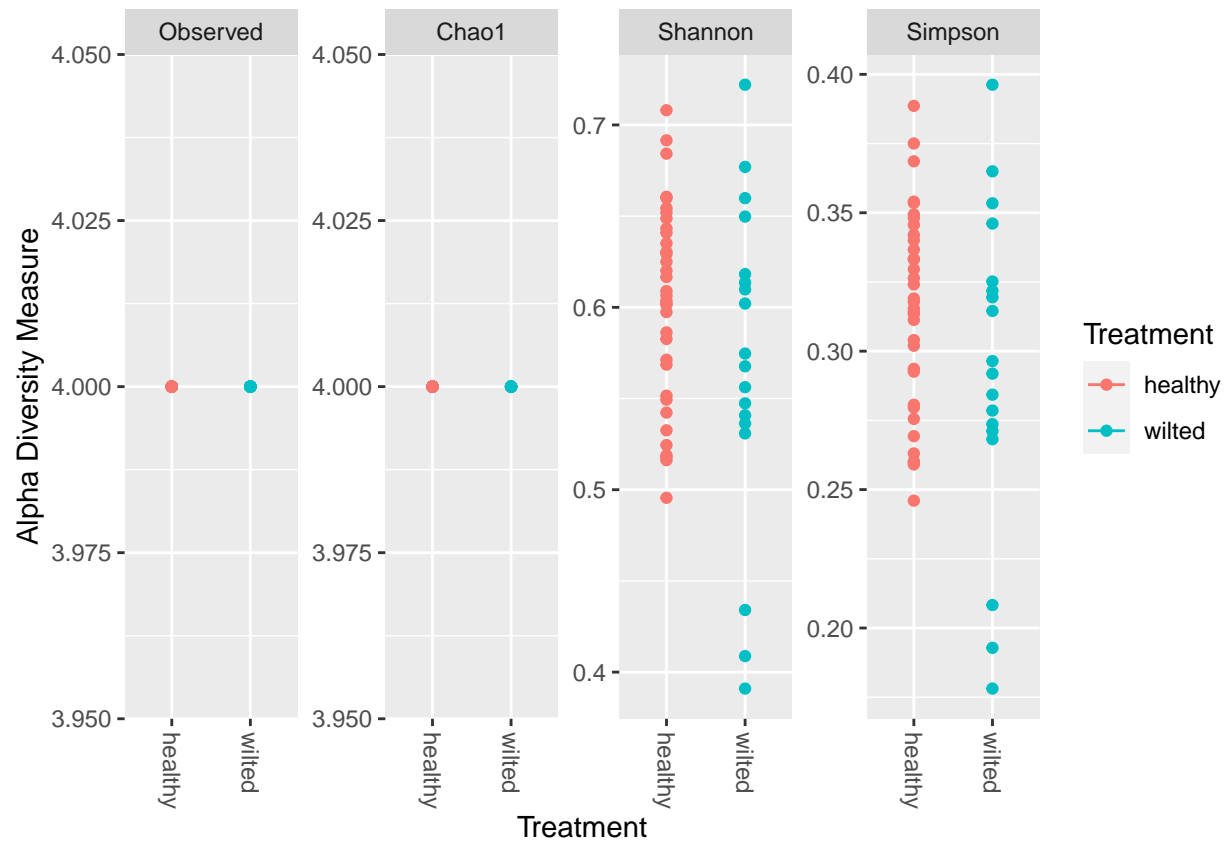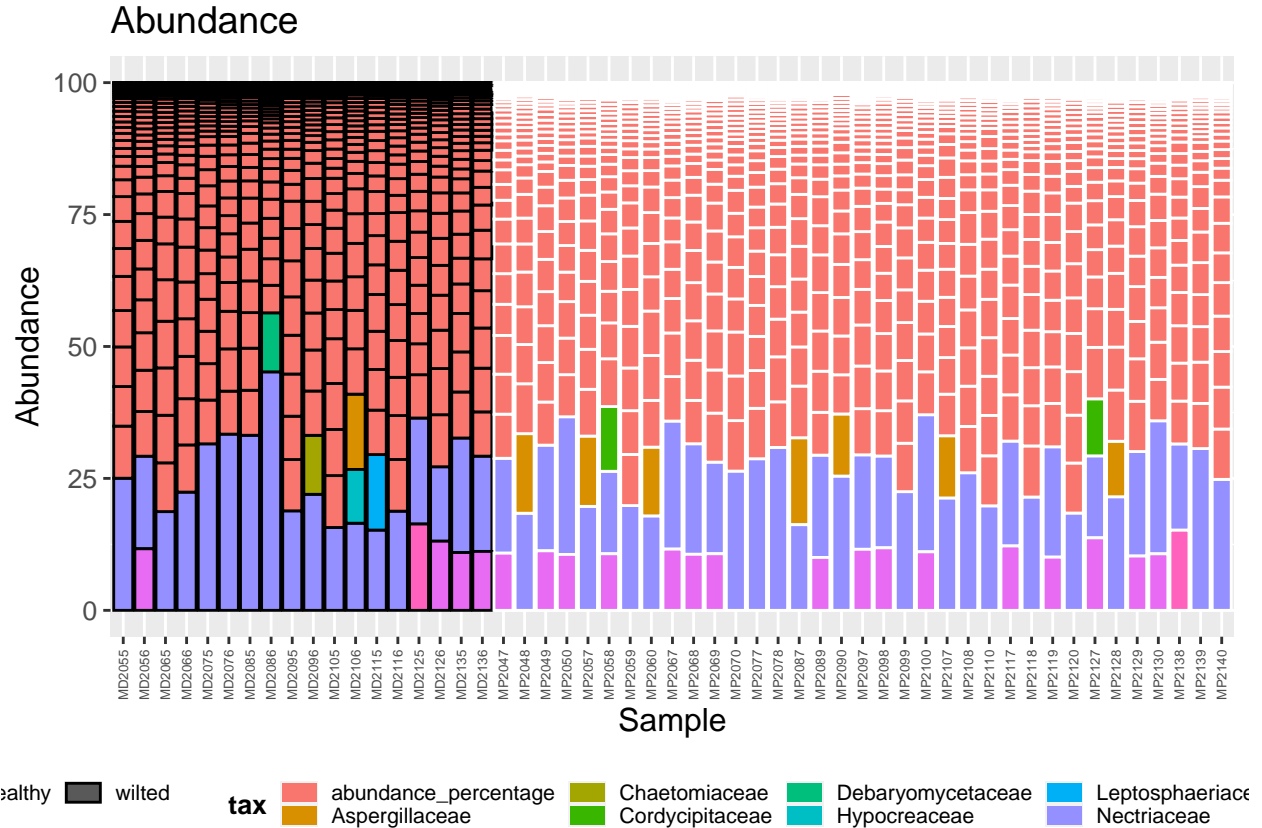
#———Eukarya by Family

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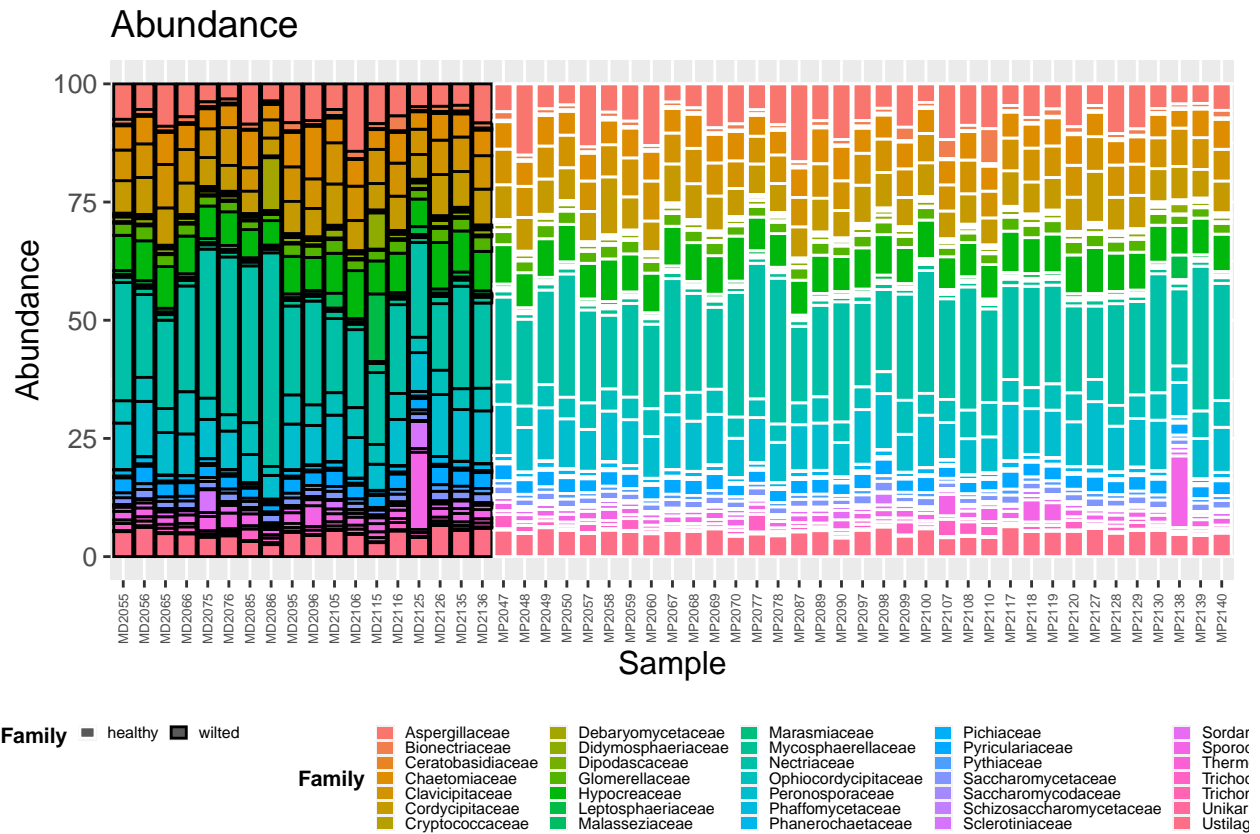
```
## [[1]]
```

Abundance

```
Barras_Species[2]
```

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

Abundance

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

```
## Wisconsin double standardization
## Run 0 stress 0.1089081
## Run 1 stress 0.1088964
## ... New best solution
## ... Procrustes: rmse 0.002397465  max resid 0.009337499
## ... Similar to previous best
## Run 2 stress 0.1089479
## ... Procrustes: rmse 0.008318336  max resid 0.0543661
## Run 3 stress 0.1089298
## ... Procrustes: rmse 0.008610539  max resid 0.05495783
## Run 4 stress 0.1088985
## ... Procrustes: rmse 0.000636777  max resid 0.00368301
## ... Similar to previous best
## Run 5 stress 0.1352082
## Run 6 stress 0.109113
## ... Procrustes: rmse 0.01003345  max resid 0.05422836
## Run 7 stress 0.1088882
## ... New best solution
## ... Procrustes: rmse 0.00173353  max resid 0.009003435
## ... Similar to previous best
## Run 8 stress 0.1089152
## ... Procrustes: rmse 0.001735834  max resid 0.009378948
## ... Similar to previous best
```

```
## Run 9 stress 0.1185617
## Run 10 stress 0.1088982
## ... Procrustes: rmse 0.00155193  max resid 0.007565839
## ... Similar to previous best
## Run 11 stress 0.1089574
## ... Procrustes: rmse 0.00861713  max resid 0.05374258
## Run 12 stress 0.1089481
## ... Procrustes: rmse 0.008203471  max resid 0.05409664
## Run 13 stress 0.4042251
## Run 14 stress 0.1089316
## ... Procrustes: rmse 0.008488576  max resid 0.05456272
## Run 15 stress 0.1089084
## ... Procrustes: rmse 0.001691858  max resid 0.009408485
## ... Similar to previous best
## Run 16 stress 0.1113091
## Run 17 stress 0.1091144
## ... Procrustes: rmse 0.0100354  max resid 0.05392358
## Run 18 stress 0.1091131
## ... Procrustes: rmse 0.009953453  max resid 0.05403308
## Run 19 stress 0.1088877
## ... New best solution
## ... Procrustes: rmse 0.0001671813  max resid 0.0009656288
## ... Similar to previous best
## Run 20 stress 0.109126
## ... Procrustes: rmse 0.01001698  max resid 0.05420395
## *** Best solution repeated 1 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.
```
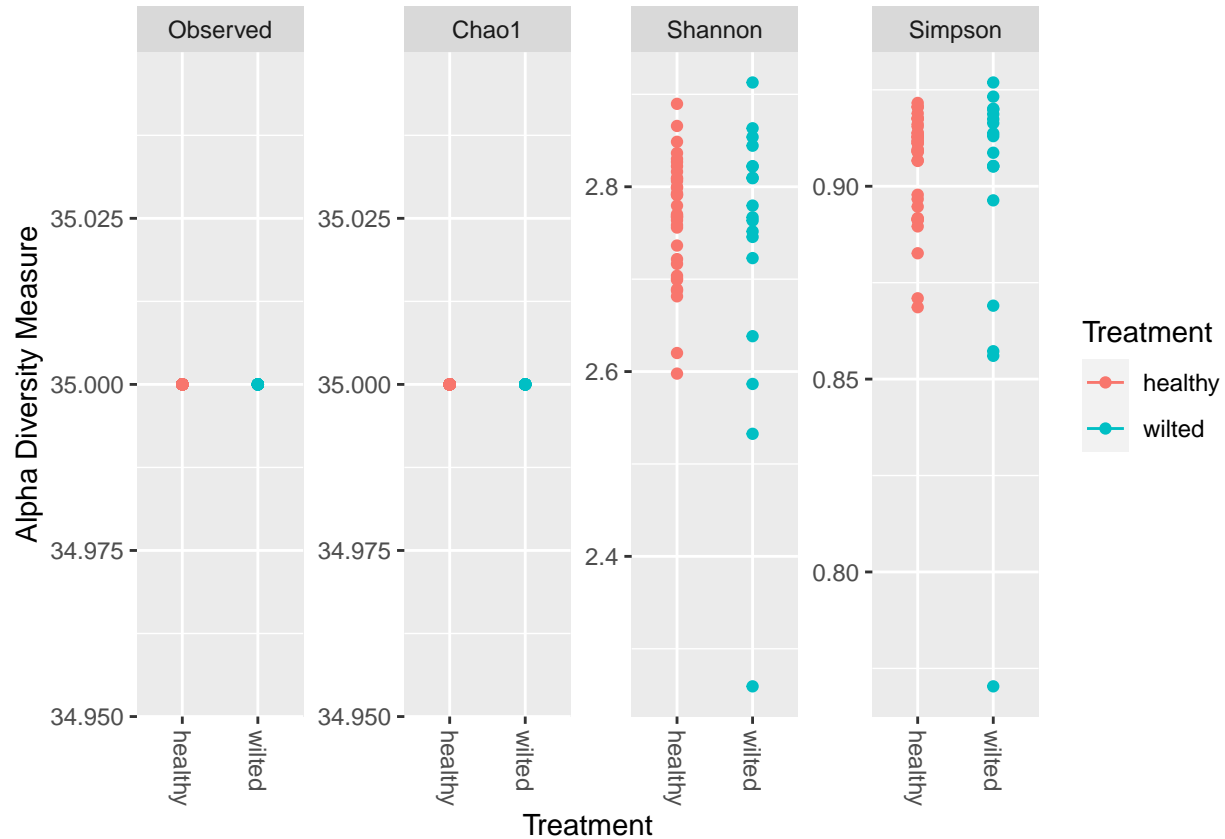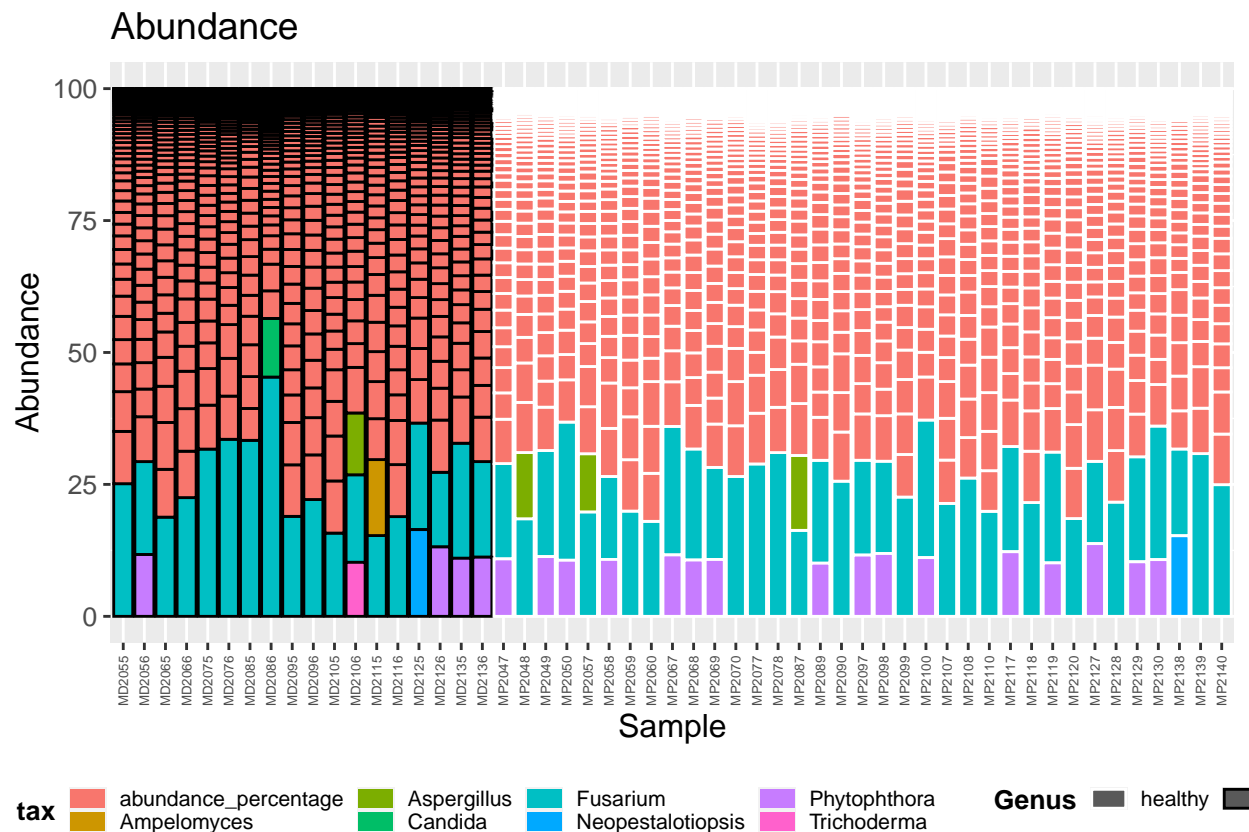

#———Eukarya by Genero

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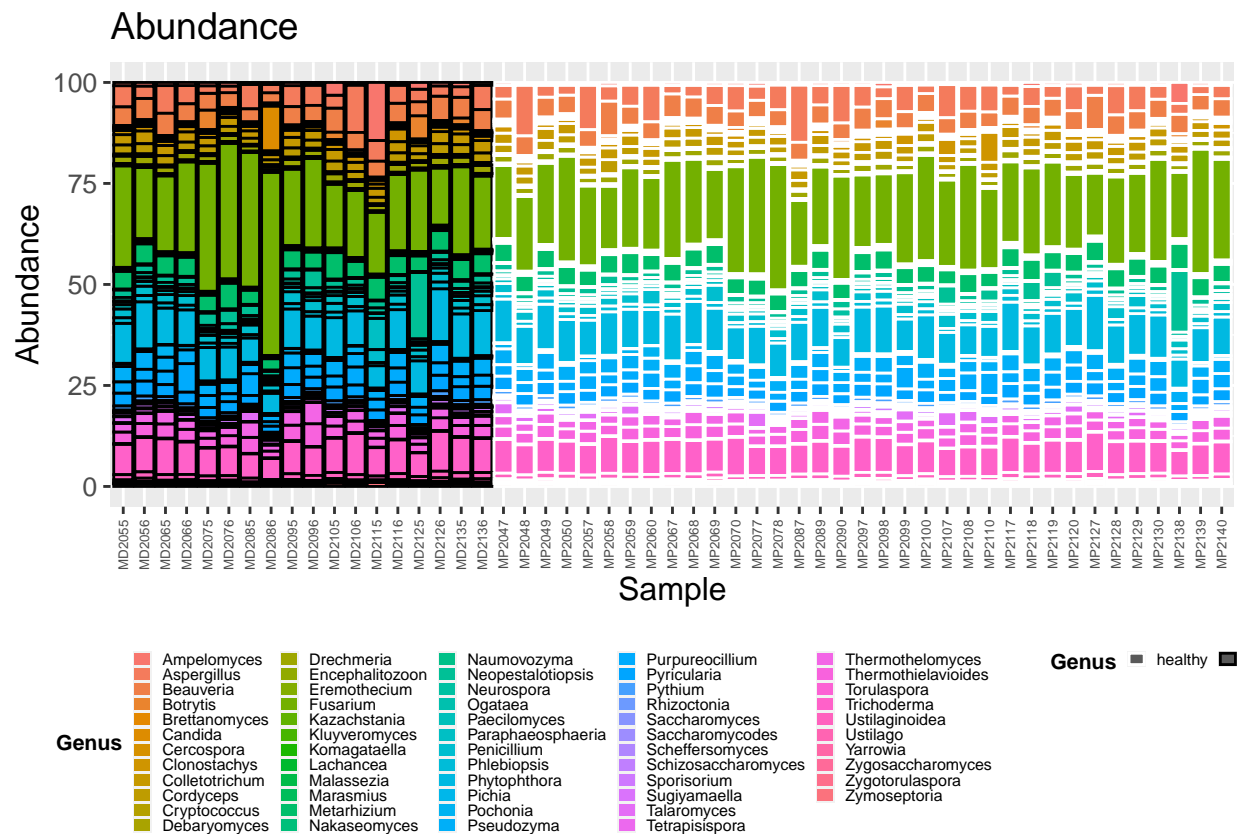
```
## [[1]]
```

Abundance

Genus: healthy, ...

```
Barras_Species[2]
```

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

Abundance

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

```
## Wisconsin double standardization
## Run 0 stress 0.110709
## Run 1 stress 0.1111514
## ... Procrustes: rmse 0.01374689  max resid 0.06906551
## Run 2 stress 0.1235012
## Run 3 stress 0.1119814
## Run 4 stress 0.1107094
## ... Procrustes: rmse 0.001118204  max resid 0.006393413
## ... Similar to previous best
## Run 5 stress 0.123502
## Run 6 stress 0.1235014
## Run 7 stress 0.1223845
## Run 8 stress 0.1107098
## ... Procrustes: rmse 0.0002377637  max resid 0.001329702
## ... Similar to previous best
## Run 9 stress 0.1236307
## Run 10 stress 0.1236309
## Run 11 stress 0.110709
## ... New best solution
## ... Procrustes: rmse 1.991006e-05  max resid 0.0001234856
## ... Similar to previous best
## Run 12 stress 0.1235025
## Run 13 stress 0.1236304
```

```
## Run 14 stress 0.1107086
## ... New best solution
## ... Procrustes: rmse 0.000252225  max resid 0.001539016
## ... Similar to previous best
## Run 15 stress 0.1107097
## ... Procrustes: rmse 0.0009435275  max resid 0.005267492
## ... Similar to previous best
## Run 16 stress 0.1223877
## Run 17 stress 0.1107172
## ... Procrustes: rmse 0.002093797  max resid 0.01195467
## Run 18 stress 0.1235015
## Run 19 stress 0.1223843
## Run 20 stress 0.1107093
## ... Procrustes: rmse 0.000821115  max resid 0.00457383
## ... Similar to previous best
## *** Best solution repeated 3 times
```
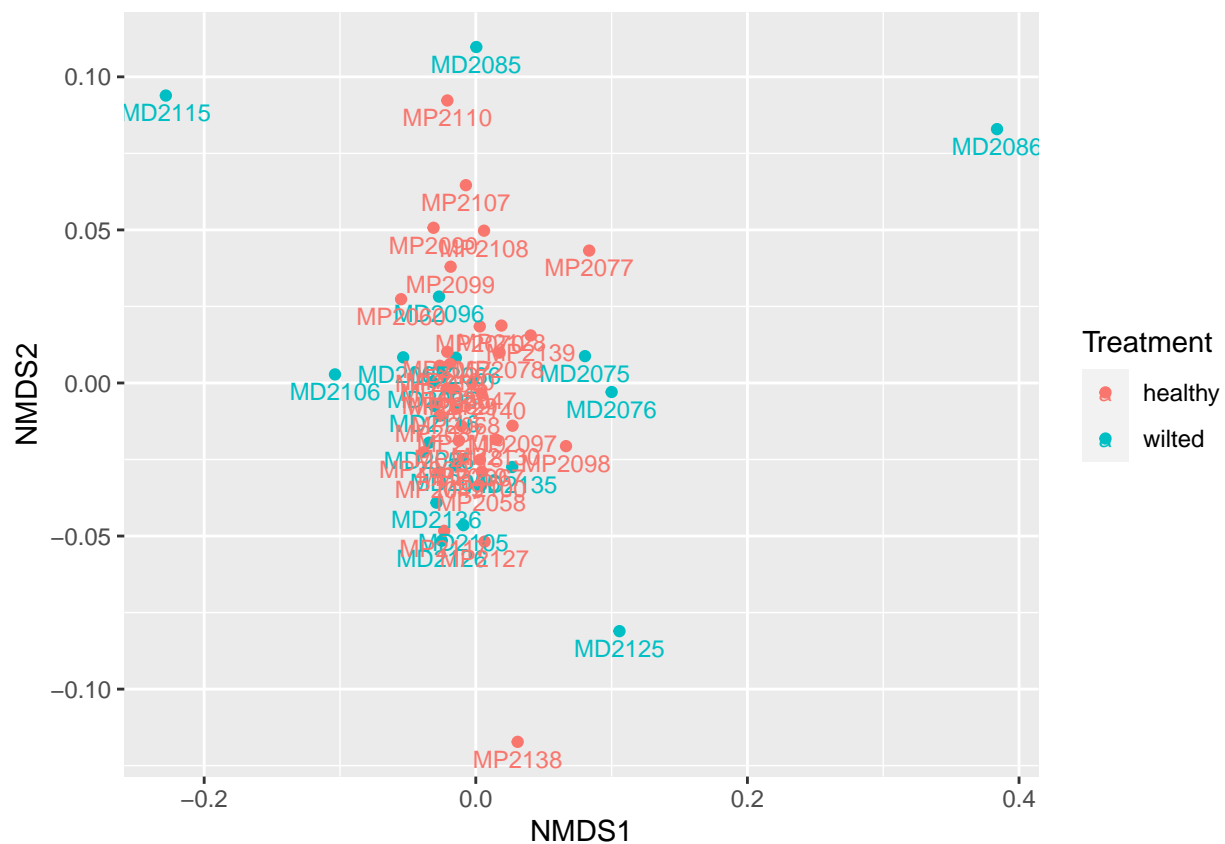


```
Alpha_diversity(merge_Eukaryota , 'Genus' , 'Treatment')
```
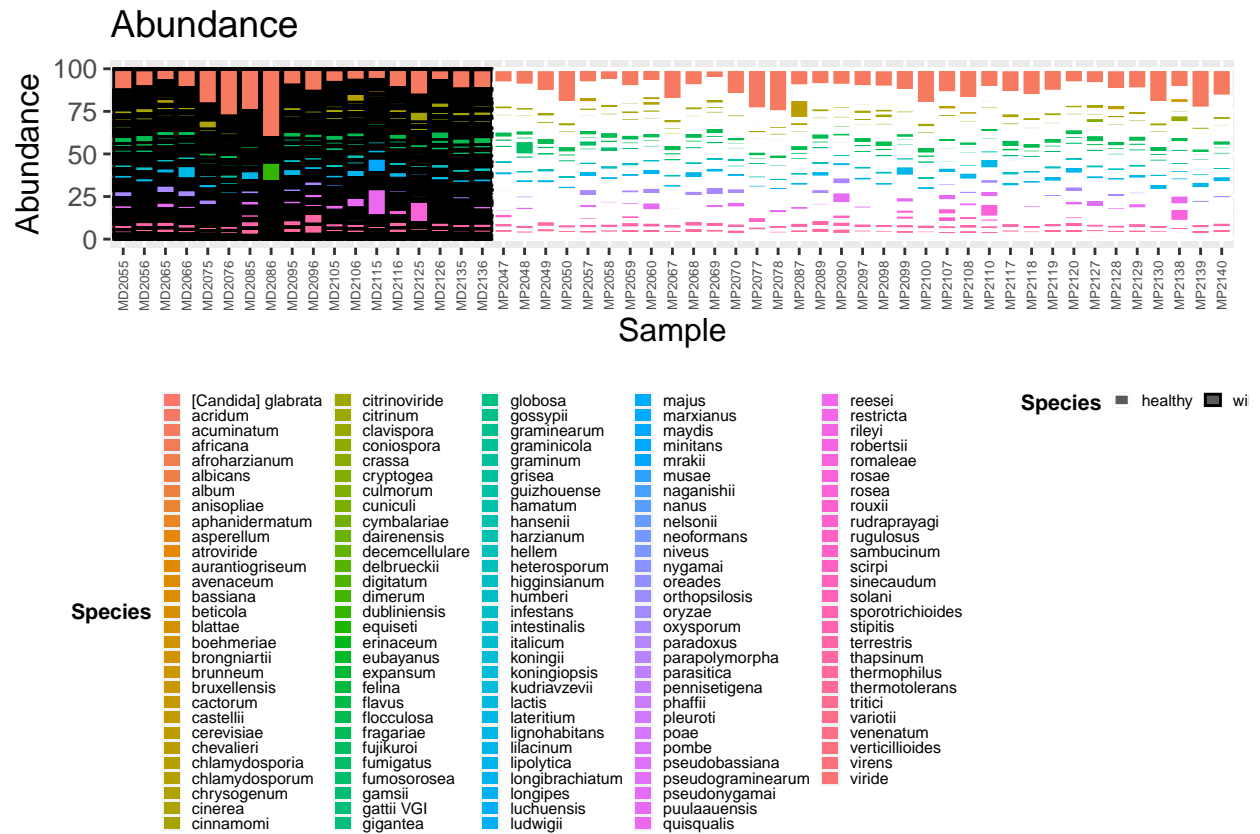
```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##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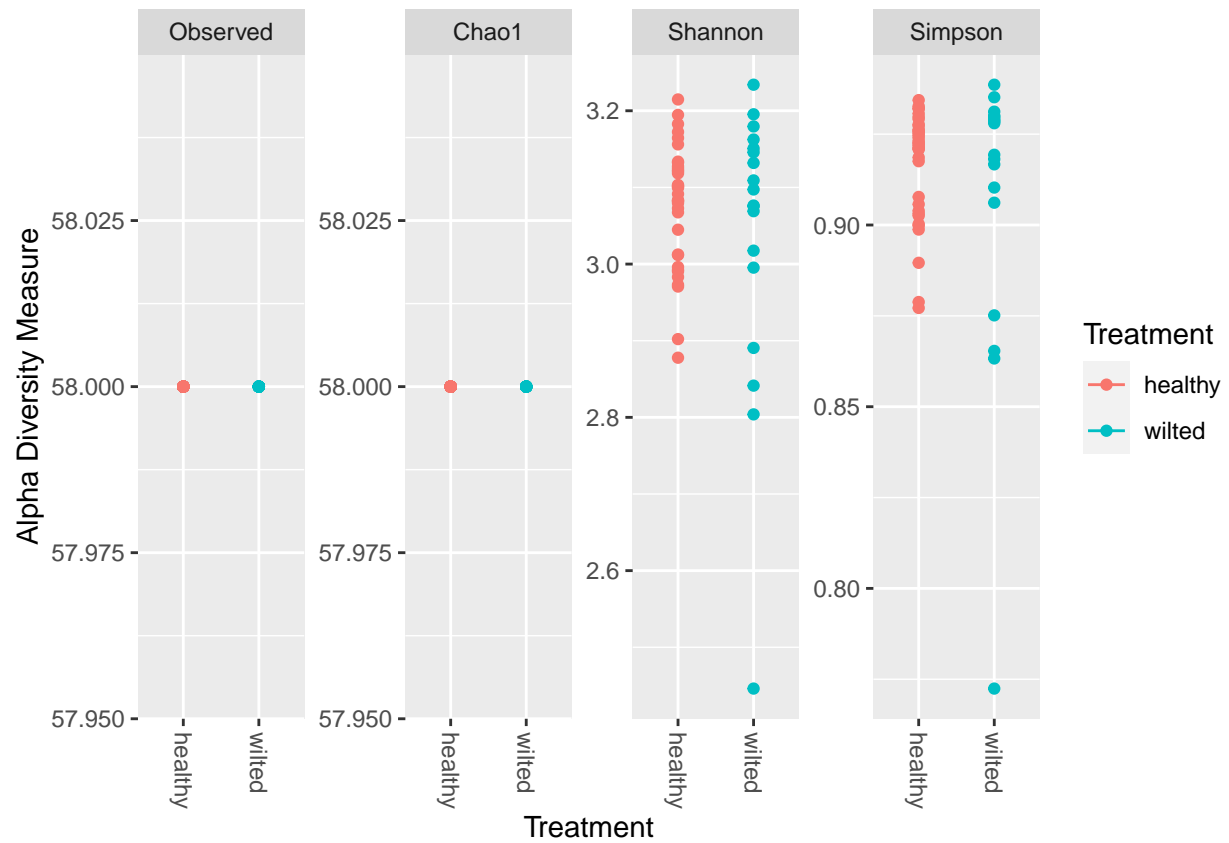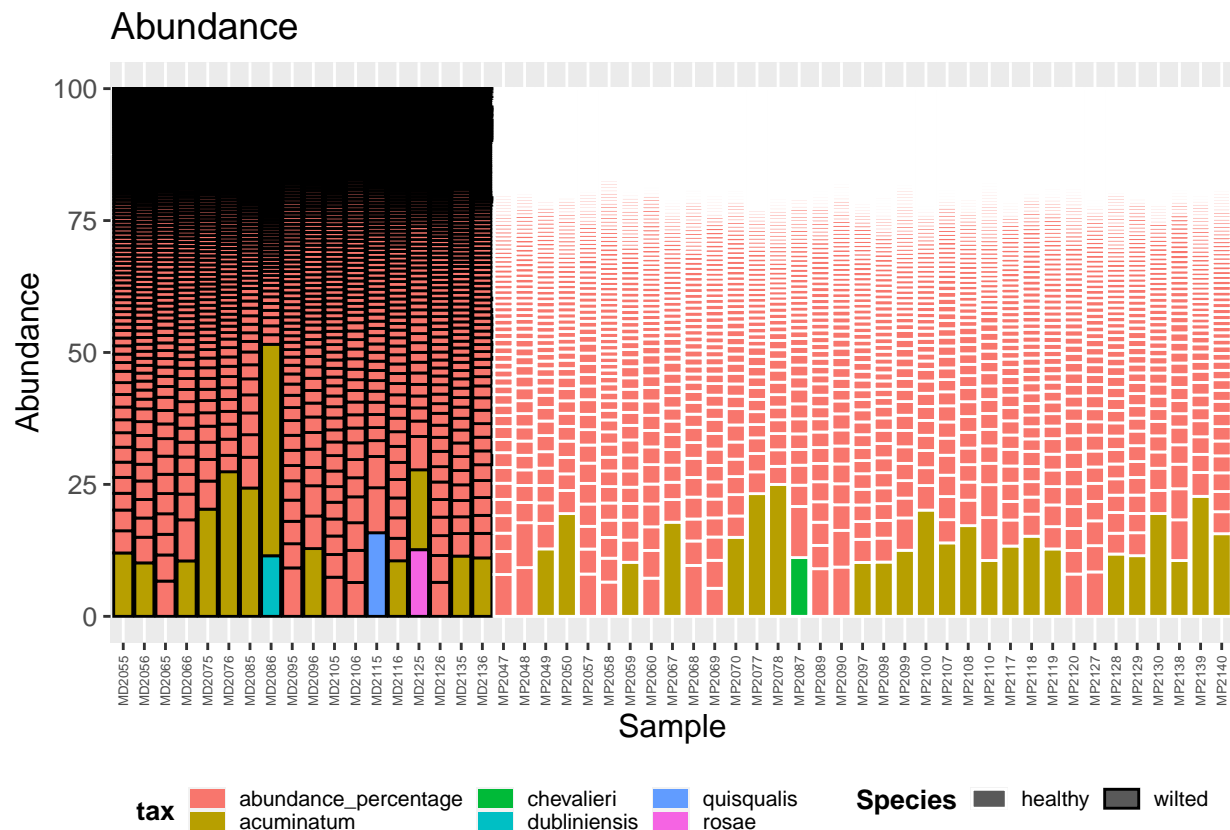
#————Eukarya by Species

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

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

Abundance

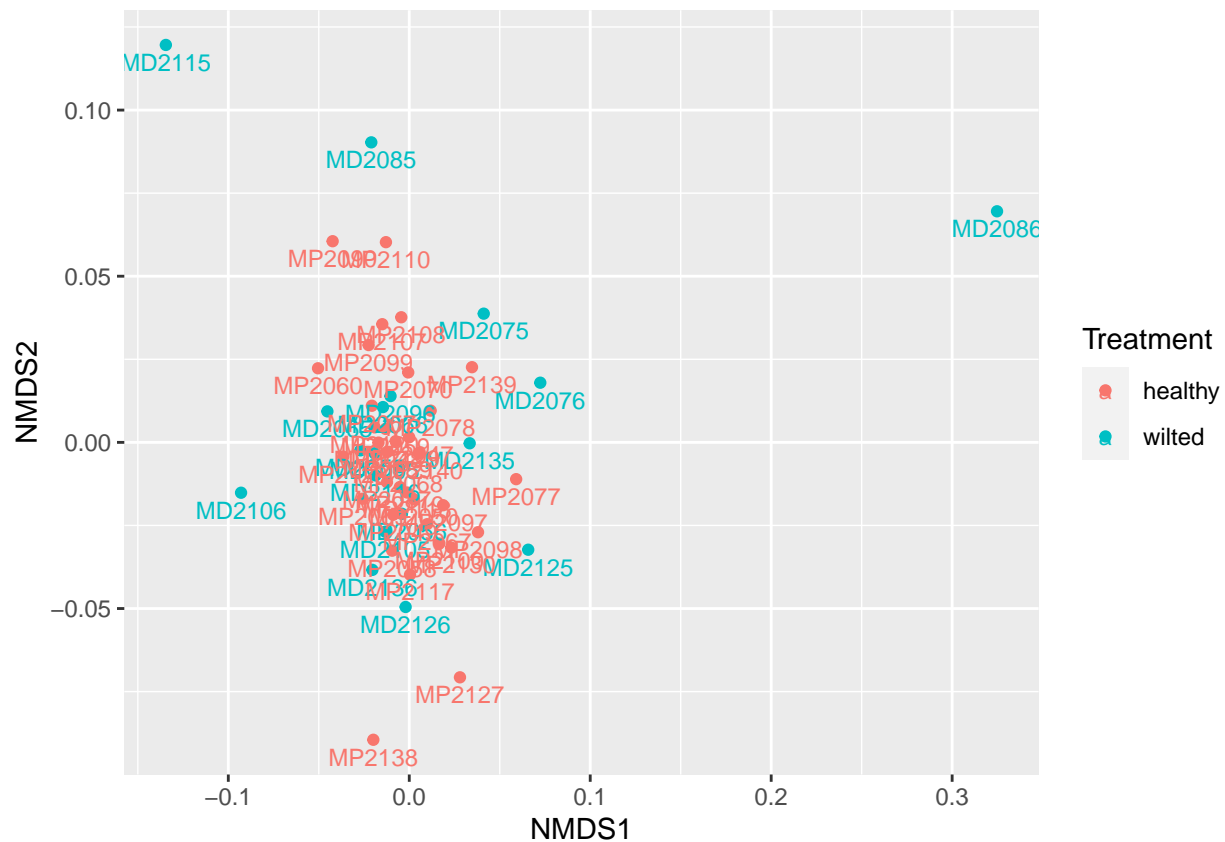| Species				
[Candida] glabrata	citrinoviride	globosa	majus	reesei
acridum	citrinum	gossypii	marxianus	restricta
acuminatum	clavispora	graminearum	maydis	rileyi
africana	coniospora	graminicola	minitans	robertsii
afroharzianum	crassa	graminum	mrakii	romaleae
albicans	cryptogea	grisea	musae	rosae
album	culmorum	guizhouense	naganishii	rosea
anisopliae	cuniculi	hamatum	nanus	rouxii
aphanidermatum	cymbalariae	hansenii	nelsonii	rudraprayagi
asperellum	dairenensis	harzianum	neoformans	rugulosus
atroviride	decemcellulare	hellem	niveus	sambucinum
aurantiogriseum	delbrueckii	heterosporum	nygamai	scirpi
avenaceum	digitatum	higginsianum	oreades	sinecaudum
bassiana	dimerum	humberi	orthopsilosis	solani
beticola	dubliniensis	infestans	oryzae	sporotrichioides
blattae	equiseti	intestinalis	oxysporum	stipitis
boehmeriae	erinaceum	italicum	paradoxus	terrestris
brongniartii	eubayanus	koningii	parapolymorpha	thapsinum
brunneum	expansum	koningiopsis	parasitica	thermophilus
bruxellensis	felina	kudriavzevii	pennisetigena	thermotolerans
cactorum	flavus	lactis	phaffii	tritici
castellii	flocculosa	lateritium	pleuroti	variotii
cerevisiae	fragariae	lignohabitans	poae	venenatum
chevalieri	fujikuroi	lilacinum	pombe	verticillioides
chlamydosporia	fumigatus	lipolytica	pseudobassiana	virens
chlamydosporum	fumosorosea	longibrachiatum	pseudograminearum	viride
chrysogenum	gamsii	longipes	pseudonygamai	
cinerea	gattii VGI	luchuensis	puulaauensis	
cinnamomi	gigantea	ludwigii	quisqualis	

Species   ■ healthy ■ wi
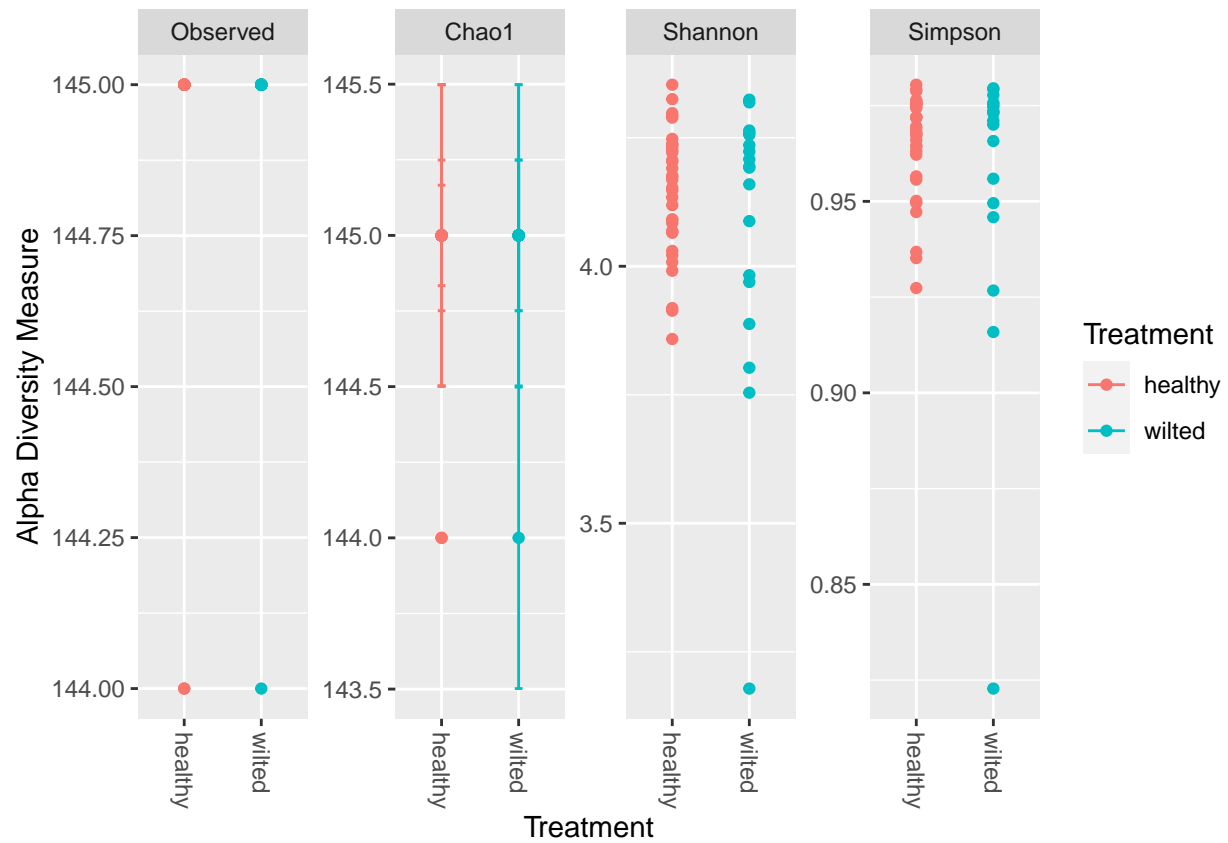
```
Barras_Species[2]
```

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

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

```
## Wisconsin double standardization
## Run 0 stress 0.1226512
## Run 1 stress 0.1226515
## ... Procrustes: rmse 0.0009565164  max resid 0.004818758
## ... Similar to previous best
## Run 2 stress 0.1233302
## Run 3 stress 0.1218539
## ... New best solution
## ... Procrustes: rmse 0.02026332  max resid 0.1282693
## Run 4 stress 0.1278289
## Run 5 stress 0.1218549
## ... Procrustes: rmse 0.0006613939  max resid 0.003265407
## ... Similar to previous best
## Run 6 stress 0.1227526
## Run 7 stress 0.1226511
## Run 8 stress 0.1218544
## ... Procrustes: rmse 0.00050139  max resid 0.002464929
## ... Similar to previous best
## Run 9 stress 0.1218543
## ... Procrustes: rmse 0.0002429245  max resid 0.001192044
## ... Similar to previous best
## Run 10 stress 0.1233307
## Run 11 stress 0.1272847
```

```
## Run 12 stress 0.1218539
## ... Procrustes: rmse 0.0001695548  max resid 0.0008627428
## ... Similar to previous best
## Run 13 stress 0.121854
## ... Procrustes: rmse 0.0003043927  max resid 0.001496288
## ... Similar to previous best
## Run 14 stress 0.1226509
## Run 15 stress 0.1218543
## ... Procrustes: rmse 0.0004881011  max resid 0.002431532
## ... Similar to previous best
## Run 16 stress 0.1226506
## Run 17 stress 0.1539498
## Run 18 stress 0.1535018
## Run 19 stress 0.1218548
## ... Procrustes: rmse 0.0003979232  max resid 0.001941218
## ... Similar to previous best
## Run 20 stress 0.122651
## *** Best solution repeated 7 times
```



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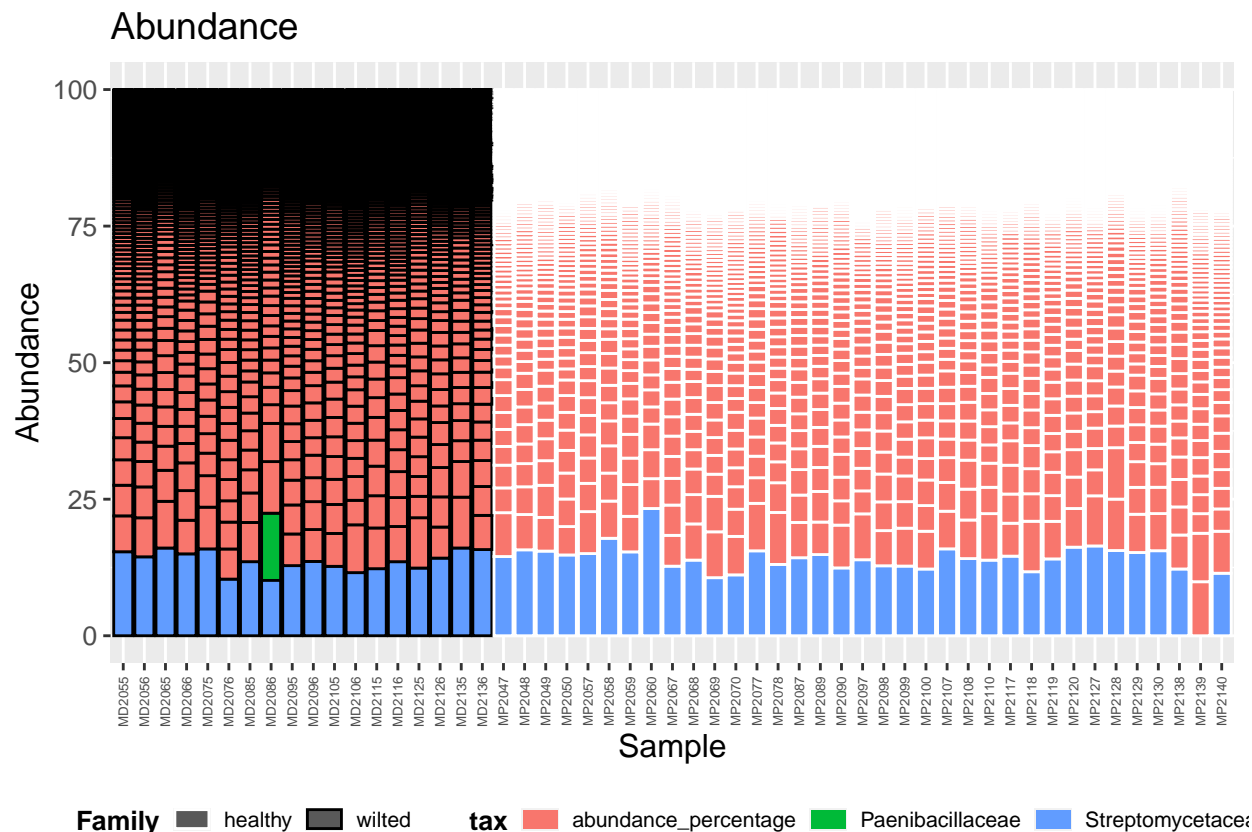
#———Bacteria by Phylum

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

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

Abundance

Phylum

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

```
Barras_Species[2]
```

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

Abundance

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

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.1520004
## Run 1 stress 0.1636958
## Run 2 stress 0.1700011
## Run 3 stress 0.1519724
## ... New best solution
## ... Procrustes: rmse 0.008285382  max resid 0.04681388
## Run 4 stress 0.1552698
## Run 5 stress 0.1519014
## ... New best solution
## ... Procrustes: rmse 0.04885038  max resid 0.3152661
## Run 6 stress 0.1614796
## Run 7 stress 0.1513921
## ... New best solution
## ... Procrustes: rmse 0.04582075  max resid 0.3024696
## Run 8 stress 0.1779282
## Run 9 stress 0.1548791
## Run 10 stress 0.1629442
## Run 11 stress 0.16964
## Run 12 stress 0.1524009
## Run 13 stress 0.1662298
## Run 14 stress 0.1613925
```

```
## Run 15 stress 0.1652755
## Run 16 stress 0.1633312
## Run 17 stress 0.1607191
## Run 18 stress 0.1672632
## Run 19 stress 0.1513905
## ... New best solution
## ... Procrustes: rmse 0.0004428603  max resid 0.002388818
## ... Similar to previous best
## Run 20 stress 0.1513906
## ... Procrustes: rmse 3.760188e-05  max resid 0.0002150336
## ... Similar to previous best
## *** Best solution repeated 2 times
```
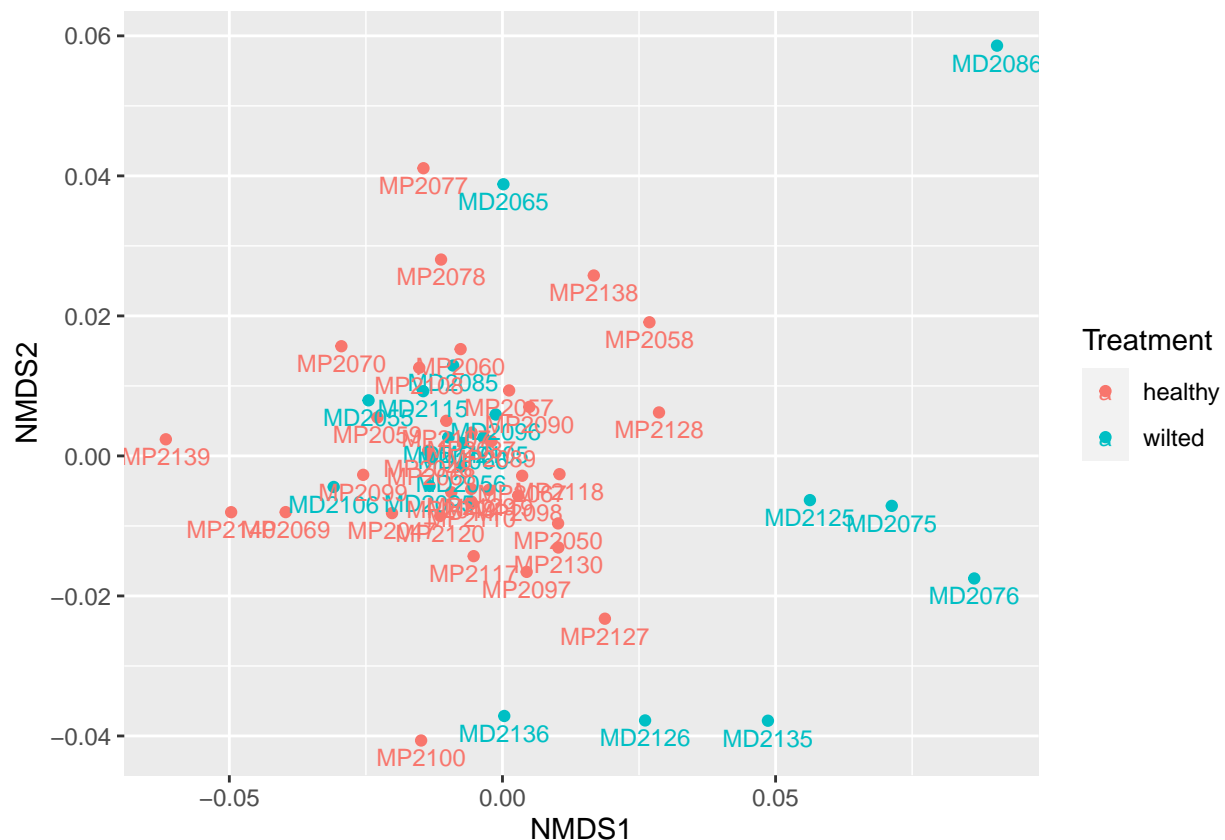


```
Alpha_diversity(merge_Bacteria , 'Phylum' , 'Treatment')
```

```
## 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

```r
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

```
Barras_Species[2]
```

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

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

```
## Wisconsin double standardization
## Run 0 stress 0.1412073
## Run 1 stress 0.1418145
## Run 2 stress 0.1390466
## ... New best solution
## ... Procrustes: rmse 0.02128683  max resid 0.1331159
## Run 3 stress 0.1405626
## Run 4 stress 0.145559
## Run 5 stress 0.1863488
## Run 6 stress 0.1412066
## Run 7 stress 0.1369866
## ... New best solution
## ... Procrustes: rmse 0.06315741  max resid 0.3787318
## Run 8 stress 0.1551948
## Run 9 stress 0.142348
## Run 10 stress 0.1405103
## Run 11 stress 0.1372656
## ... Procrustes: rmse 0.01219911  max resid 0.0572946
## Run 12 stress 0.1369866
## ... Procrustes: rmse 5.037779e-05  max resid 0.0001538958
## ... Similar to previous best
## Run 13 stress 0.1412071
## Run 14 stress 0.1402344
```

```
## Run 15 stress 0.1373769
## ... Procrustes: rmse 0.01547261  max resid 0.05919644
## Run 16 stress 0.1412072
## Run 17 stress 0.1373766
## ... Procrustes: rmse 0.01563171  max resid 0.05932202
## Run 18 stress 0.1441744
## Run 19 stress 0.1552141
## Run 20 stress 0.1625797
## *** Best solution repeated 1 times
```
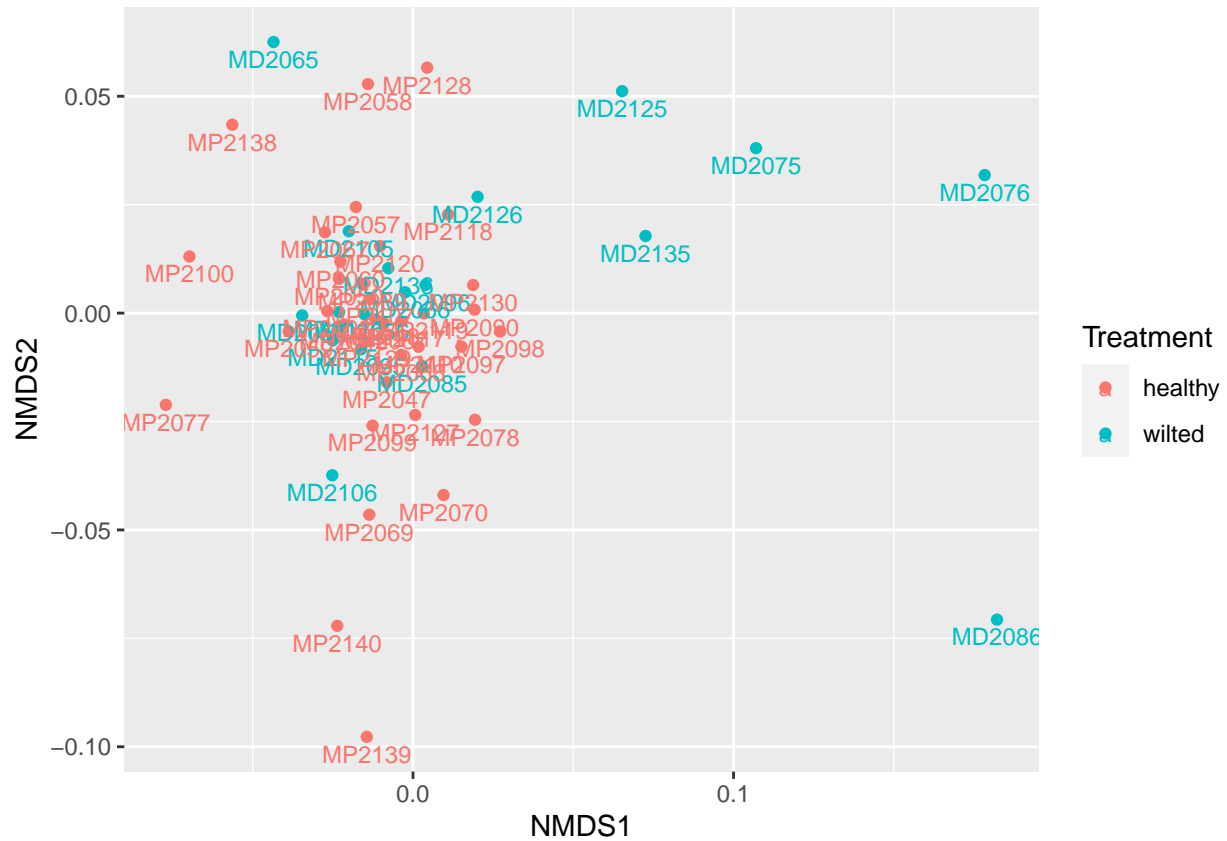


```
Alpha_diversity(merge_Bacteria , 'Family' , 'Treatment')
```
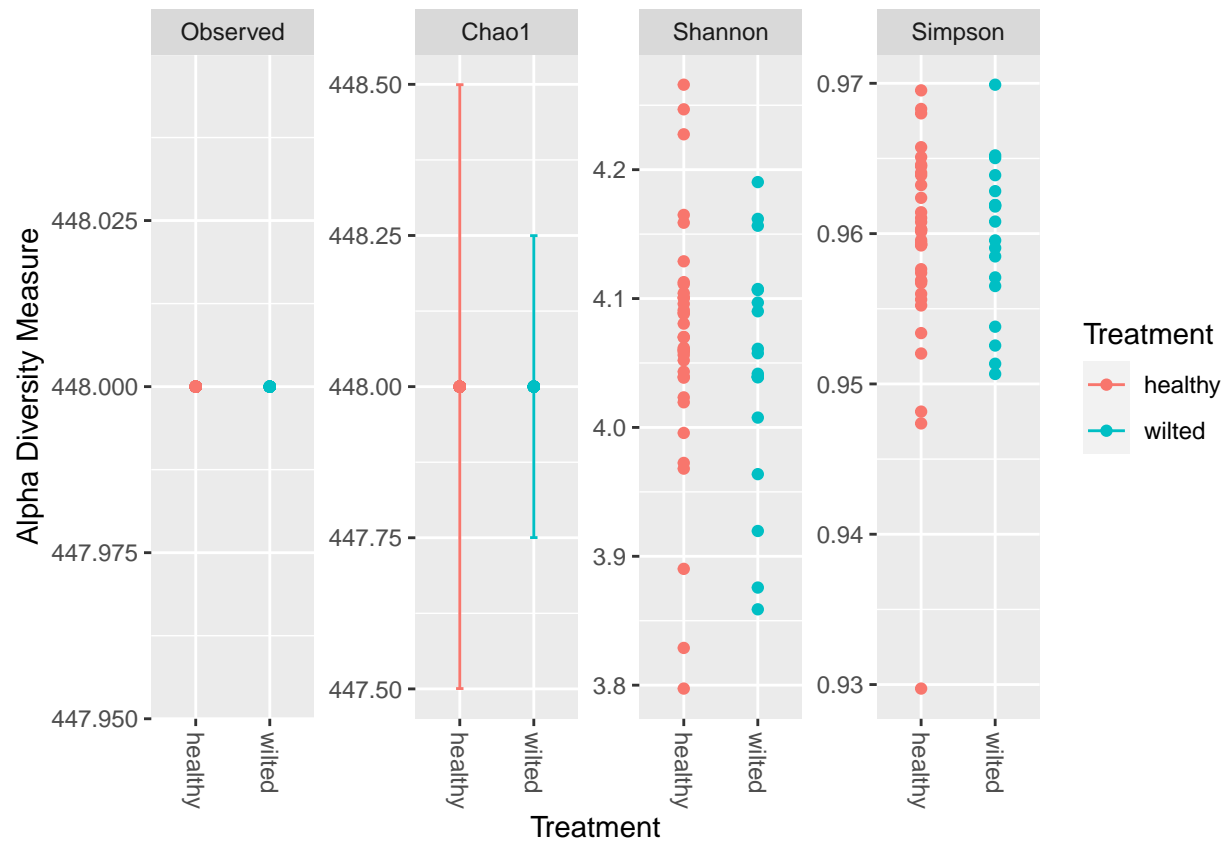
#———Bacteria by Genero

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

[[1]]

lex
flexum
habitans
luna
marina
ncola
rhabdus
rufa
salimonas
salinus
sediminimonas
sphaera
talea
iibacter
hidicoccus
hnia
nobacterium
angium
bacter
cibacterium
ibacter
imonas
natoleum
nicicoccus
nophonus
robacter
a
cacaulis
lassotoga
ntibacter
obium
acter
ntiacibacter
ntimicrobium
ntimonas
ticoccus
imonas
liella
idibacter
wickia
acterium
rcus
hizobium
spira
spirillum
obacter
llus
erioplanes
eriovorax
eroides
duia
esiella
onella
ia
lea
lovibrio
giatoa
urinckia

Desulfarculus
Desulfatibacillum
Desulfitobacterium
Desulfobacca
Desulfobacter
Desulfobacula
Desulfobulbus
Desulfocapsa
Desulfococcus
Desulfocurvibacter
Desulfofarcimen
Desulfoglaeba
Desulfohalobium
Desulfoluna
Desulfolutivibrio
Desulfomarina
Desulfomicrobium
Desulfomonile
Desulfonema
Desulforamulus
Desulforapulum
Desulfosarcina
Desulfoscipio
Desulfosediminicola
Desulfosporosinus
Desulfosudis
Desulfotalea
Desulfotomaculum
Desulfovibrio
Desulfurispirillum
Desulfurivibrio
Desulfobacterium
Desulfuromonas
Devosia
Devriesea
Dialister
Diaminobutyricimonas
Diaphorobacter
Dichelobacter
Dickeya
Dictyoglomus
Dietzia
Dinoroseobacter
Dissulfurimicrobium
Dissulfurispira
Dokdonella
Dokdonia
Dolichospermum
Dolosigranulum
Dongshaea
Dorea
Draconibacterium
Duganella
Duncaniella
Dyadobacter
Dyella
Dysgonomonas
Dysosmobacter

Labrenzia
Labrys
Laceyella
Lachnoanaerobaculum
Lachnoclostridium
Lachnospira
Lacibacter
Lacimicrobium
Lacinutrix
Lacipirellula
Lacrimispora
Lacticaseibacillus
Lactiplantibacillus
Lactobacillus
Lactococcus
Lacunisphaera
Lancefieldella
Lapidilactobacillus
Laribacter
Larkinella
Latilactobacillus
Lautropia
Lawsonella
Lawsonia
Leadbetterella
Leclercia
Lederbergia
Leeuwenhoekiella
Legionella
Leifsonia
Leisingera
Lelliottia
Leminorella
Lentibacillus
Lentilactobacillus
Lentilitoribacter
Lentzea
Leptodesmis
Leptolyngbya
Leptospira
Leptospirillum
Leptothermofonsia
Leptothrix
Leptotrichia
Leucobacter
Leuconostoc
Levilactobacillus
Liberibacter
Lichenicola
Lichenihabitans
Ligilactobacillus
Lignipirellula
Limihaloglobus
Limnobacter
Limnobaculum
Limnochorda
Limnoglobus
Limnohabitans

Paremcibacter
Paroceanicella
Parolsenella
Parvibaculum
Parvimonas
Parvularcula
Pasteurella
Paucibacter
Paucilactobacillus
Pauljensenia
Pectinatus
Pectobacterium
Pediococcus
Pedobacter
Pedococcus
Pelagerythrobacter
Pelagibacterium
Pelagovum
Pelistega
Pelobacter
Pelodictyon
Pelolinea
Pelosinus
Pengzhenrongella
Peptacetobacter
Peptoclostridium
Peptoniphilus
Peribacillus
Periweissella
Permianibacter
Persephonella
Persicimonas
Peteryoungia
Petrimonas
Petrocella
Petrotoga
Phaeobacter
Phascolarctobacterium
Phenylobacterium
Phnomibacter
Phocaeicola
Phoenicibacter
Photobacterium
Photorhabdus
Phototrophicus
Phreatobacter
Phycicoccus
Phycisphaera
Phyllobacterium
Phytobacter
Phytohabitans
Pigmentiphaga
Pikeienuella
Pimelobacter
Pirellula
Pirellulimonas
Piscirickettsia
Pistricoccus

Subtercola
Succinivibrio
Suicoccus
Sulfidibacter
Sulfitobacter
Sulfuricaulis
Sulfuricella
Sulfuricurvum
Sulfuriferula
Sulfuriflexus
Sulfurifustis
Sulfurihydrogenibium
Sulfurimicrobium
Sulfurimonas
Sulfuriroseicoccus
Sulfuritalea
Sulfuritortus
Sulfurivermis
Sulfurospirillum
Sulfurovum
Sutcliffiella
Sutterella
Suttonella
Swingsia
Symbiobacterium
Symmachiella
Synechococcus
Synechocystis
Syntrophobacter
Syntrophobotulus
Syntrophomonas
Syntrophotalea
Syntrophothermus
Syntrophus
Tabrizicola
Tamlana
Tannerella
Tardibacter
Tardiphaga
Tateyamaria
Tatlockia
Tatumella
Tautonia
Taylorella
Telmatocola
Tenacibaculum
Tenuifilum
Tepidanaerobacter
Tepidibacter
Tepidiforma
Tepidimonas
Tepiditoga
Terasakiella
Teredinibacter
Terribacillus
Terricaulis
Terriglobus
Terrihabitans

Barras_Species[2]

[[1]]

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

```
## Wisconsin double standardization
## Run 0 stress 0.1467945
## Run 1 stress 0.145778
## ... New best solution
## ... Procrustes: rmse 0.04626627  max resid 0.2220378
## Run 2 stress 0.1433318
## ... New best solution
## ... Procrustes: rmse 0.08271459  max resid 0.3946675
## Run 3 stress 0.1467201
## Run 4 stress 0.1531013
## Run 5 stress 0.1467425
## Run 6 stress 0.146185
## Run 7 stress 0.1505679
## Run 8 stress 0.1500532
## Run 9 stress 0.145519
## Run 10 stress 0.151215
## Run 11 stress 0.1512369
## Run 12 stress 0.1490812
## Run 13 stress 0.148721
## Run 14 stress 0.1432834
## ... New best solution
## ... Procrustes: rmse 0.004246344  max resid 0.02586992
## Run 15 stress 0.1454653
```

```
## Run 16 stress 0.1432838
## ... Procrustes: rmse 0.0007481338   max resid 0.003205415
## ... Similar to previous best
## Run 17 stress 0.1519958
## Run 18 stress 0.1499637
## Run 19 stress 0.1438174
## Run 20 stress 0.1484465
## *** 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]]
```

`Barras_Species[2]`

`## [[1]]`

Abundance


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

```
## Wisconsin double standardization
## Run 0 stress 0.1597841
## Run 1 stress 0.1616467
## Run 2 stress 0.1596992
## ... New best solution
## ... Procrustes: rmse 0.05927183  max resid 0.3719294
## Run 3 stress 0.1703226
## Run 4 stress 0.1633768
## Run 5 stress 0.1622795
## Run 6 stress 0.166837
## Run 7 stress 0.1577449
## ... New best solution
## ... Procrustes: rmse 0.02327626  max resid 0.1144114
## Run 8 stress 0.1676656
## Run 9 stress 0.1603708
## Run 10 stress 0.1596212
## Run 11 stress 0.1635446
## Run 12 stress 0.1605549
## Run 13 stress 0.1637696
## Run 14 stress 0.1641623
## Run 15 stress 0.1602436
## Run 16 stress 0.1603294
## Run 17 stress 0.1587399
```

```
## Run 18 stress 0.1789824
## Run 19 stress 0.1571292
## ... New best solution
## ... Procrustes: rmse 0.03053161  max resid 0.1408118
## Run 20 stress 0.1576528
## *** Best solution was not repeated -- monoMDS stopping criteria:
##      4: no. of iterations >= maxit
##     16: stress ratio > sratmax
```



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