

230306_Reporte1Exploracion

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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/Data_all")
fresa_kraken <- import_biom("fresa_kraken_all.biom")
class(fresa_kraken)
```

```
## [1] "phyloseq"
## attr(,"package")
## [1] "phyloseq"
```

```
## como tenemos diferencias de longitud en los nombres de las muestras, al cortar los nombres, quedan 1
## usando la libreria stringi
sample_names(fresa_kraken) <- stri_replace_all_regex(sample_names(fresa_kraken), '\\\\.', 'A')
## renombrar las columnas del tax_table
colnames(fresa_kraken@tax_table@.Data) <- c("Kingdom", "Phylum", "Class", "Order", "Family", "Genus", "h")
## quitar los primeros caracteres de los nombres del tax_table
fresa_kraken@tax_table@.Data <- substr(fresa_kraken@tax_table@.Data, 4, 100)
## recortar los nombres de las muestras
colnames(fresa_kraken@otu_table@.Data) <- substr(colnames(fresa_kraken@otu_table@.Data), 1, 6)
## cargar los metadatos
metadata_fresa <- read.csv2("/home/camila/GIT/Tesis_Maestria/Data/fresa_solena/Data_all/metadata.csv", h)
rownames(metadata_fresa) <- sample_names(fresa_kraken)
## unir los metadatos al objeto phyloseq
fresa_kraken@sam_data <- sample_data(metadata_fresa)
```

```
# filtro de calidad
samples_to_remove <- c("MP2079","MP2080","MP2088","MP2109","MP2137")
samples<-!(sample_names(fresa_kraken) %in% samples_to_remove)
names(samples)<-as.character(sample_names(fresa_kraken))
fresa_kraken_fil <- prune_samples(samples, fresa_kraken)
nsamples(fresa_kraken) # 85
```

```
## [1] 85
```

```
nsamples(fresa_kraken_fil) # 80
```

```
## [1] 80
```

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 phyloseq 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()'

```

```

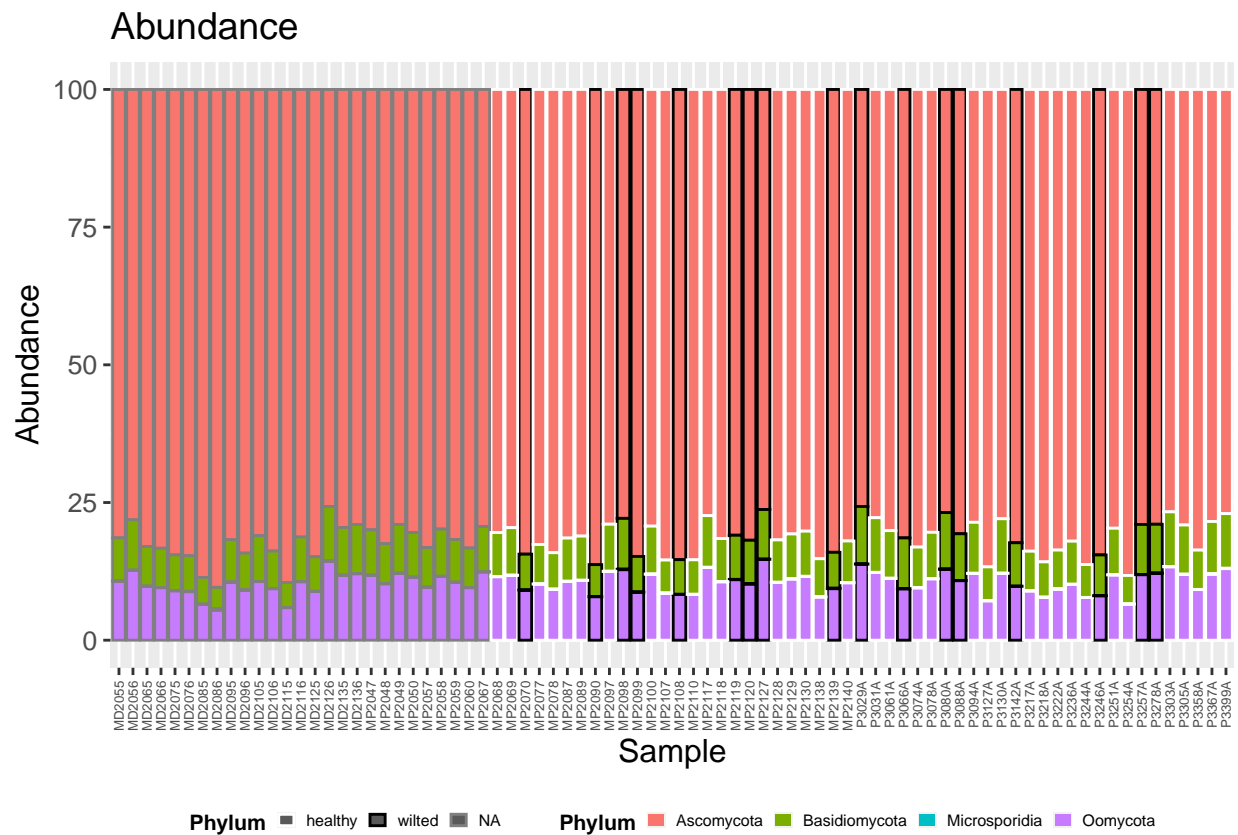
Barras_Phylum[1] # normal

```

```

## [[1]]

```

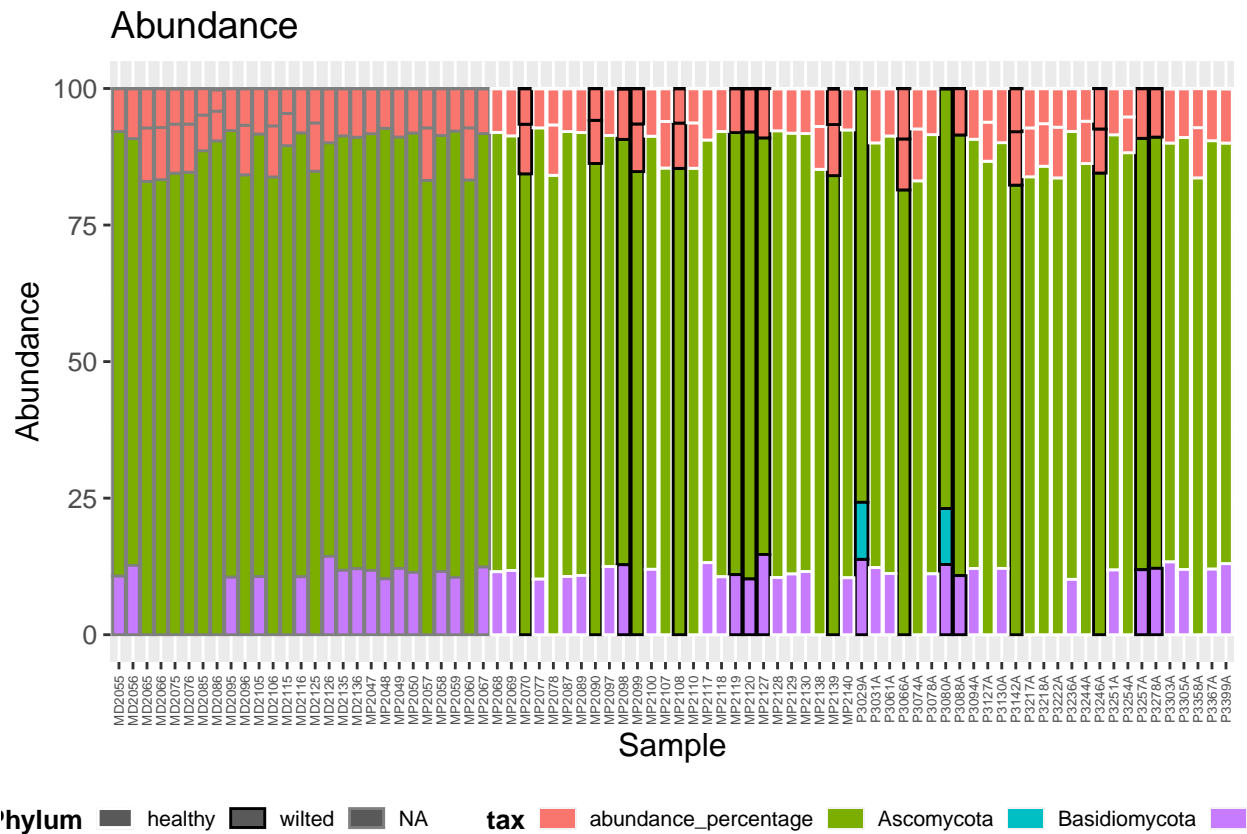


```

Barras_Phylum[2]

```

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



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

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.01092347
## Run 1 stress 9.734801e-05
## ... New best solution
## ... Procrustes: rmse 0.02230386 max resid 0.05599817
## Run 2 stress 9.871748e-05
## ... Procrustes: rmse 0.0001228726 max resid 0.0003500669
## ... Similar to previous best
## Run 3 stress 9.819744e-05
## ... Procrustes: rmse 9.857134e-05 max resid 0.0002705246
## ... Similar to previous best
## Run 4 stress 0.001167197
## Run 5 stress 0.0001449023
## ... Procrustes: rmse 0.0002674023 max resid 0.0006336985
## ... Similar to previous best
## Run 6 stress 9.814744e-05
## ... Procrustes: rmse 2.469828e-06 max resid 1.147763e-05
## ... Similar to previous best
## Run 7 stress 5.445962e-05
## ... New best solution
```

```

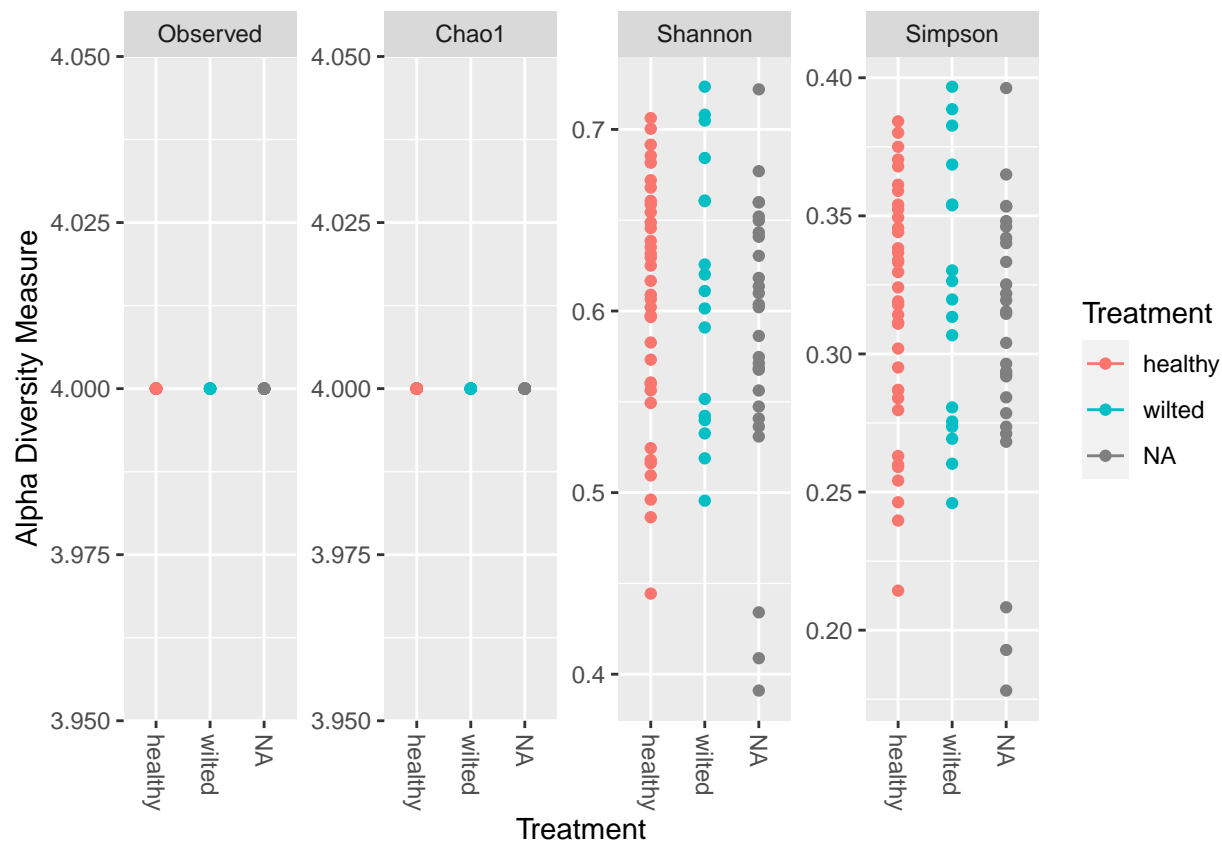
## ... Procrustes: rmse 0.0001020114  max resid 0.0002247589
## ... Similar to previous best
## Run 8 stress 9.522178e-05
## ... Procrustes: rmse 2.77495e-05  max resid 5.373292e-05
## ... Similar to previous best
## Run 9 stress 9.928758e-05
## ... Procrustes: rmse 9.8982e-05  max resid 0.0002412854
## ... Similar to previous best
## Run 10 stress 9.567226e-05
## ... Procrustes: rmse 9.071014e-05  max resid 0.0002201253
## ... Similar to previous best
## Run 11 stress 9.546742e-05
## ... Procrustes: rmse 0.000115702  max resid 0.0002830266
## ... Similar to previous best
## Run 12 stress 9.916533e-05
## ... Procrustes: rmse 8.248923e-05  max resid 0.0001793601
## ... Similar to previous best
## Run 13 stress 6.239085e-05
## ... Procrustes: rmse 1.963294e-05  max resid 4.511147e-05
## ... Similar to previous best
## Run 14 stress 9.930775e-05
## ... Procrustes: rmse 6.361762e-05  max resid 0.0001497356
## ... Similar to previous best
## Run 15 stress 0.0001609772
## ... Procrustes: rmse 0.0003290465  max resid 0.000790323
## ... Similar to previous best
## Run 16 stress 0.0001376356
## ... Procrustes: rmse 0.0002811157  max resid 0.0006678026
## ... Similar to previous best
## Run 17 stress 9.688643e-05
## ... Procrustes: rmse 8.353791e-05  max resid 0.0001828628
## ... Similar to previous best
## Run 18 stress 4.265144e-05
## ... New best solution
## ... Procrustes: rmse 1.546682e-05  max resid 4.158713e-05
## ... Similar to previous best
## Run 19 stress 9.586864e-05
## ... Procrustes: rmse 2.010005e-05  max resid 0.0001050013
## ... Similar to previous best
## Run 20 stress 9.040026e-05
## ... Procrustes: rmse 3.165034e-05  max resid 8.116249e-05
## ... Similar to previous best
## *** Best solution repeated 3 times

```

```

## Warning in metaMDS(veganifyOTU(physeq), distance, ...): stress is (nearly) zero:
## you may have insufficient data

```

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

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.01092347
## Run 1 stress 9.335705e-05
## ... New best solution
## ... Procrustes: rmse 0.0223114 max resid 0.05607995
## Run 2 stress 9.05933e-05
## ... New best solution
## ... Procrustes: rmse 9.334717e-05 max resid 0.0002510353
## ... Similar to previous best
## Run 3 stress 8.295263e-05
## ... New best solution
## ... Procrustes: rmse 0.0001070632 max resid 0.0002674128
## ... Similar to previous best
## Run 4 stress 9.459767e-05
## ... Procrustes: rmse 2.538734e-05 max resid 7.767238e-05
## ... Similar to previous best
## Run 5 stress 6.333525e-05
## ... New best solution
## ... Procrustes: rmse 2.811014e-05 max resid 7.472418e-05
## ... Similar to previous best
## Run 6 stress 8.947329e-05
## ... Procrustes: rmse 3.872243e-05 max resid 0.0001050772
```

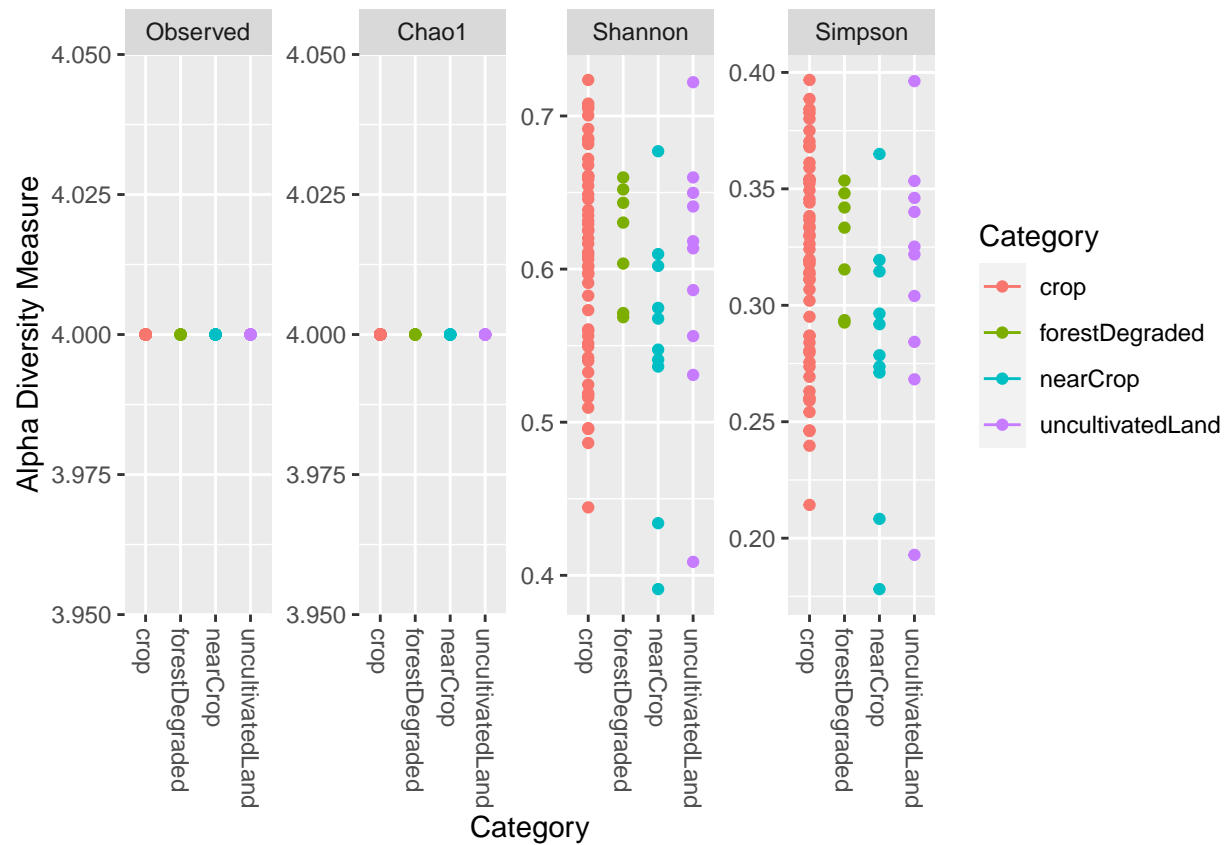


```

## ... Similar to previous best
## Run 7 stress 9.420623e-05
## ... Procrustes: rmse 4.92327e-05  max resid 0.000135095
## ... Similar to previous best
## Run 8 stress 9.691644e-05
## ... Procrustes: rmse 0.0001108939  max resid 0.0002399508
## ... Similar to previous best
## Run 9 stress 9.770556e-05
## ... Procrustes: rmse 9.135358e-05  max resid 0.0001946187
## ... Similar to previous best
## Run 10 stress 6.32783e-05
## ... New best solution
## ... Procrustes: rmse 2.9795e-05  max resid 0.0001080258
## ... Similar to previous best
## Run 11 stress 9.297361e-05
## ... Procrustes: rmse 8.763944e-05  max resid 0.0002378802
## ... Similar to previous best
## Run 12 stress 9.554237e-05
## ... Procrustes: rmse 6.618609e-05  max resid 0.0002140865
## ... Similar to previous best
## Run 13 stress 9.838965e-05
## ... Procrustes: rmse 6.238972e-05  max resid 0.000184277
## ... Similar to previous best
## Run 14 stress 9.005017e-05
## ... Procrustes: rmse 5.407641e-05  max resid 0.0001296094
## ... Similar to previous best
## Run 15 stress 9.72548e-05
## ... Procrustes: rmse 6.160573e-05  max resid 0.0002030988
## ... Similar to previous best
## Run 16 stress 9.854852e-05
## ... Procrustes: rmse 3.23828e-05  max resid 8.60709e-05
## ... Similar to previous best
## Run 17 stress 7.382101e-05
## ... Procrustes: rmse 3.769402e-05  max resid 0.0001091618
## ... Similar to previous best
## Run 18 stress 9.911898e-05
## ... Procrustes: rmse 0.0001054754  max resid 0.0003025607
## ... Similar to previous best
## Run 19 stress 9.742706e-05
## ... Procrustes: rmse 3.960747e-05  max resid 7.743144e-05
## ... Similar to previous best
## Run 20 stress 9.181024e-05
## ... Procrustes: rmse 6.712639e-05  max resid 0.0002175394
## ... Similar to previous best
## *** Best solution repeated 11 times

## Warning in metaMDS(veganifyOTU(physeq), distance, ...): stress is (nearly) zero:
## you may have insufficient data

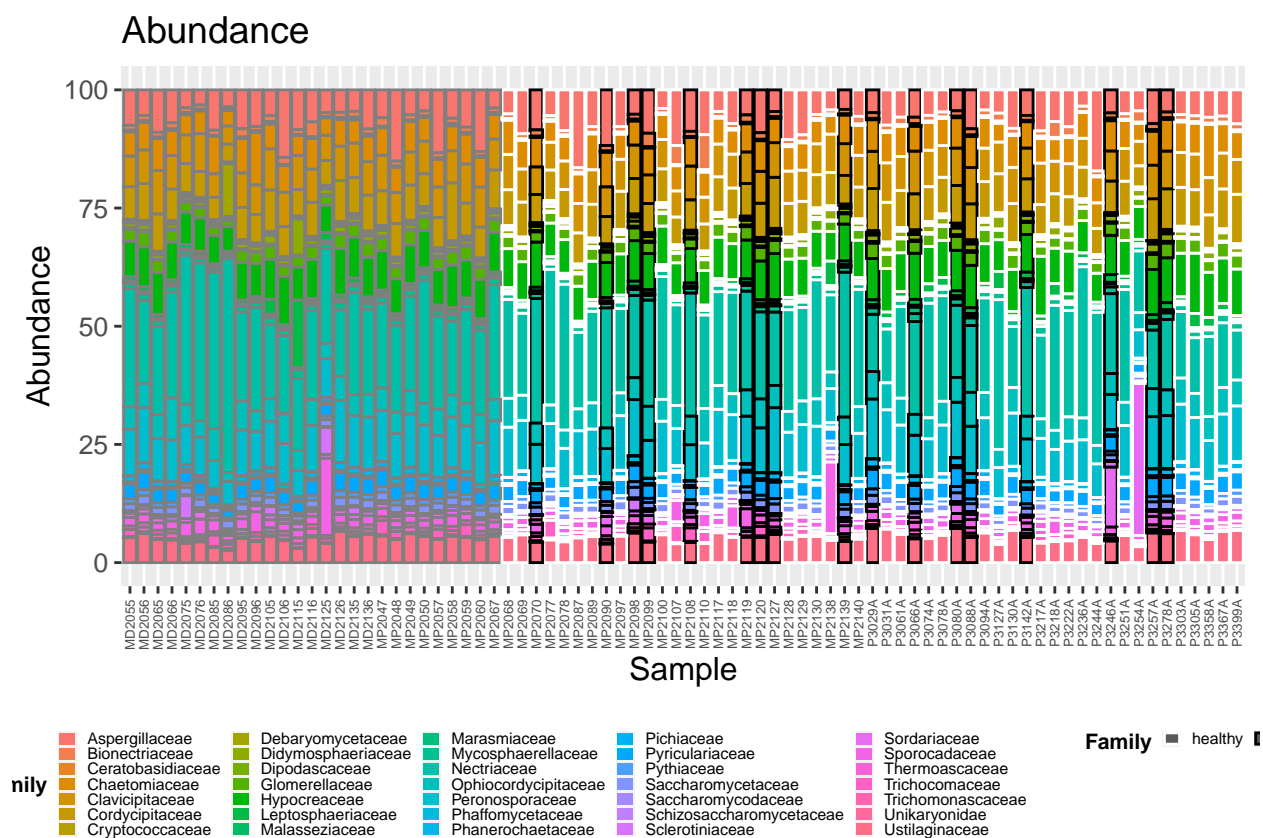
```

#———Eukarya by Family

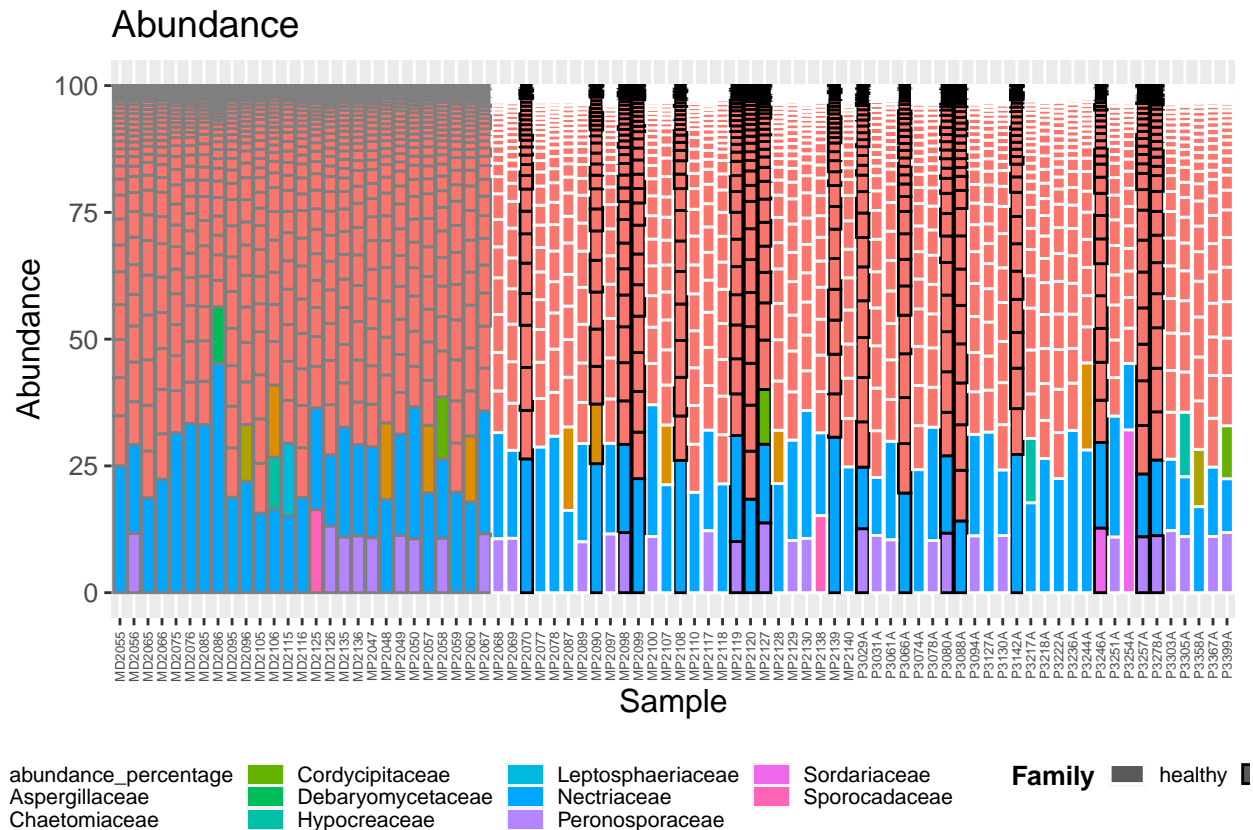
```
Barras_Species <- Abundance_barras(merge_Eukaryota, 'Family', 'Treatment', 10.0)
Barras_Species[1]
```

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



Barras_Species[2]

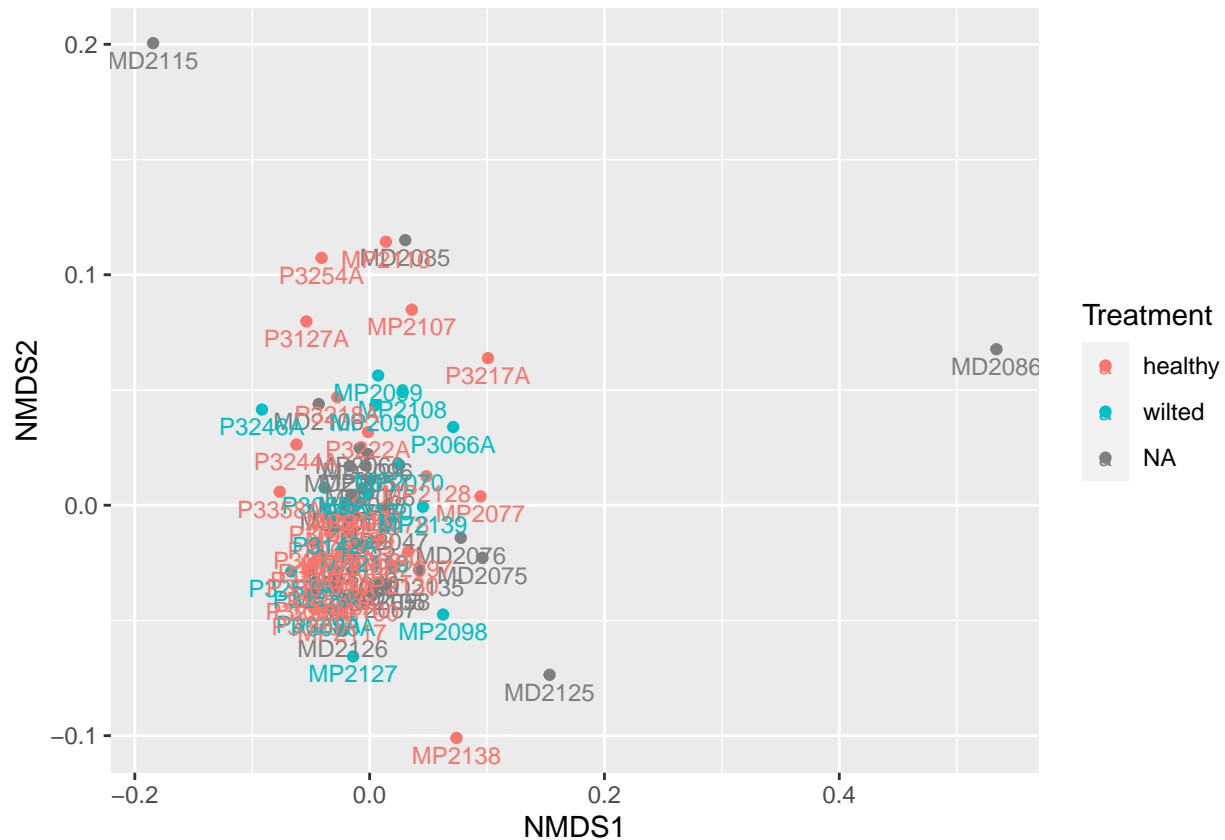
[[1]]



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

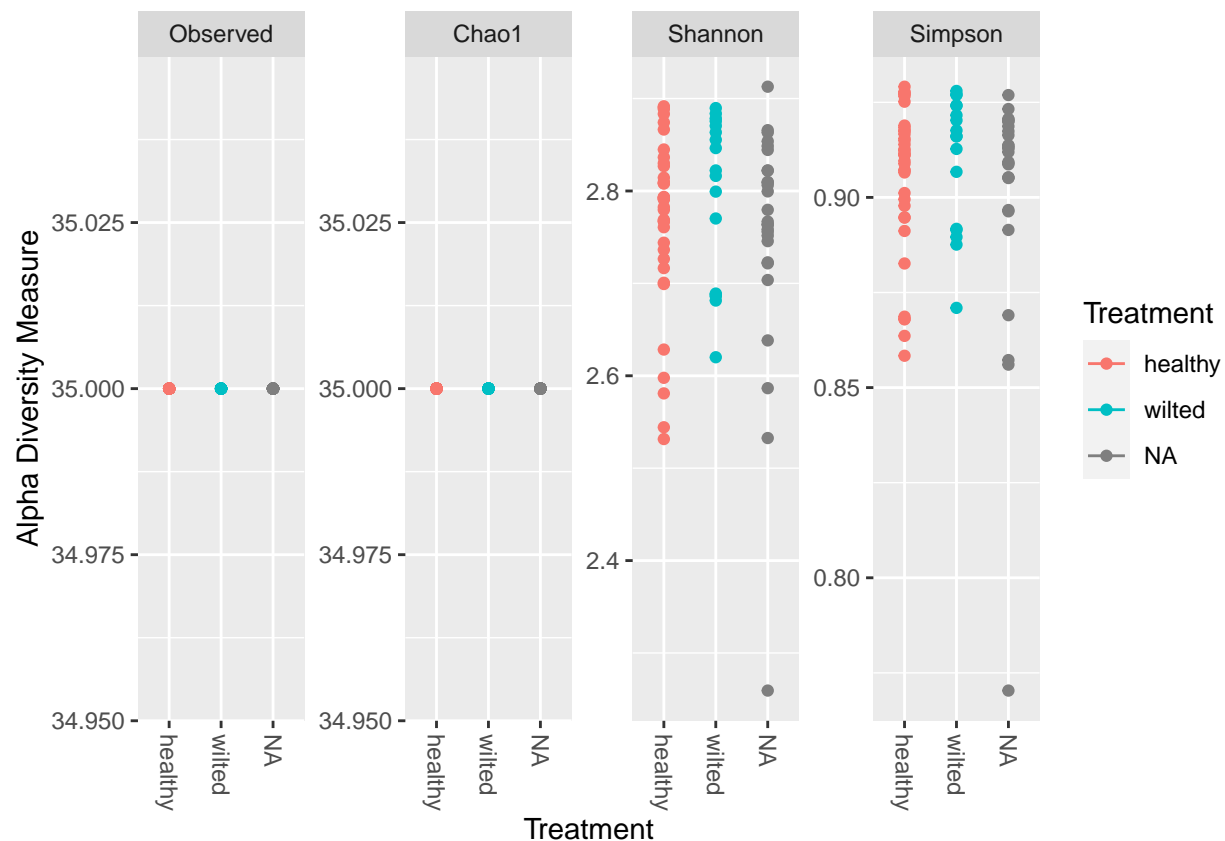
```
## Wisconsin double standardization
## Run 0 stress 0.136765
## Run 1 stress 0.1371023
## ... Procrustes: rmse 0.008825574 max resid 0.07706356
## Run 2 stress 0.1375698
## Run 3 stress 0.1367639
## ... New best solution
## ... Procrustes: rmse 0.001002787 max resid 0.00643578
## ... Similar to previous best
## Run 4 stress 0.1382601
## Run 5 stress 0.1414158
## Run 6 stress 0.1424672
## Run 7 stress 0.1448042
## Run 8 stress 0.1443076
## Run 9 stress 0.1370173
## ... Procrustes: rmse 0.01446446 max resid 0.1233838
## Run 10 stress 0.1456562
## Run 11 stress 0.1388323
## Run 12 stress 0.155677
## Run 13 stress 0.1367785
## ... Procrustes: rmse 0.001519871 max resid 0.00796185
## ... Similar to previous best
## Run 14 stress 0.1412243
```

```
## Run 15 stress 0.1371028
## ... Procrustes: rmse 0.008985293  max resid 0.07707036
## Run 16 stress 0.1376853
## Run 17 stress 0.152514
## Run 18 stress 0.4090803
## Run 19 stress 0.1441295
## Run 20 stress 0.1388286
## *** Best solution repeated 2 times
```



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

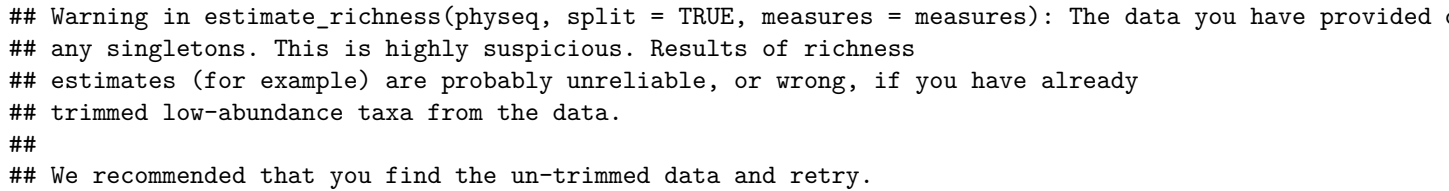
```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided contains
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the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

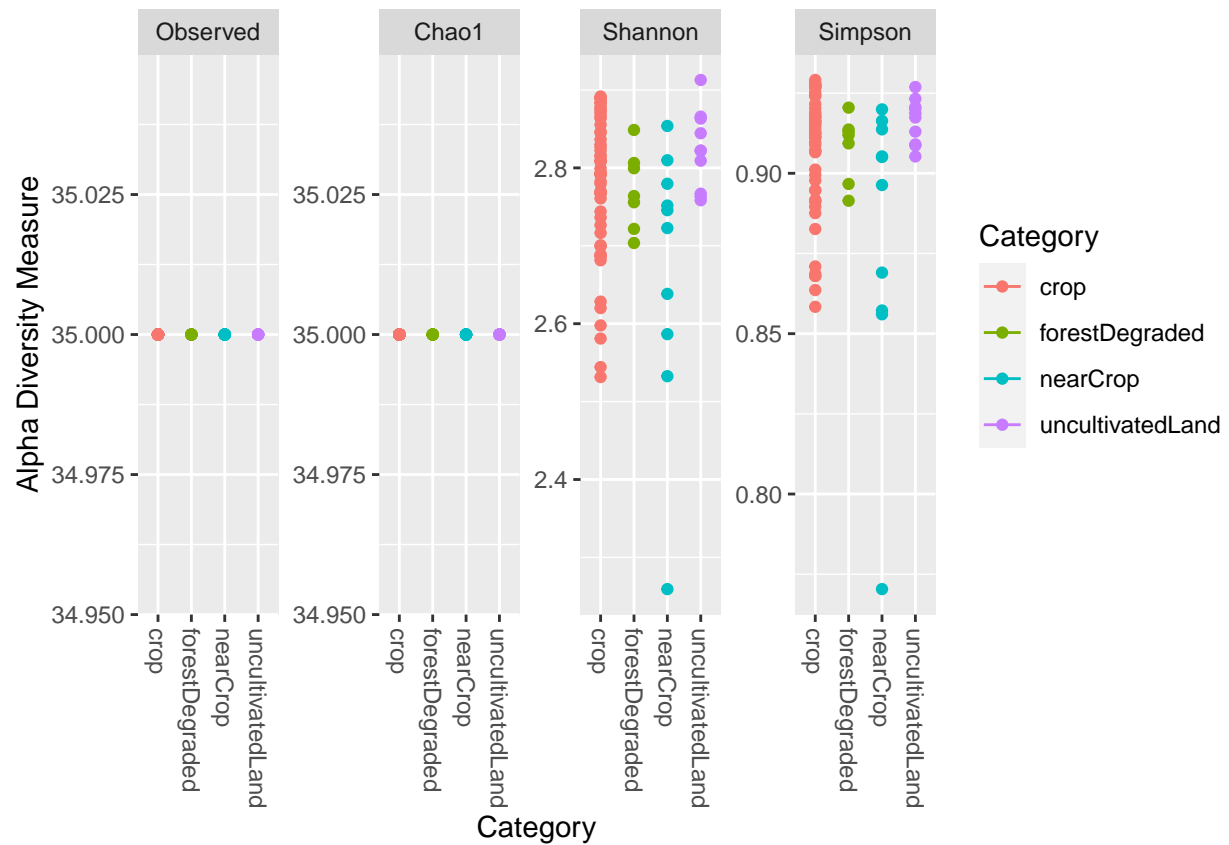


```
Beta_diversity(merge_Eukaryota , 'Family' , 'Category', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.136765
## Run 1 stress 0.1426953
## Run 2 stress 0.1375597
## Run 3 stress 0.1426931
## Run 4 stress 0.158903
## Run 5 stress 0.1481642
## Run 6 stress 0.1371009
## ... Procrustes: rmse 0.008803992 max resid 0.07709067
## Run 7 stress 0.137101
## ... Procrustes: rmse 0.008804207 max resid 0.07708579
## Run 8 stress 0.1428083
## Run 9 stress 0.1370891
## ... Procrustes: rmse 0.01445755 max resid 0.1215379
## Run 10 stress 0.1371022
## ... Procrustes: rmse 0.008824543 max resid 0.07706358
## Run 11 stress 0.141876
## Run 12 stress 0.1496806
## Run 13 stress 0.1385872
## Run 14 stress 0.1428099
## Run 15 stress 0.1640928
## Run 16 stress 0.1424547
## Run 17 stress 0.1375701
```

```
Alpha_diversity(merge_Eukaryota , 'Family' , 'Category')
```

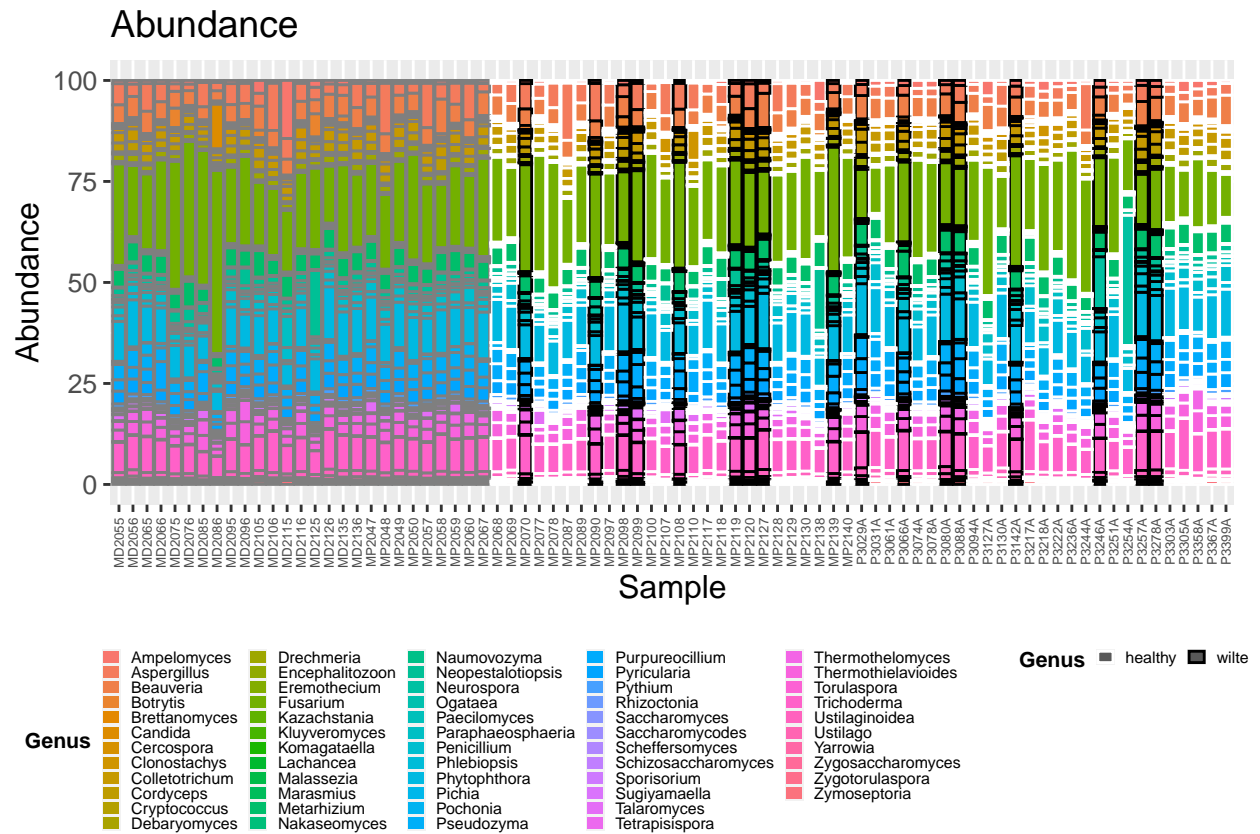




#—— Eukarya by Genero

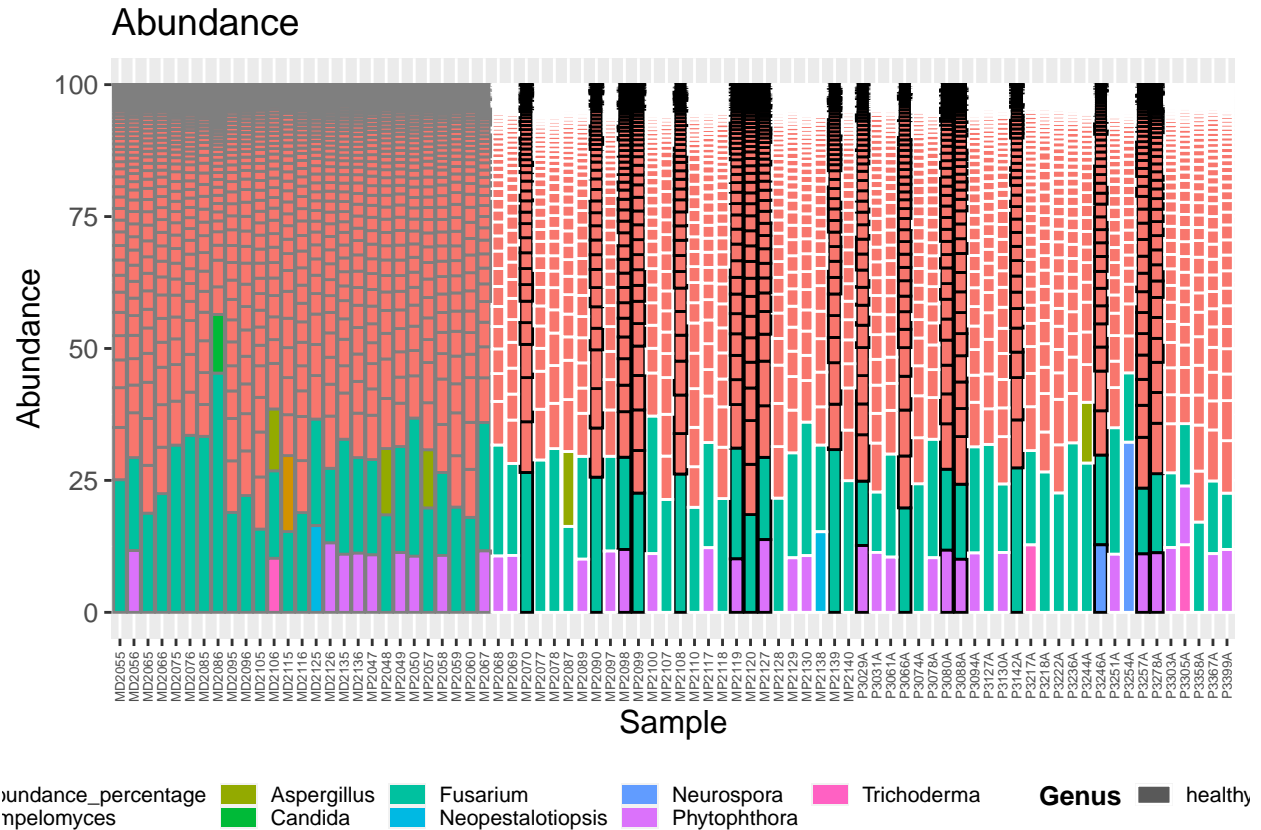
```
Barras_Species <- Abundance_barras(merge_Eukaryota, 'Genus', 'Treatment', 10.0)
Barras_Species[1]
```

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



Barras_Species [2]

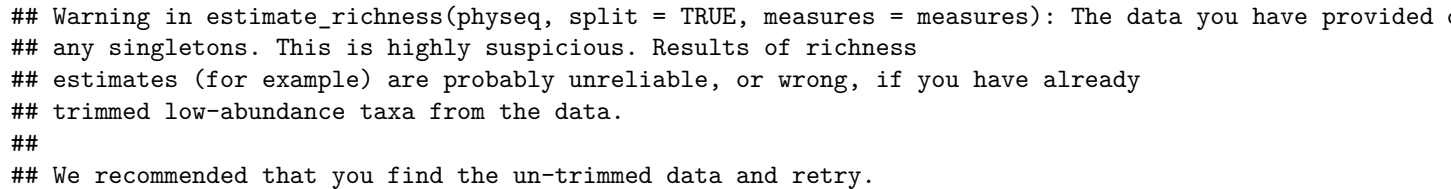
[[1]]

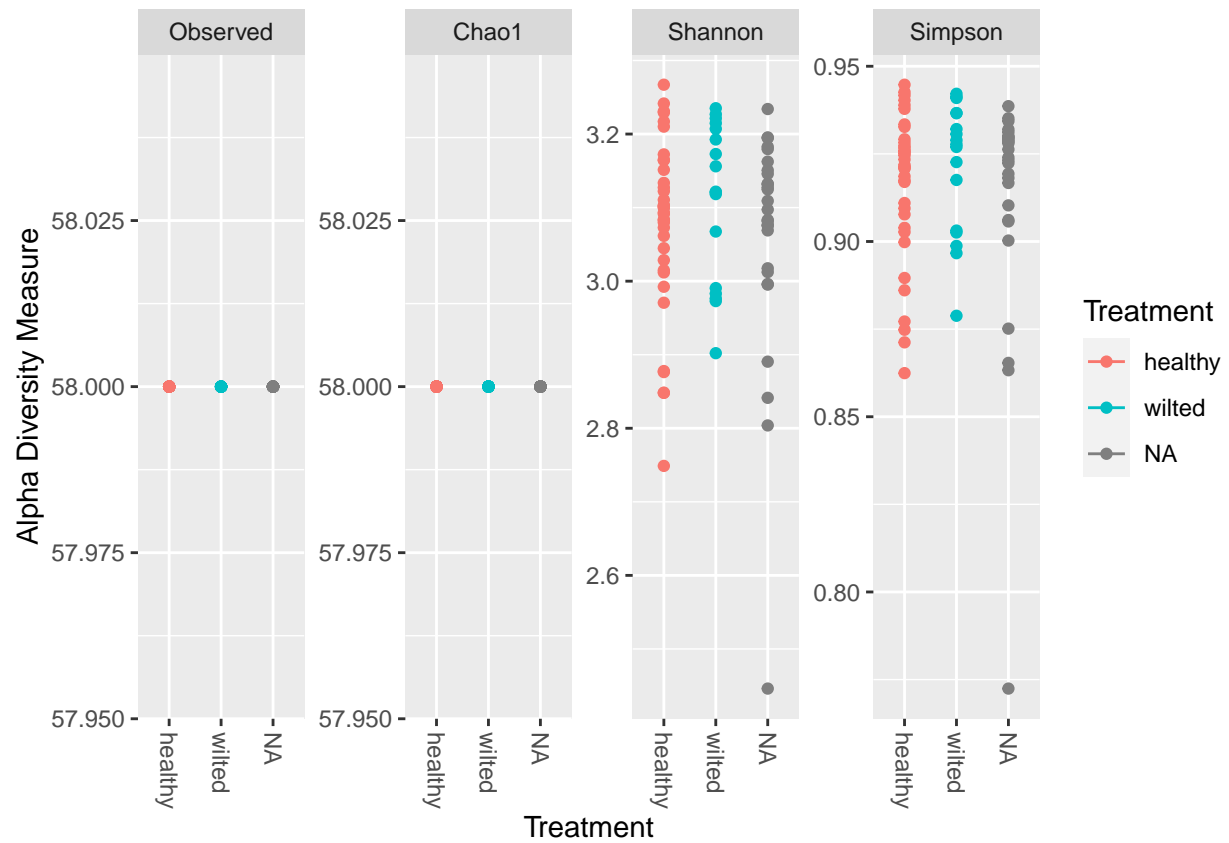


```
Beta_diversity(merge_Eukaryota , 'Genus' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1425943
## Run 1 stress 0.1556068
## Run 2 stress 0.157223
## Run 3 stress 0.1430761
## ... Procrustes: rmse 0.02756276 max resid 0.1227383
## Run 4 stress 0.1535271
## Run 5 stress 0.1545259
## Run 6 stress 0.1430704
## ... Procrustes: rmse 0.01572318 max resid 0.08365698
## Run 7 stress 0.1527883
## Run 8 stress 0.1406338
## ... New best solution
## ... Procrustes: rmse 0.02876197 max resid 0.1880479
## Run 9 stress 0.1650957
## Run 10 stress 0.1489875
## Run 11 stress 0.1554675
## Run 12 stress 0.1523229
## Run 13 stress 0.1398565
## ... New best solution
## ... Procrustes: rmse 0.01919991 max resid 0.08750119
## Run 14 stress 0.1463
## Run 15 stress 0.1404287
```

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

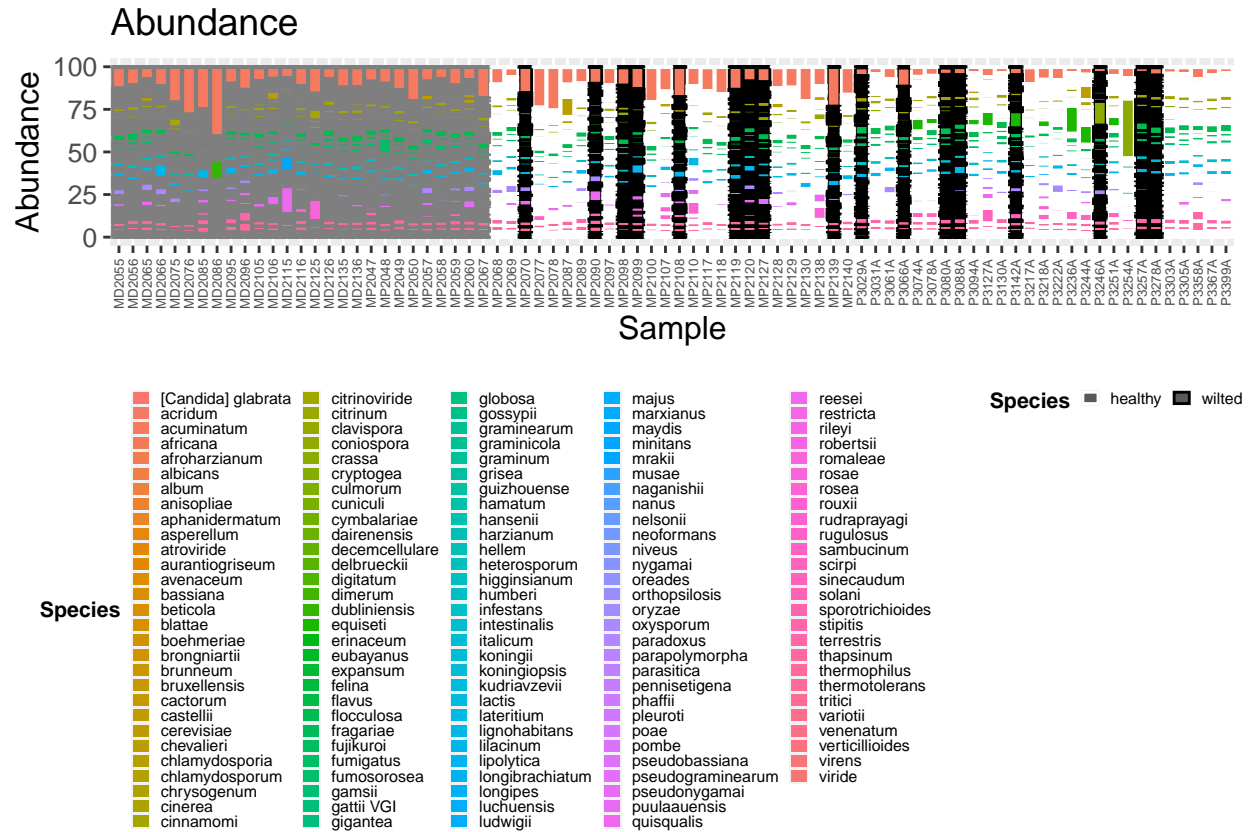




#———Eukarya by Species

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

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



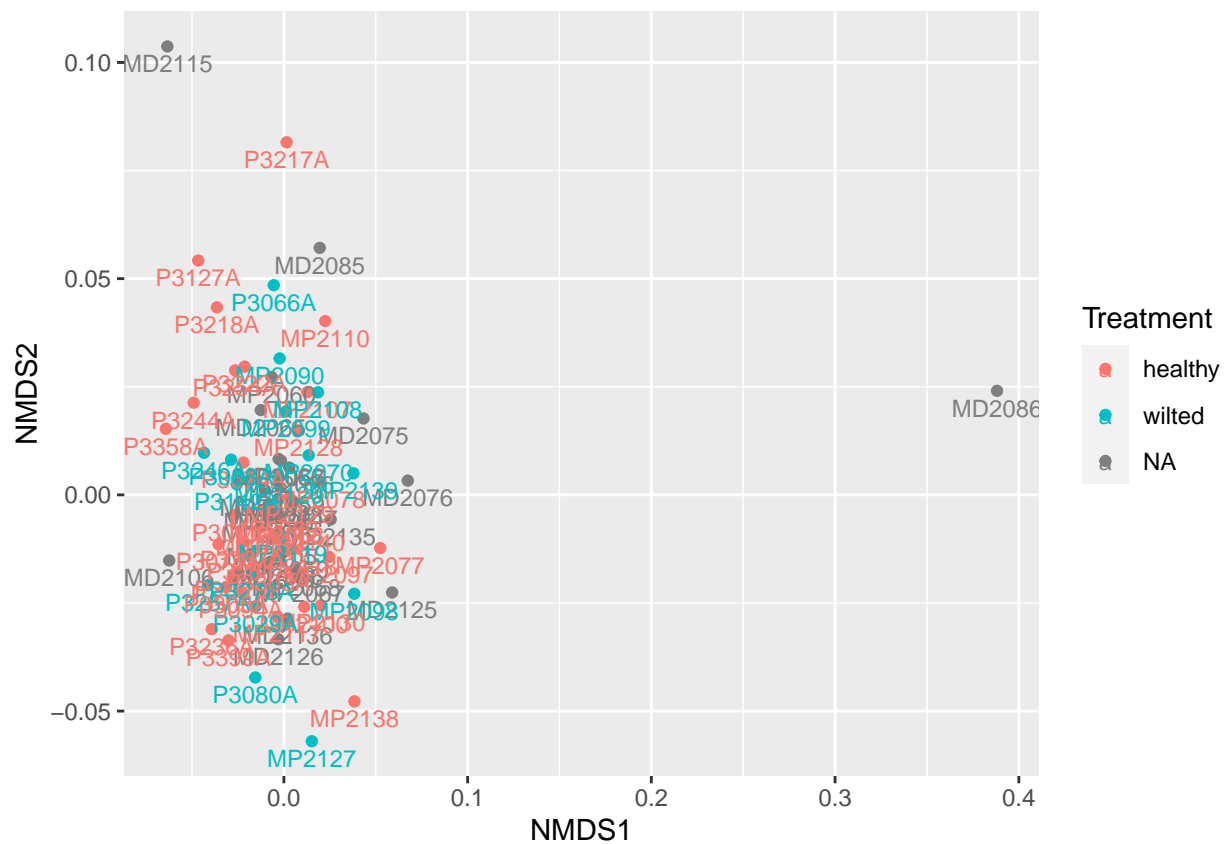
Barras_Species [2]

[[1]]

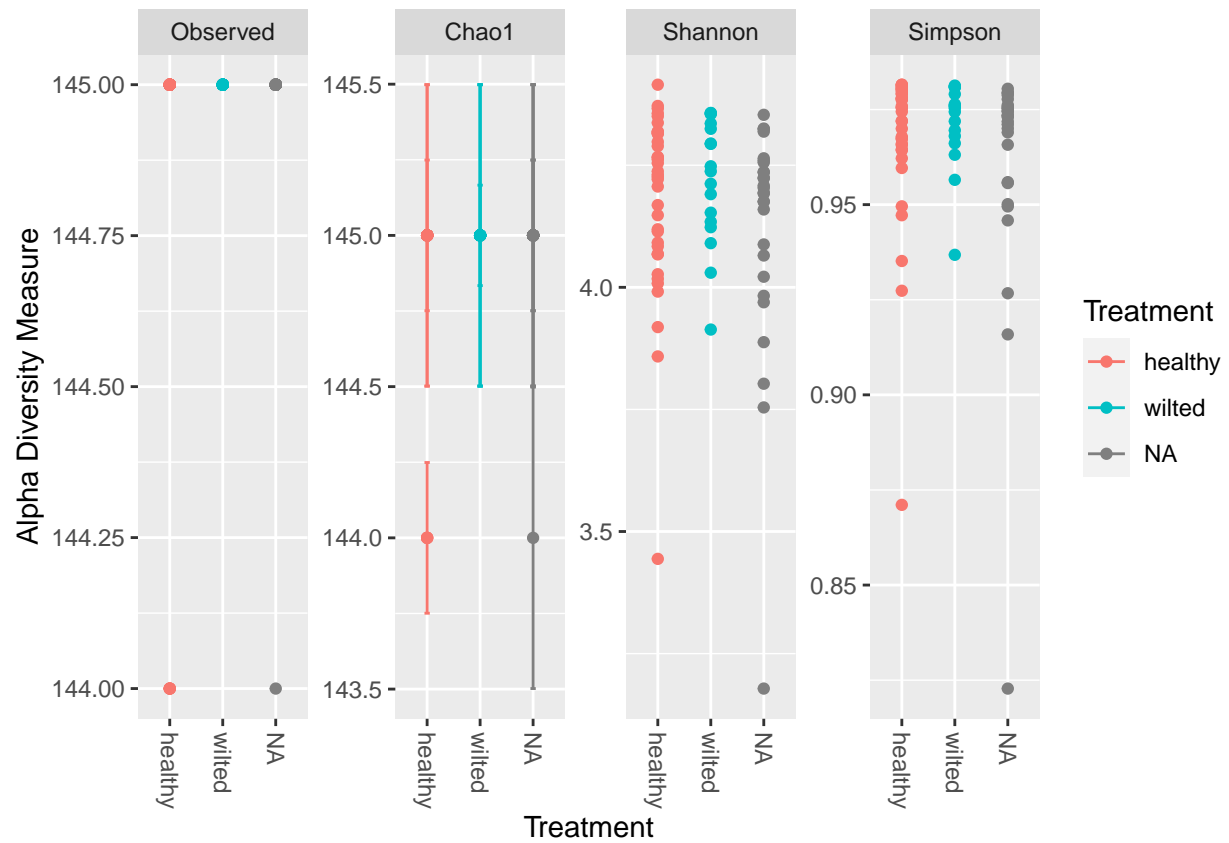

```

## Run 12 stress 0.1394575
## Run 13 stress 0.1394577
## Run 14 stress 0.1394569
## Run 15 stress 0.1394577
## Run 16 stress 0.1394573
## Run 17 stress 0.1394571
## Run 18 stress 0.1388439
## ... Procrustes: rmse 0.0003470212  max resid 0.001990059
## ... Similar to previous best
## Run 19 stress 0.1388444
## ... Procrustes: rmse 0.0004392323  max resid 0.002517098
## ... Similar to previous best
## Run 20 stress 0.1394611
## *** Best solution repeated 3 times

```



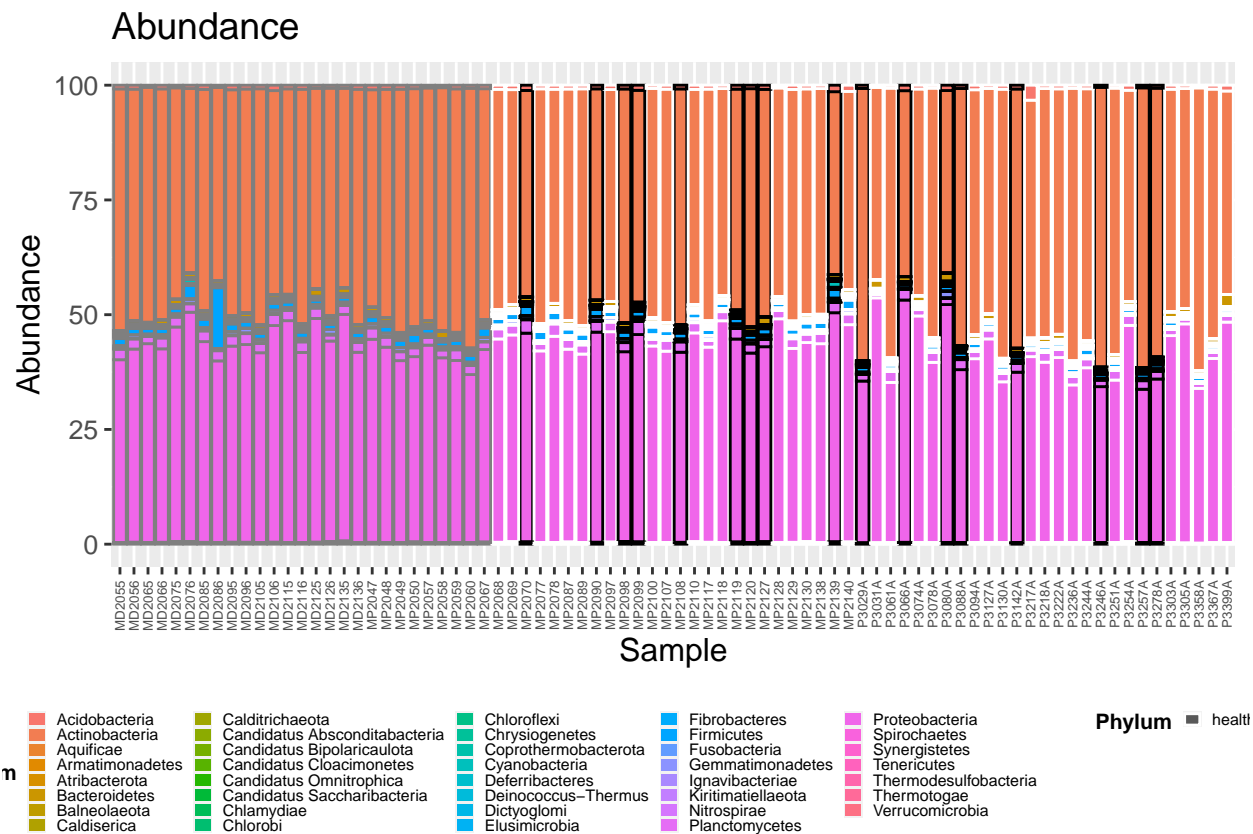
```
Alpha_diversity(merge_Eukaryota , 'Species' , 'Treatment')
```

#——Bacteria by Phylum

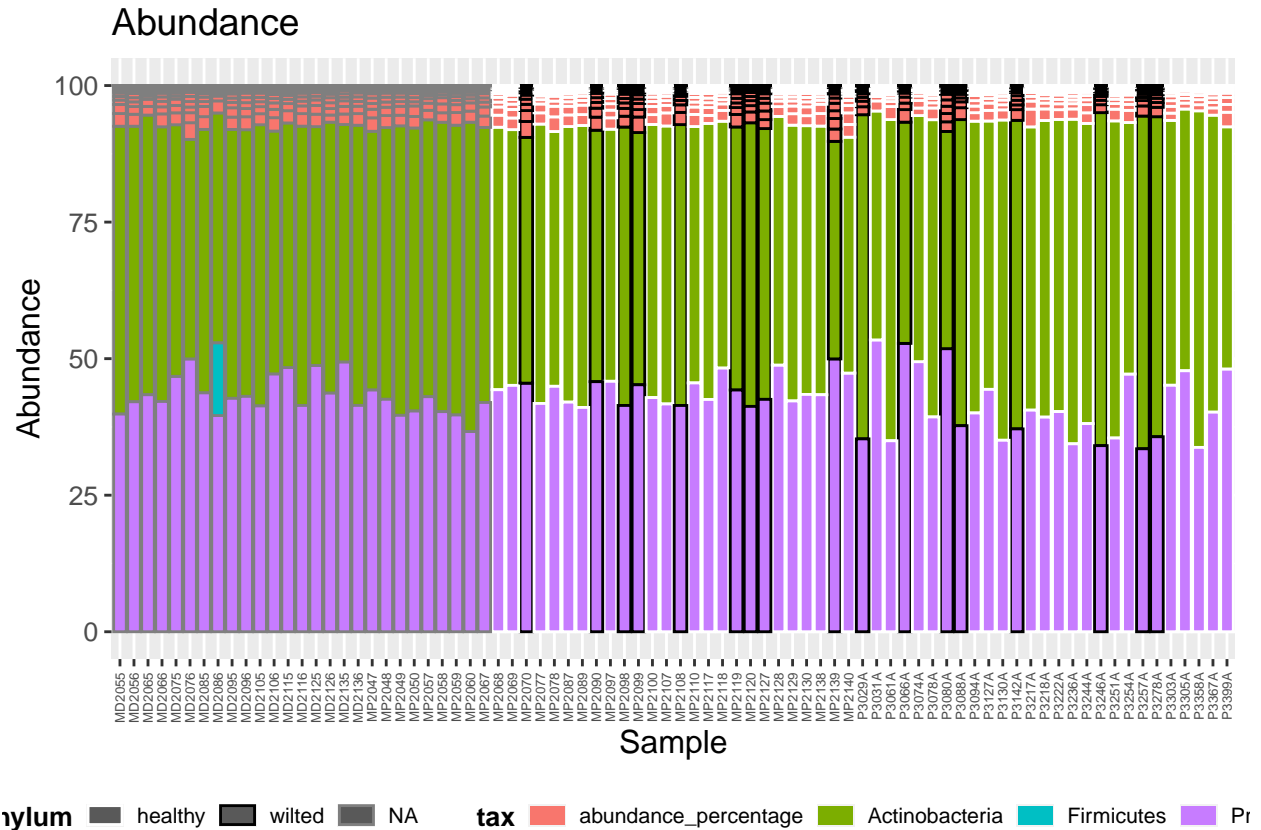
```
Barras_Species <- Abundance_barras(merge_Bacteria, 'Phylum', 'Treatment', 10.0)
Barras_Species[1]
```

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



Barras_Species[2]

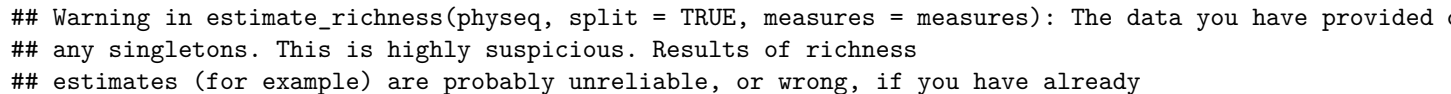
[[1]]



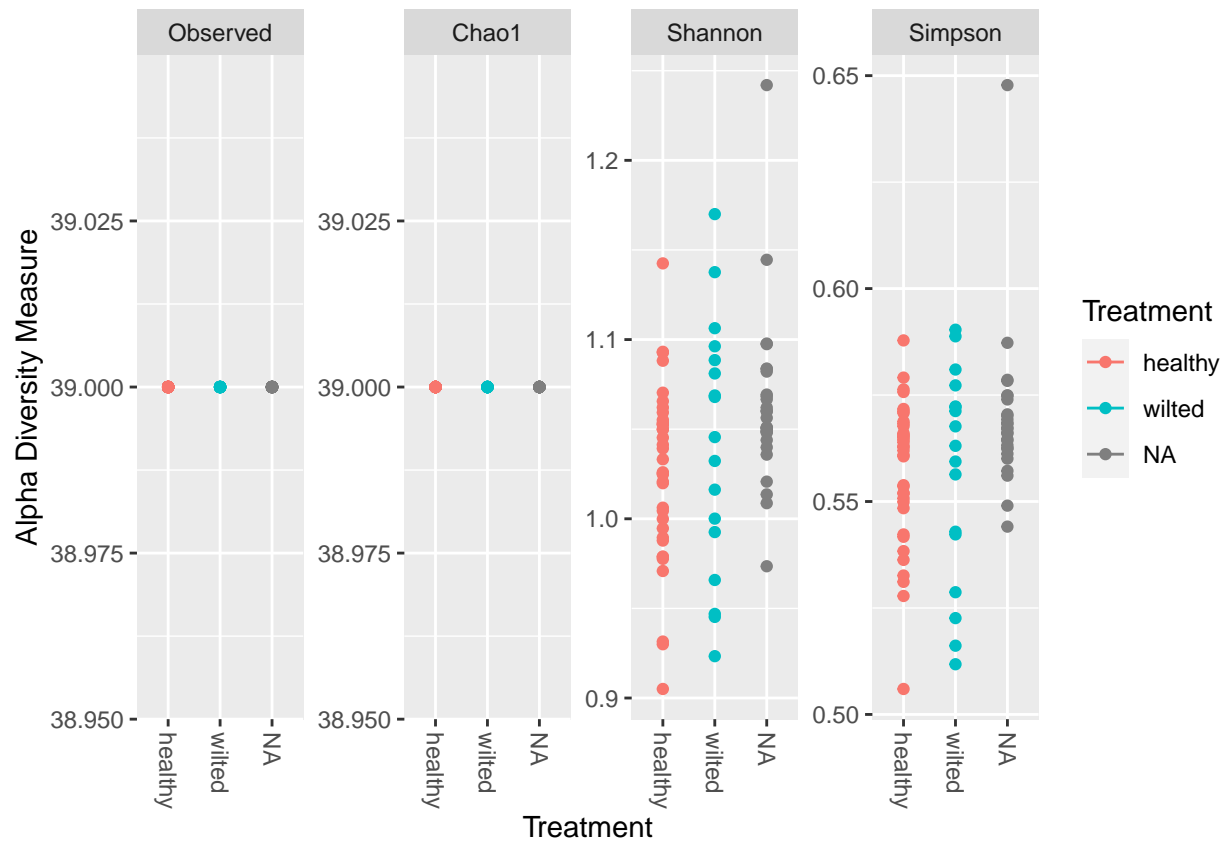
```
Beta_diversity(merge_Bacteria , 'Phylum' , 'Treatment', 'bray')
```

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.1704433
## Run 1 stress 0.1708577
## ... Procrustes: rmse 0.01316983 max resid 0.06454964
## Run 2 stress 0.1712858
## Run 3 stress 0.1716125
## Run 4 stress 0.169571
## ... New best solution
## ... Procrustes: rmse 0.02946184 max resid 0.2259082
## Run 5 stress 0.1696863
## ... Procrustes: rmse 0.0166448 max resid 0.09703316
## Run 6 stress 0.1704877
## Run 7 stress 0.1779854
## Run 8 stress 0.1683153
## ... New best solution
## ... Procrustes: rmse 0.01148517 max resid 0.06885598
## Run 9 stress 0.1683139
## ... New best solution
## ... Procrustes: rmse 0.001687889 max resid 0.01121499
## Run 10 stress 0.1796243
## Run 11 stress 0.1683149
## ... Procrustes: rmse 0.001764232 max resid 0.01125403
```

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



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



```
#———Bacteria by Familia
```

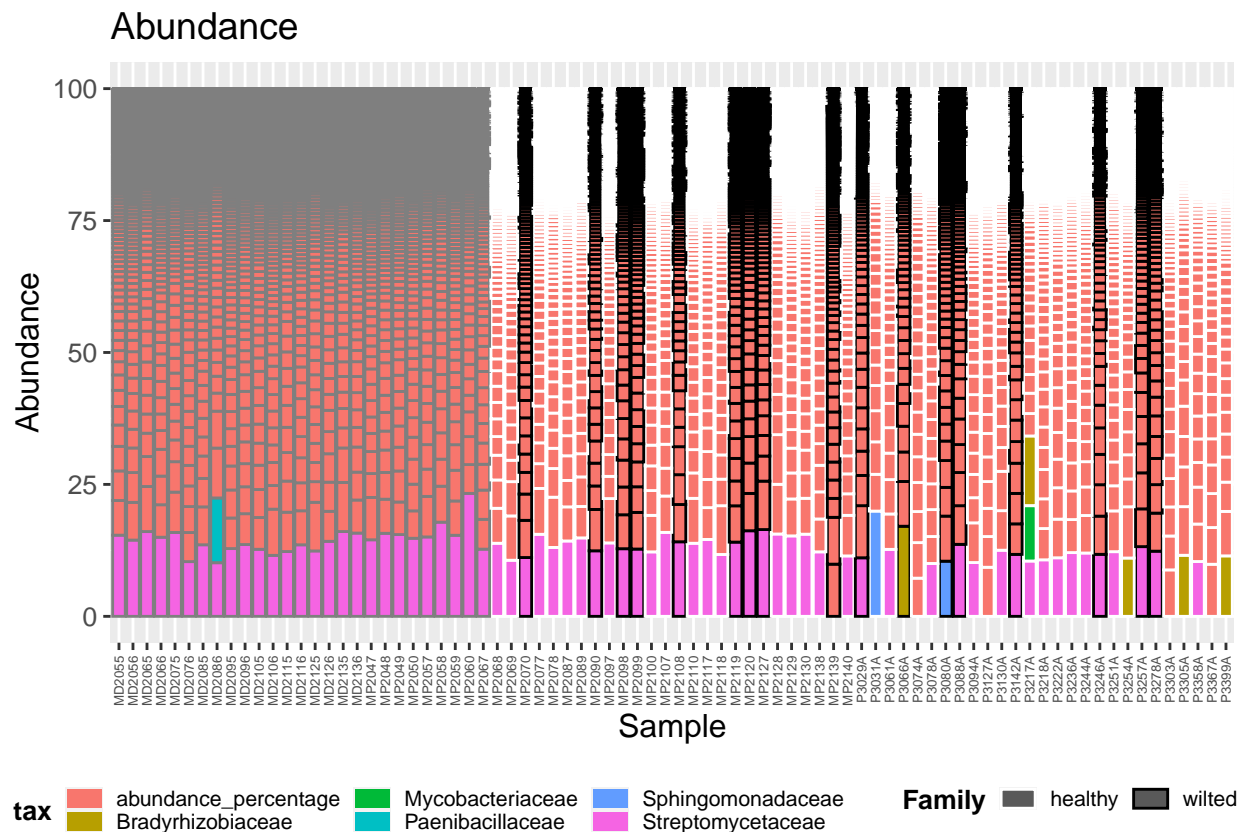
```
Barras_Species <- Abundance_barras(merge_Bacteria, 'Family', 'Treatment', 10.0)
Barras_Species[1]
```

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

Chloromonadaceae	Flavobacterioidaceae	Nocardiaceae	Sporobolaceae
Clostridiaceae	Halobacteroidaceae	Nocardioidaceae	Sporomusaceae
Clostridiales Family XVI. Incertae Sedis	Halomonadaceae	Nocardiopsaceae	Staphylococcaceae
Clostridiales Family XVII. Incertae Sedis	Halotheobacillaceae	Nostocaceae	Stappiaceae
Cohaesibacteraceae	Hapalosiphonaceae	Oceanospirillaceae	Stellaceae
Coleofasciculaceae	Helicobacteraceae	Oculatellaceae	Steroidobacteraceae
Colwelliaceae	Hellobacteriaceae	Odoribacteraceae	Sterolibacteriaceae
Comamonadaceae	Holospiraceae	Oleiphilaceae	Streptococcaceae
Conexibacteraceae	Hydrogenimonaceae	Opitutaceae	Streptomyetaceae
Coprothermobacteraceae	Hydrogenophilaceae	Orbaceae	Streptosporangiaceae
Coriobacteriaceae	Hydrogenothermaceae	Ornithinimicrobiaceae	Succinivibrionaceae
Corynebacteriaceae	Hyellaceae	Oscillatoriaceae	Sulfuricellaceae
Coxiellaceae	Hymenobacteraceae	Oscillospiraceae	Sulfurospirillaceae
Crocinitomicaceae	Hyphomicrobiaceae	Oxalobacteraceae	Sulfurovaceae
Cyclobacteriaceae	Hyphomonadaceae	Paenibacillaceae	Sutterellaceae
Cytophagaceae	Iamiaceae	Paludibacteraceae	Symbiobacteriaceae
Deferribacteraceae	Ichthyobacteriaceae	Parachlamydiaceae	Synechococcaceae
Dehalococcoidaceae	Idiomarinaceae	Parvibaculaceae	Synergistaceae
Deinococcaceae	Ignavibacteriaceae	Parvularculaceae	Syntrophaceae
Demequinaceae	Ilumatobacteraceae	Pasteurellaceae	Syntrophobacteraceae
Dermabacteraceae	Immundisolibacteraceae	Pectobacteriaceae	Syntrophomonadaceae
Dermacoccaceae	Intrasporangiaceae	Pelagibacteraceae	Syntrophotaleaceae
Dermatophilaceae	Isosphaeraceae	Peptococcaceae	Tannerellaceae
Dermocarpellaceae	Jatrophihabitantaceae	Peptoniphilaceae	Tenuifilaceae
Desulfallaceae	Jiangellaceae	Peptostreptococcaceae	Tepidanaerobacteraceae
Desulfarculaceae	Jonesiaceae	Petrotoceae	Tepidiformaceae
Desulfatobacteriaceae	Kaistiaceae	Phototrophicaceae	Tepidisphaeraceae
Desulfobacteraceae	Kangiellaceae	Phreatobacteraceae	Terasakiellaceae
Desulfobulbaceae	Kineosporiaceae	Phycisphaeraceae	Thalassospiraceae
Desulfocapsaceae	Kiritimatiellaceae	Phyllobacteriaceae	Thermaceae
Desulfohalobiaceae	Koferiaceae	Pirellulaceae	Thermincolaceae
Desulfomicrobiaceae	Koleobacteraceae	Piscirickettsiaceae	Thermoactinomycetaceae
Desulfosudaceae	Kordiimonadaceae	Planctomycetaceae	Thermoanaerobacteraceae
Desulfotomaculaceae	Kosmotogaceae	Planococcaceae	Thermoanaerobacteriales Family III. Incertae Sec
Desulfotrivirionaceae	Kribbellaceae	Pleomorphomonadaceae	Thermoanaerobacteriales Family IV. Incertae Sec
Desulfurellaceae	Ktedonosporobacteraceae	Polyangiaceae	Thermodesulfobacteriaceae
Desulfurobacteriaceae	Kytococcaceae	Porphyromonadaceae	Thermodesulfobiaceae
Desulfurodonadaceae	Labilitrichaceae	Prevotellaceae	Thermodesulfotrivirionaceae
Devosiaceae	Lachnospiraceae	Prochlorococcaceae	Thermoguttaceae
Dictyoglomaceae	Lacipirellulaceae	Prochlorotrichaceae	Thermohalobacteraceae
Dietziaceae	Lactobacillaceae	Prolixibacteraceae	Thermomicrobiaceae
Dissulfurispiriaceae	Lawsonellaceae	Promicromonosporaceae	Thermomonosporaceae
Dysgonomonadaceae	Legionellaceae	Propionibacteriaceae	Thermosediminibacteraceae
Ectothiorhodospiraceae	Leptolyngbyaceae	Proteinivoraceae	Thermostichaceae
Eggerthellaceae	Leptospiaceae	Pseudanabaenaceae	Thermosynechococcaceae
Egibacteraceae	Leptotrichiaceae	Pseudoalteromonadaceae	Thermotogaceae
Egicoccaceae	Lichenihabitantaceae	Pseudomonadaceae	Thermotomaculaceae
Elioraeaceae	Limnochordaceae	Pseudonocardiaceae	Thioalkalibacteraceae
Elusimicrobiaceae	Listeriaceae	Psychromonadaceae	Thioalkalispiraceae
Emcibacteraceae	Litoricolaceae	Puniceicoccaceae	Thiobacillaceae
Endomicrobiaceae	Magnetococcaceae	Rhabdochlamydiaceae	Thiotrichaceae
Endozoicomonadaceae	Mangrovivirgaceae	Rhizobiaceae	Thiovulaceae
Enterobacteriaceae	Maricaulaceae	Rhodanobacteraceae	Tichowtungiaceae
Enterococcaceae	Marinifilaceae	Rhodobacteraceae	Tissierellaceae
Entomoplasmataceae	Marinilabiliaceae	Rhodocyphaceae	Tolypothrichaceae
Erwinaceae	Marinobacteraceae	Rhodospirillaceae	Treponemataceae
Erysipelotrichaceae	Mariprofundaceae	Rhodothermaceae	Tropherymataceae
Erythrobacteraceae	Marinimicrobiaceae	Rickettsiaceae	Trichomonadaceae

Barras_Species [2]

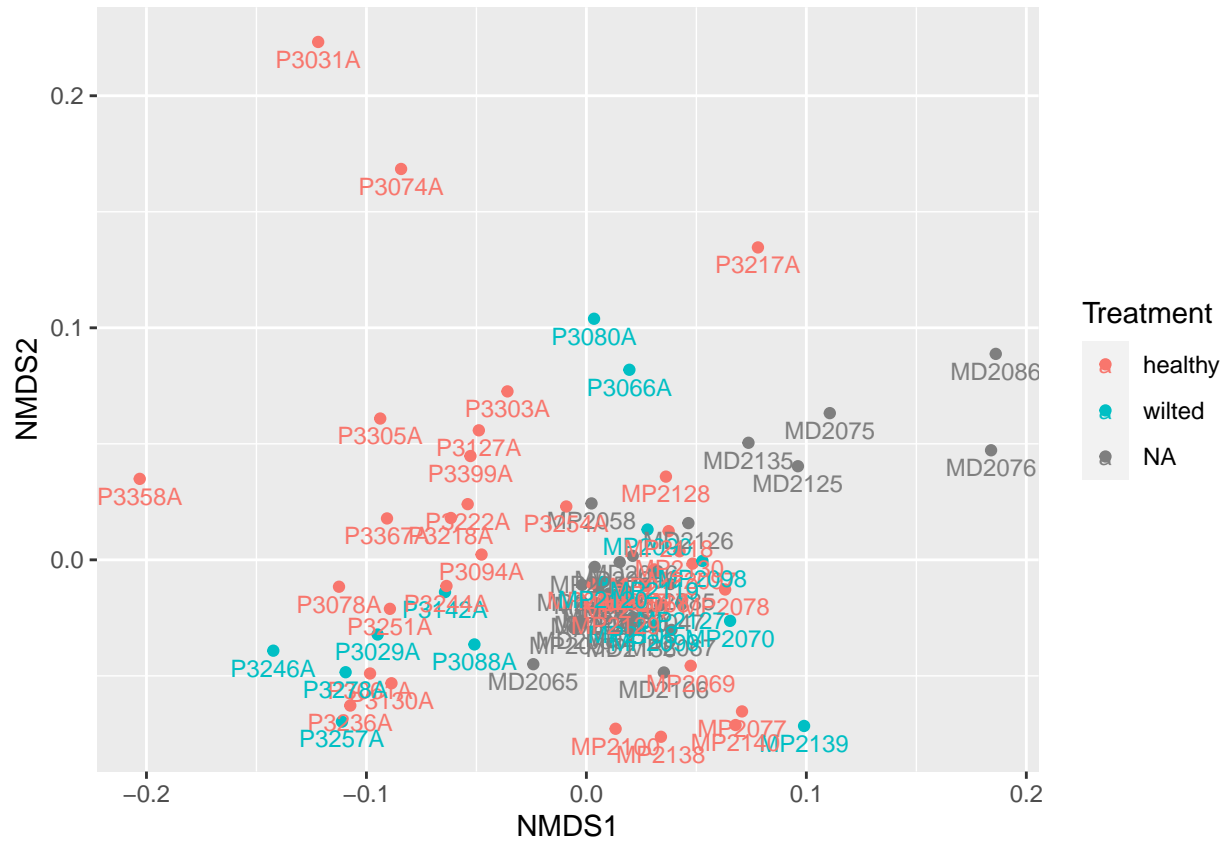
[[1]]



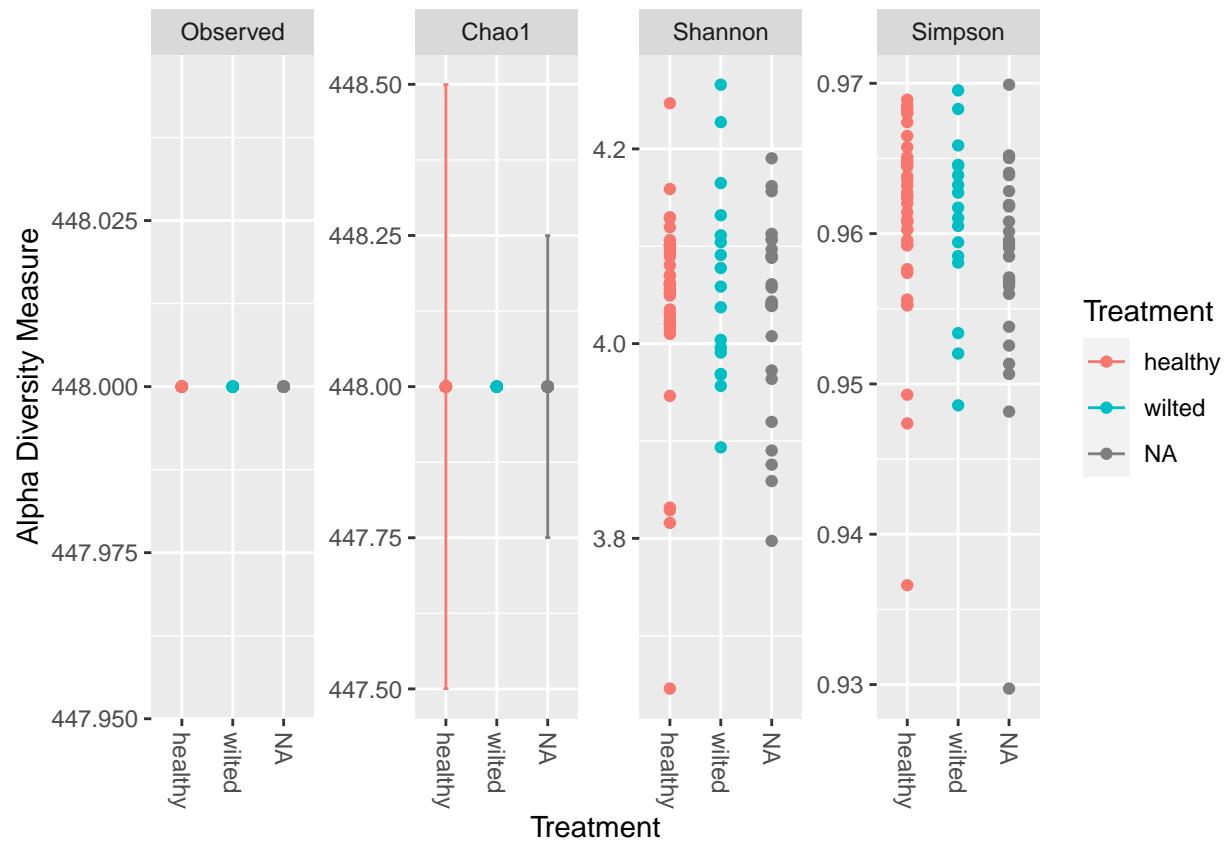
```
Beta_diversity(merge_Bacteria , 'Family' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.132377
## Run 1 stress 0.1405609
## Run 2 stress 0.1391985
## Run 3 stress 0.1519021
## Run 4 stress 0.1527065
## Run 5 stress 0.1432062
## Run 6 stress 0.1705558
## Run 7 stress 0.1395452
## Run 8 stress 0.1391766
## Run 9 stress 0.163441
## Run 10 stress 0.1411044
## Run 11 stress 0.1637101
## Run 12 stress 0.1444844
## Run 13 stress 0.1566534
## Run 14 stress 0.1486548
## Run 15 stress 0.1337582
## Run 16 stress 0.141046
## Run 17 stress 0.155059
## Run 18 stress 0.1626394
## Run 19 stress 0.1405614
## Run 20 stress 0.1622084
## *** Best solution was not repeated -- monoMDS stopping criteria:
```

```
##      2: no. of iterations >= maxit
##     18: stress ratio > sratmax
```



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

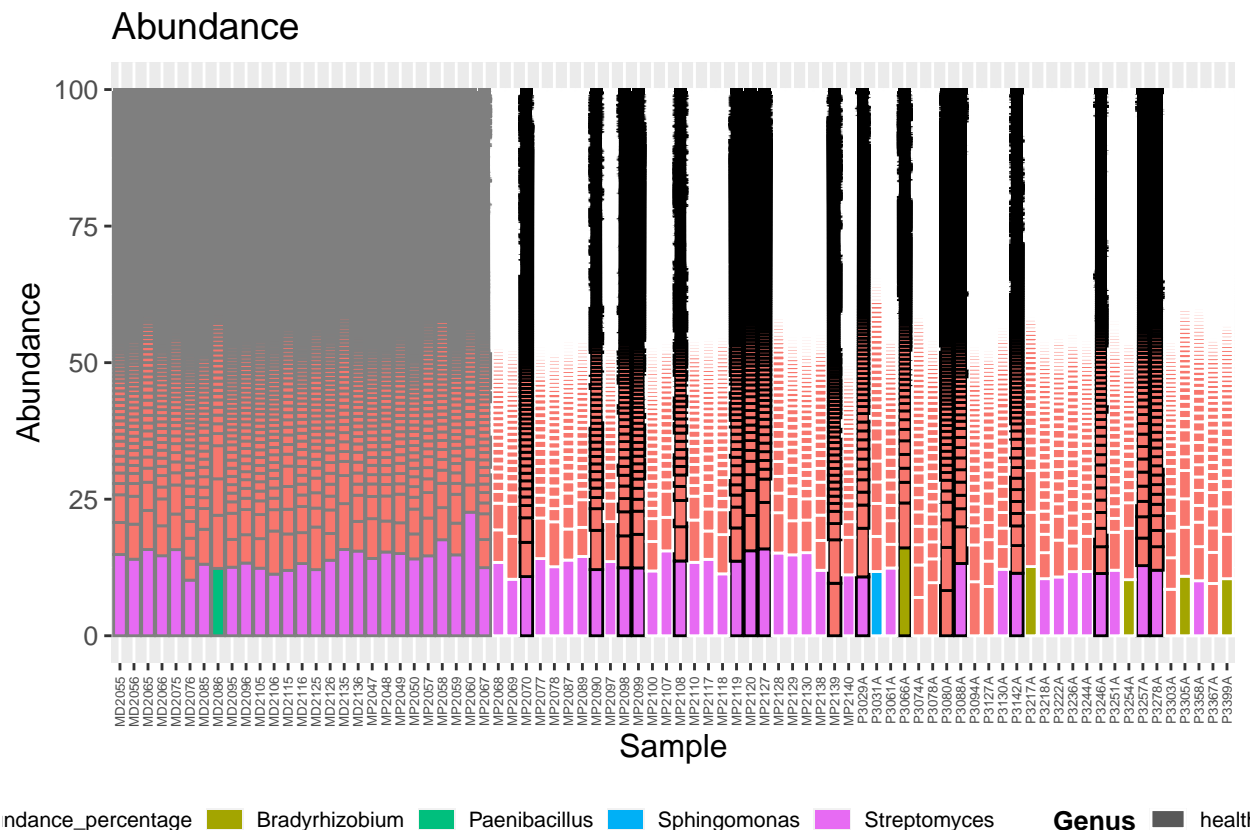
#——Bacteria by Genero

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

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

Aquifex	Desulfatococcus	Lactenzia	Paronibacter
Aquiflexum	Desulfatibaculum	Labrys	Paroceanicella
Aquihabitans	Desulfotibacterium	Laceyella	Parolsenella
Aquiluna	Desulfobacca	Lachnoanaerobaculum	Parvibaculum
Aquimarina	Desulfobacter	Lachnoclostridium	Parvimonas
Aquincola	Desulfobacula	Lachnospira	Parvularcula
Aquirhabdus	Desulfobulbus	Lacibacter	Pasteurella
Aquirufa	Desulfocapsa	Lacimicrobium	Paucibacter
Aquisalmonas	Desulfococcus	Lacinutrix	Paucilactobacillus
Aquisalinus	Desulfocurvibacter	Lactipirella	Pauljensenia
Aquisedimentimonas	Desulfofarctum	Lactimispira	Pectinatus
Aquisphaera	Desulfohalobium	Lactocaseibacillus	Pectinobacterium
Aquitalea	Desulfohalobium	Lactiplantibacillus	Pedococcus
Arabibacter	Desulfoluna	Lactobacillus	Pedobacter
Archidicoccus	Desulfolutivibrio	Lactococcus	Pedococcus
Arachnia	Desulfomarina	Lacunisphaera	Pelagerythrobacter
Arcanobacterium	Desulfomicrobium	Lancefieldella	Pelagibacterium
Archangium	Desulfomonile	Lapidilactobacillus	Pelagovum
Arcobacter	Desulfonema	Laribacter	Pelistega
Arcticibacterium	Desulforamulus	Larkinella	Pelobacter
Arenibacter	Desulforapulum	Latilactobacillus	Pelodictyon
Arenimonas	Desulfosarcina	Latropia	Pelolinea
Aromatoleum	Desulfoscapio	Lawsonella	Pelosinus
Arsenicococcus	Desulfoseditiminicola	Lawsonia	Pengzhenrongella
Arsenophonus	Desulfosporosinus	Leadbetterella	Pepiactobacter
Arenobacter	Desulfosudis	Lecleria	Pepiactobacterium
Asaia	Desulfotalea	Lederbergia	Peptoniphilus
Asticcaaulis	Desulfotomaculum	Leeuwenhoekeilla	Peribacillus
Athalassotoga	Desulfovibrio	Legionella	Periweissella
Atlantibacter	Desulfurispirillum	Leifsonia	Permanibacter
Atopobium	Desulfurivibrio	Leisingera	Persephonella
Atribacter	Desulfurobacterium	Lelliottia	Perseimonas
Aurantiaciabacter	Desulfuromonas	Leminorella	Pteryoungia
Aurantimicrobium	Devosia	Lentibacillus	Petrimonas
Aurantimonas	Devriesea	Lentilactobacillus	Petrocella
Auraticoccus	Dialister	Lentilitoribacter	Petrogla
Aureimonas	Diaminobutyricimonas	Leptzea	Phaeobacter
Aureliella	Diphorobacter	Leptodesmis	Phascolarctobacterium
Aurifidibacter	Dichelobacter	Leptolyngbya	Phenyllobacterium
Austwickia	Dickeya	Leptospira	Phnomibacter
Austrohalobium	Dicthyglomus	Leptospirillum	Phocoecia
Azoarcus	Dietzia	Leptothermofonsia	Phoenicibacter
Azorhizobium	Dinoroseobacter	Leptothrix	Photobacterium
Azospira	Dissulfurimicrobium	Leptotrichia	Photorhabdus
Azospirillum	Dissulfurispira	Leucobacter	Phototrophicus
Azotobacter	Dokdonella	Leuconostoc	Phreatobacter
Bacillus	Dokdonia	Levilactobacillus	Phycococcus
Bacterioplanes	Dolichospermum	Liberibacter	Phycisphaera
Bacteriovorax	Dolosigranulum	Lichenicola	Phyllobacterium
Bacteroides	Dongshaeta	Lichenihabitans	Phytobacter
Baekduia	Dorea	Ligilactobacillus	Phytohaptans
Barnesiella	Draconibacterium	Lignipirella	Pigmentiphaga
Baronella	Duganella	Limalnaloglobus	Pikeienuella
Basfia	Duncanella	Linnobacter	Pinelobacter
Basilea	Dysodacter	Linnobaculum	Pirellula
Bdellovibrio	Dyella	Linnochorda	Pirellulimonas
Beggiatoa	Dysgonomonas	Linnoglobus	Piscirickettsia
Bellerophon	Dysgonobacter	Linnobaculum	Pistisporus

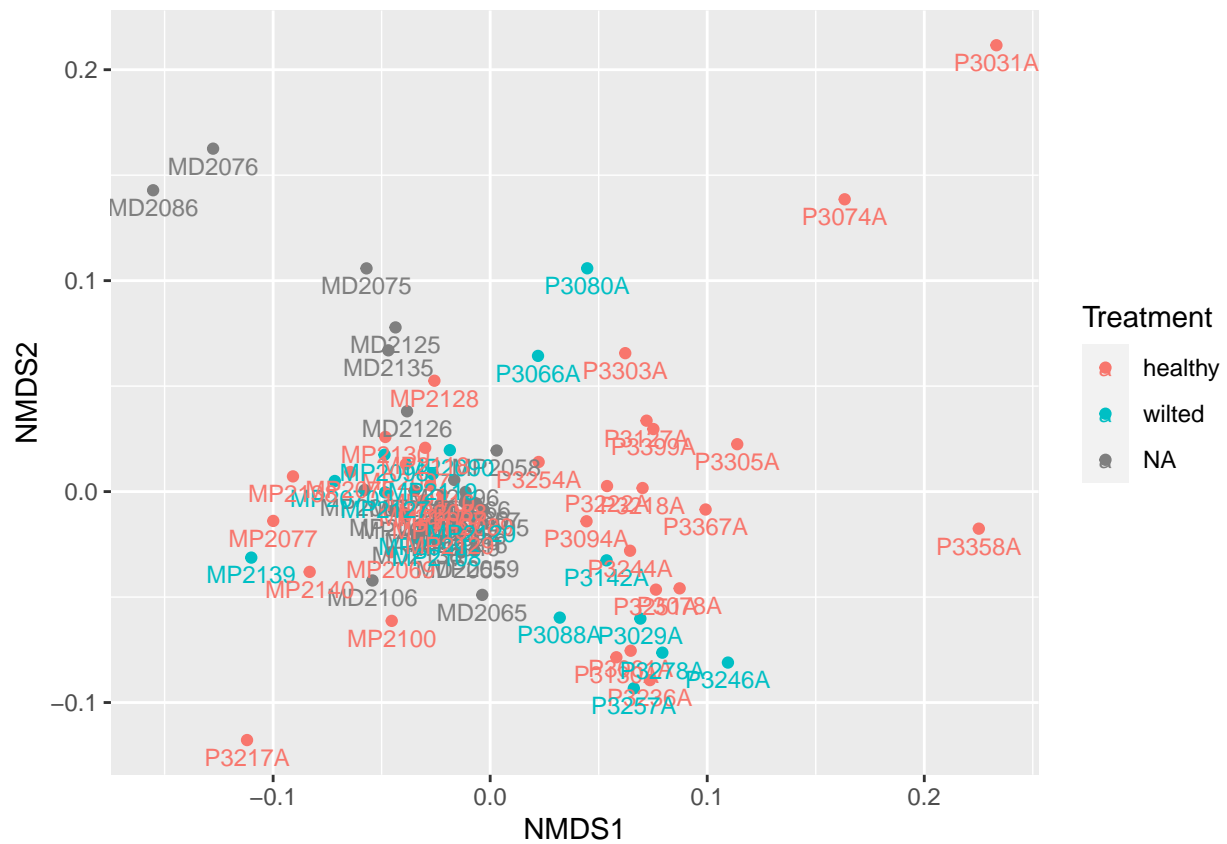
```
## [[1]]
```



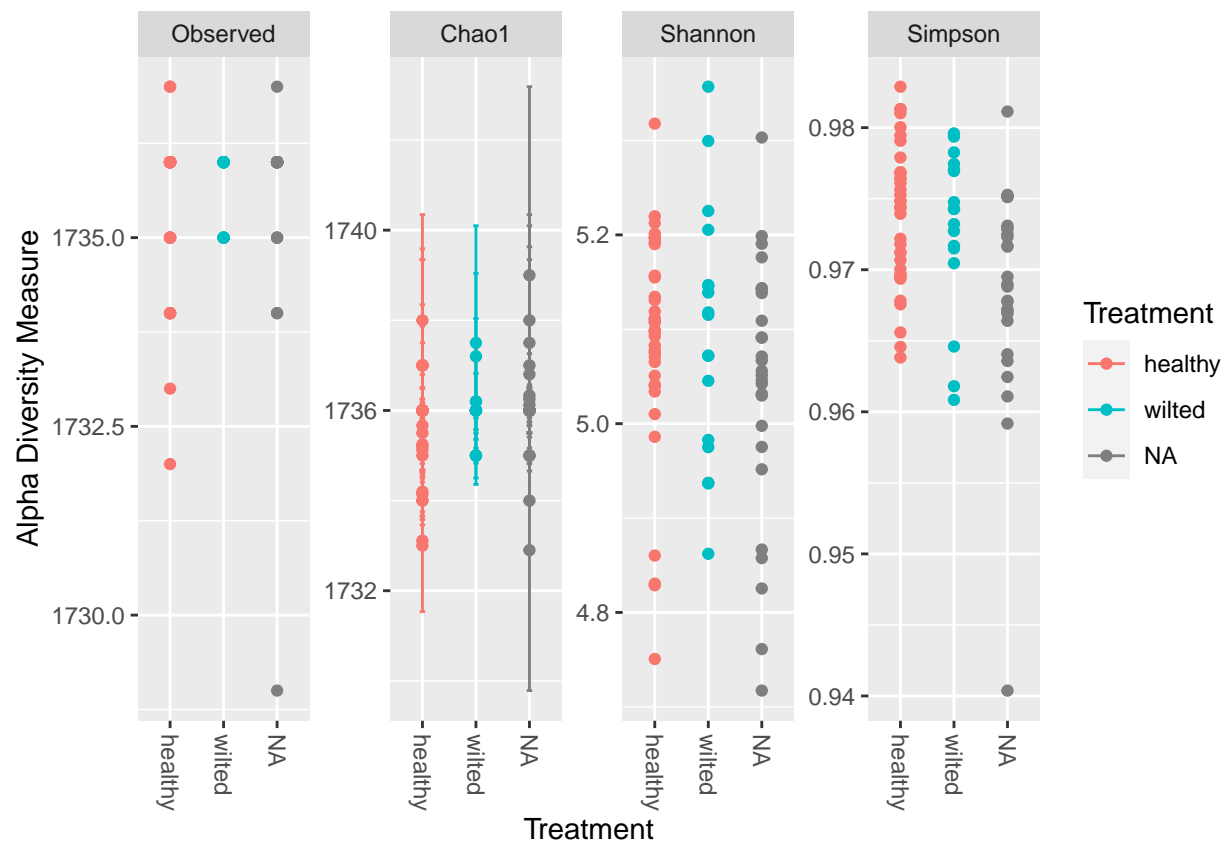
```
Beta_diversity(merge_Bacteria , 'Genus' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1323538
## Run 1 stress 0.1318739
## ... New best solution
## ... Procrustes: rmse 0.04483879 max resid 0.3308961
## Run 2 stress 0.1320811
## ... Procrustes: rmse 0.04682465 max resid 0.3312729
## Run 3 stress 0.1322392
## ... Procrustes: rmse 0.01733447 max resid 0.1405044
## Run 4 stress 0.1383274
## Run 5 stress 0.1328271
## Run 6 stress 0.1266989
## ... New best solution
## ... Procrustes: rmse 0.02281745 max resid 0.1891363
## Run 7 stress 0.1412309
## Run 8 stress 0.1321914
## Run 9 stress 0.148244
## Run 10 stress 0.1420427
## Run 11 stress 0.1467141
## Run 12 stress 0.1323434
## Run 13 stress 0.1324735
## Run 14 stress 0.148499
## Run 15 stress 0.1330579
```

```
## Run 16 stress 0.1682506
## Run 17 stress 0.1489298
## Run 18 stress 0.1517771
## Run 19 stress 0.1554539
## Run 20 stress 0.1333587
## *** Best solution was not repeated -- monoMDS stopping criteria:
##      1: no. of iterations >= maxit
##     19: stress ratio > sratmax
```



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



#——Bacteria by Species

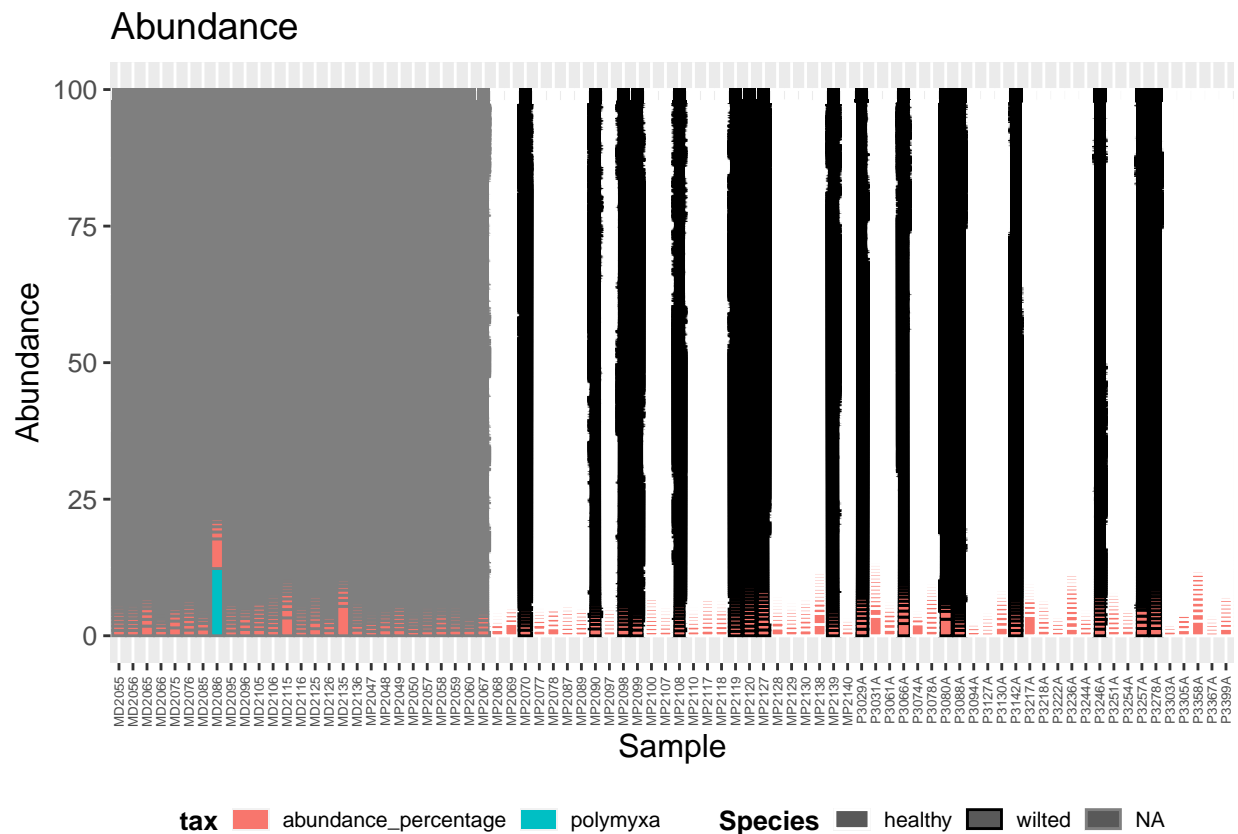
```
Barras_Species <- Abundance_barras(merge_Bacteria, 'Species', 'Treatment', 10.0)
Barras_Species[1]
```

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

	lactus	sp. (masutermes uarwiniensis)	sp. N1-13	sp. ACS2
	lactucae	sp. (Nauphoeta cinerea)	sp. KT25b	sp. XES5
	lacunae	sp. (Periplaneta americana)	sp. KTR9	sp. XF20
	lacus	sp. 001	sp. KUDC0405	sp. XG20
	lacuslunae	sp. 007	sp. KUDC0406	sp. XGS-
	lacustris	sp. 008	sp. KUDC1026	sp. XGS7
	laguerreae	sp. 02C 26	sp. KUDC1714	sp. XH2
	laidlawii	sp. 09C 129	sp. KUIN-1	sp. Xi13
	laixinhei	sp. 09RB8471	sp. Kuro-4	sp. XLW
	laikuanensis	sp. 09RB8910	sp. KW1	sp. xlx-2
	laminatus	sp. 1_2014MBL_MicDiv	sp. KX20019	sp. XM-1
	lanienae	sp. 1_2015MBL_MicDiv	sp. KY-GH-1	sp. XS-3
	lanii	sp. 1-1C	sp. KY-YJ-3	sp. XSG
	lansingensis	sp. 1.5R	sp. KY3	sp. XT11
	lanthieri	sp. 1(2017)	sp. KY5	sp. XWY-
	lapagei	sp. 103DPR2	sp. KY70	sp. XY-1
	lapidicaptus	sp. 1063	sp. KY75	sp. XY-2
	lapsinans	sp. 107-1	sp. L-07	sp. Y-01
	lari	sp. 1070	sp. L-2-11	sp. Y1
	lariciata	sp. 10FS3-1	sp. L-8-10	sp. Y16C
	larrymoorei	sp. 10M-3C3	sp. L-8-3	sp. Y2R2
	larvae	sp. 10RB9215	sp. L-A4	sp. Y3
	lata	sp. 11-1-2	sp. L12M9	sp. Y32M
	latens	sp. 11-B-312	sp. L1A13	sp. Y33
	laterosporus	sp. 113-1-2	sp. L1A34	sp. Y33R
	laumondii	sp. 113-3-3	sp. L1A9	sp. Y39-
	lautus	sp. 113-3-9	sp. L1139	sp. Y412
	lavamentivorans	sp. 1137	sp. L1SW	sp. Y412
	lavendulae	sp. 113P3	sp. L2A1	sp. Y5-1
	leachii	sp. 114	sp. L2A11	sp. Y8
	leadbetteri	sp. 11515TR	sp. L3-i22	sp. Y9
	leeuwenhoekii	sp. 116-D4	sp. L3-i23	sp. YAU1
	leguminosarum	sp. 119287	sp. L3A3	sp. YAU1
	lehensis	sp. 11B	sp. L3A6	sp. YB32
	lekithochrous	sp. 11kri321	sp. L3A8	sp. YBL2
	lemovicicum	sp. 12200R-103	sp. L5	sp. YBS0
	lemurum	sp. 13-15	sp. L51/94	sp. YC-J
	lenghuensis	sp. 131	sp. L5B5	sp. YC-J
	lenta	sp. 131-2-1	sp. L6-1	sp. YC-F
	lentiflavum	sp. 131-2-5	sp. L9-4	sp. YC1
	lentis	sp. 131-3-5	sp. LA-2-3-30-S1-D2	sp. YCS0
	lentocellum	sp. 13159349	sp. LA112445	sp. YF1
	lentus	sp. 135	sp. LA31	sp. YG1
	leopoldii	sp. 140616W15	sp. LAB-08	sp. YGD1
	leprae	sp. 14171R-50	sp. LADL05-105	sp. YGS1
	lepromatosis	sp. 14181154	sp. LAS2	sp. YH-1
	leptomitiformis	sp. 143-21	sp. LB1	sp. YH12
	lettingae	sp. 144S4	sp. LBG001	sp. YIK1:
	liangguodongii	sp. 15-184	sp. LBUM 1475	sp. YIM 1
	liangshanensis	sp. 1513	sp. LBUM 1480	sp. YIM 1
	liaowanqingii	sp. 155	sp. LBUM 1482	sp. YJ47
	libanensis	sp. 1566	sp. LBUM920	sp. YJN-
	licheniformis	sp. 157MF	sp. LC2018020214	sp. YJN-
	lienii	sp. 15A4	sp. LC6	sp. YJN-
	liflandii	sp. 15R	sp. LCT2	sp. YL-1
	ligni	sp. 1608163	sp. Leaf245	sp. YL32
	lignieresii	sp. 1643	sp. Leaf58	sp. YLB-
	lifanlianica	sp. 1654 15	sp. LeafP3	sp. YLG

Barras_Species [2]

[[1]]



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

```
## Wisconsin double standardization
## Run 0 stress 0.1456926
## Run 1 stress 0.1551344
## Run 2 stress 0.153833
## Run 3 stress 0.1545858
## Run 4 stress 0.1462371
## Run 5 stress 0.1568186
## Run 6 stress 0.1398761
## ... New best solution
## ... Procrustes: rmse 0.03959896 max resid 0.3261456
## Run 7 stress 0.1490098
## Run 8 stress 0.1445075
## Run 9 stress 0.1575396
## Run 10 stress 0.1591801
## Run 11 stress 0.1482487
## Run 12 stress 0.151126
## Run 13 stress 0.1706569
## Run 14 stress 0.1634706
## Run 15 stress 0.1430293
## Run 16 stress 0.1497951
## Run 17 stress 0.1407344
## Run 18 stress 0.1577634
## Run 19 stress 0.1481045
```

```
## Run 20 stress 0.1739684
## *** Best solution was not repeated -- monoMDS stopping criteria:
##      2: no. of iterations >= maxit
##      18: stress ratio > sratmax
```

