Intestinal microbiome landscaping: Insight in community assemblage and implications for microbial modulation strategies

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12 december 2016

```r
library("reshape")
```

```
## Warning: package 'reshape' was built under R version 3.3.1
```

```r
library("ggplot2")
```

```
## Warning: package 'ggplot2' was built under R version 3.3.1
```

```r
library("qgraph")
```

```
## Warning: package 'qgraph' was built under R version 3.3.1
```

Before we start with the anlaysis there are a few steps that need to be completed.

1] Download the compelte repository (right hand corner)
file downloaded = Intestinal-Microbiome-Western-Adults-master.zip 2] Unzip the file "Intestinal-Microbiome-Western-Adults-master.zip"
3] set this as the working directory

```r
setwd("D:/Intestinal-Microbiome-Western-Adults-master")

# You can check the working directory now by typing
getwd()
```

```
## [1] "D:/Intestinal-Microbiome-Western-Adults-master"
```

We will noe read the files. you have to chose the file ("genome_koabundance.txt") in the new select window that will pop-ip after you run the script "file= choose.files(multi=F)"

```r
setwd("D:/Intestinal-Microbiome-Western-Adults-master")

file= choose.files(multi=F)
ko_abundance= read.table(file,sep="\t", header=T, row.names=1)
```

Creating the plots

```r
#we now calculate the Spearman rank correlation
genome.cor<- cor(ko_abundance, method="spearman")
```

```
#check the file
head(genome.cor)

#load the following packages
library("reshape")
library("ggplot2")

#format the data for use in ggplot2
cor.dat <- melt(genome.cor)

###Identifying the correlation distribution profile
cor.dist.plot <- ggplot(cor.dat, aes(x=value), geom = "histogram", size= 2, c
olor = "#CC79A7") + stat_bin(binwidth = 0.01, fill = "#807dba") + theme(axis.
title.x = element_text(colour = "black", size= 4), axis.title.y = element_tex
t(colour = "black", size=4)) + labs(x= " Correlation values Spearman correlat
ion", y= "Counts" , size= 4) + theme_grey()

print(cor.dist.plot)
```
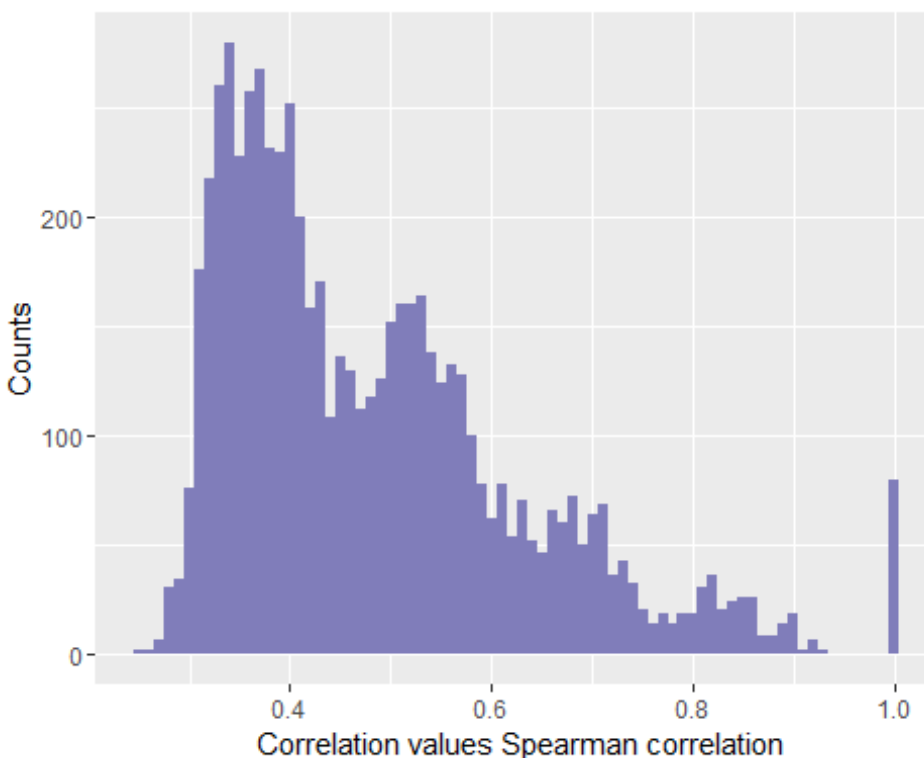


```
#Plot the pairwise Spearman's correlation
cor.pair.plot <- ggplot(cor.dat, aes(value, X1), geom= "bar", fill= ..count..
) + geom_jitter(aes(x=value,y=X1), color = "#807dba", shape=18) + labs(x= " C
orrelation values (Pearson coefficient)", y= "Genome of representative core b
acteria") + scale_x_continuous(limits = c(0.2, 1)) + theme_bw() + theme(axis.
text.y = element_text(size=8, face = "italic"))
print(cor.pair.plot)
```
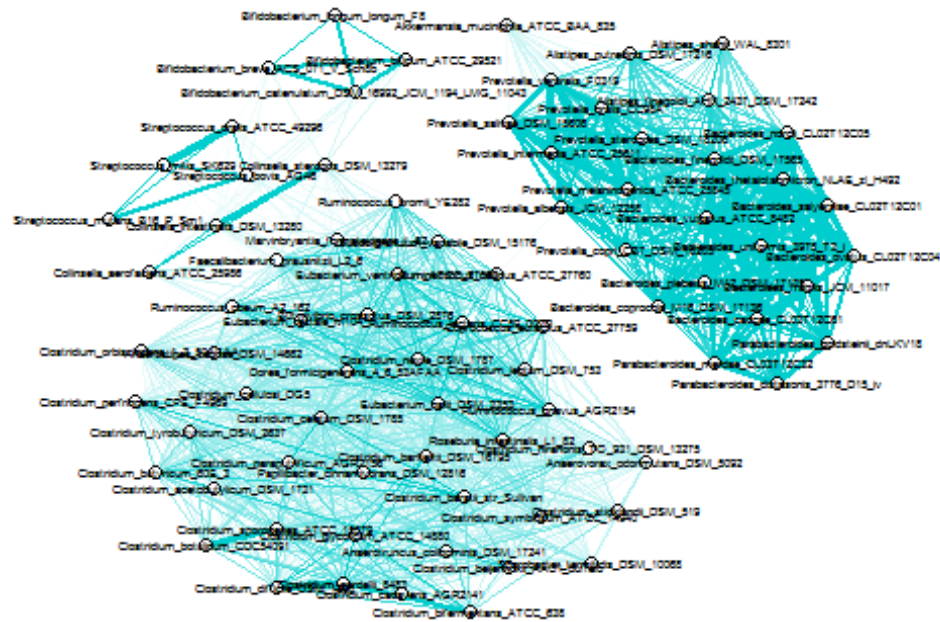
```r
library("qgraph")

#set node attribute
labels_row <- rownames(genome.cor)
set.seed(12134)
qab <- qgraph(genome.cor, minimum = 0.5, fade = TRUE, vsize = 1.5, layout = "
spring", vTrans = 255, node.labels= TRUE, edge.labels=FALSE, rotation= "45",
labels = labels_row, label.cex = 0.4, label.scale= F, edge.color= "#00CDCD")
```

Further colouring based on phylum affiliation was done in Adobe Illustrator!!