SH_Graph

Importing data and pre-processing

```r
library(phyloseq)
library(ggplot2)
library(tidyverse)
library(RColorBrewer)
library(cowplot)
library(metacoder)
SH_ITS_data0 <- import_biom(BIOMfilename = "otu_table.biom")
SH_ITS_data0
```

```
## phyloseq-class experiment-level object
## otu_table()   OTU Table:         [ 59629 taxa and 18 samples ]
## tax_table()   Taxonomy Table:    [ 59629 taxa by 7 taxonomic ranks ]
```

```r
sam.data <- read.csv (file = "mapping_file_ITS_R1_corrected.csv", row.names = 1, header
 = TRUE)
sample_data (SH_ITS_data0) <- sam.data
```

Checking sequencing depth

```r
# Make a data frame with a column for the read counts of each sample
sample_sum_df <- data.frame(sum = sample_sums(SH_ITS_data0))
# Histogram of sample read counts
ggplot(sample_sum_df, aes(x = sum)) +
  geom_histogram(color = "black", fill = "indianred", binwidth = 2500) +
  ggtitle("Distribution of sample sequencing depth") +
  xlab("Read counts") +
  theme_gray() + theme(axis.title.y = element_blank())
```

Distribution of sample sequencing depth
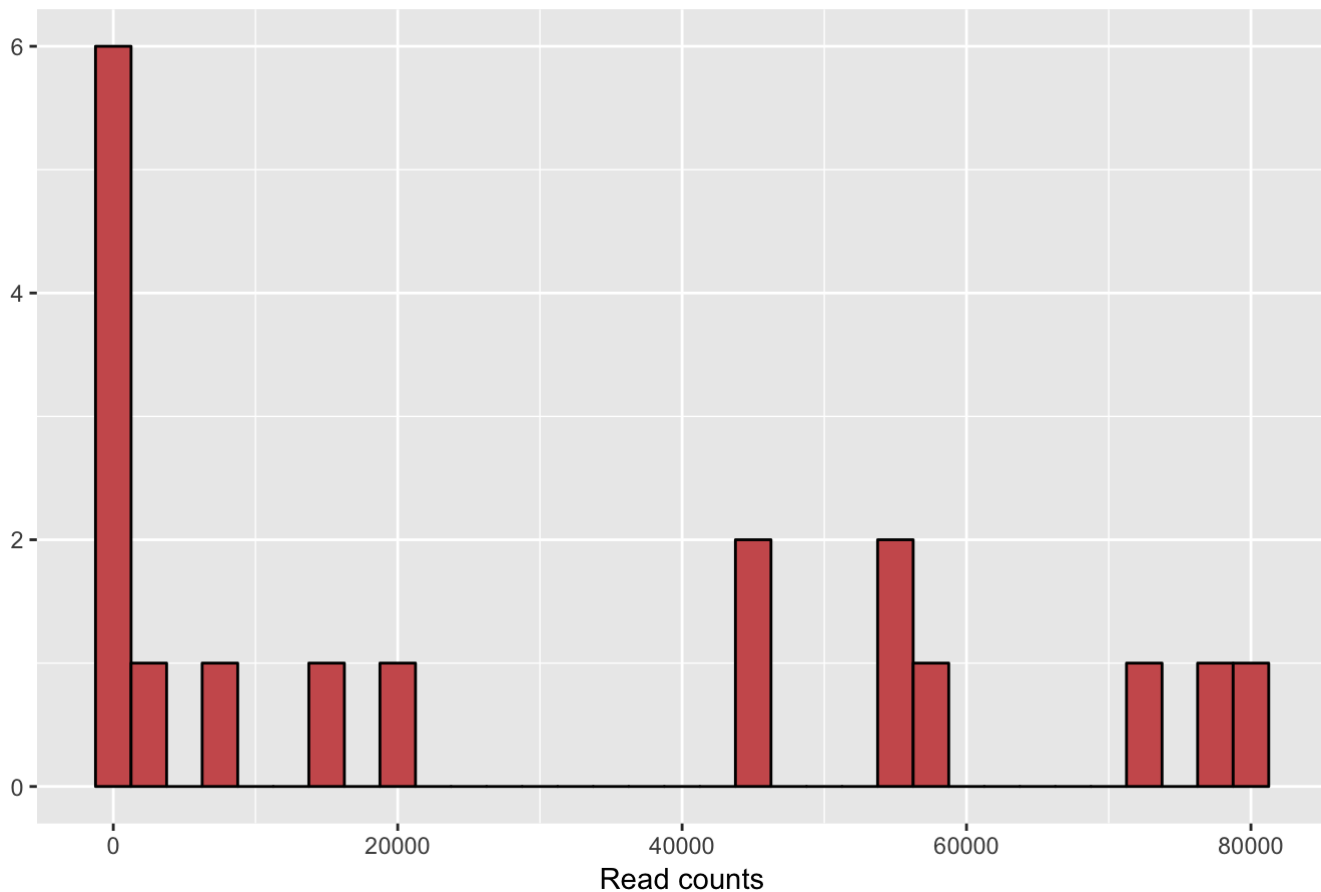
Standardizing by sequencing depth

```
#Standardize abundances to the median sequencing depth
total <- median(sample_sums(SH_ITS_data0))
standf <- function(x, t=total) round(t * (x/sum(x)))
SH_ITS_data0.std <- transform_sample_counts(SH_ITS_data0, standf)
```

Filtering "no hits"

```
#Renaming taxonomy levels on tax_table
colnames(tax_table(SH_ITS_data0.std)) <- c("Kingdom", "Phylum", "Class","Order", "Family", "Genus", "Species")
#Filtering no hit at Kingdom level
SH_ITS_data <- subset_taxa(SH_ITS_data0.std, Kingdom != "No blast hit")
```

Taxa abudance at different rank levels

```
#summarizing by tax rank
SH_ITS.phylum <- tax_glom(SH_ITS_data, "Phylum")
plot_bar(SH_ITS_data, fill = "Phylum", x = "Group") + theme_gray()
```
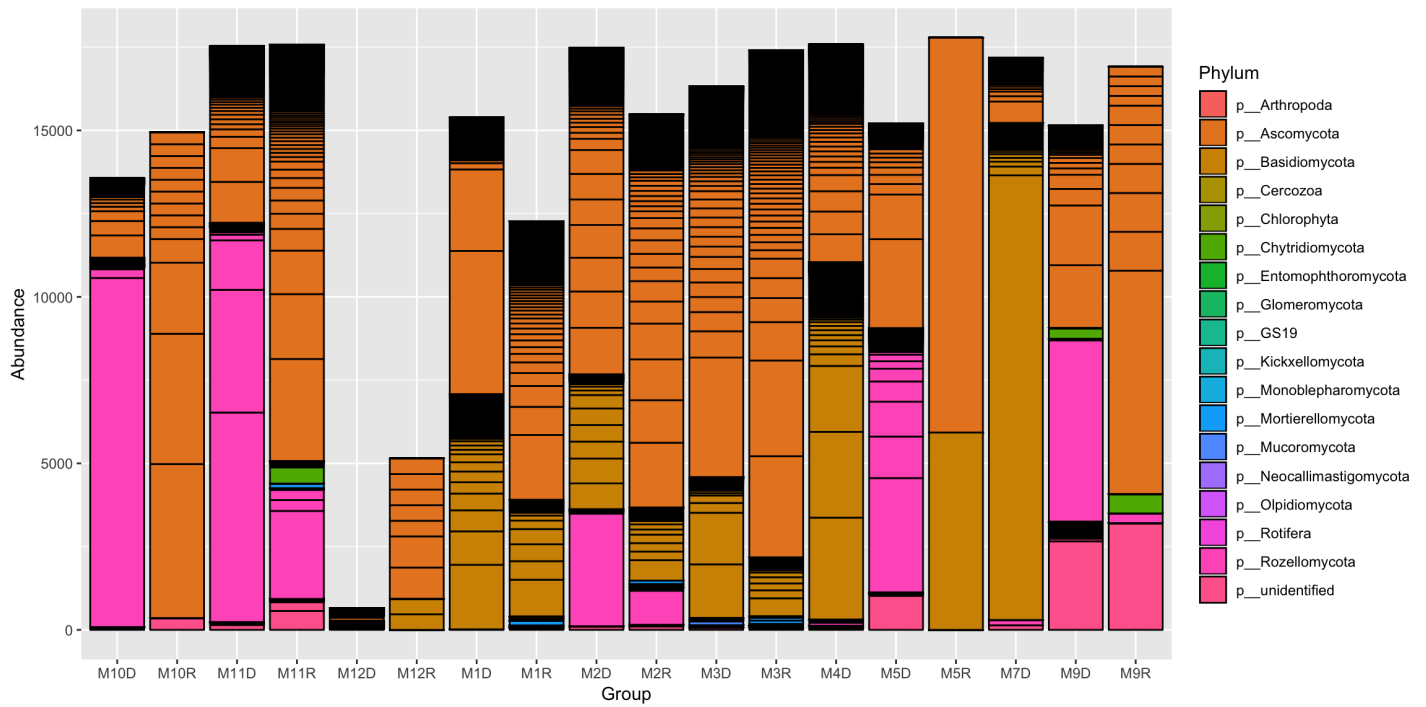
```
plot_bar(SH_ITS.phylum, fill = "Phylum", x = "Group") + theme_gray()
```
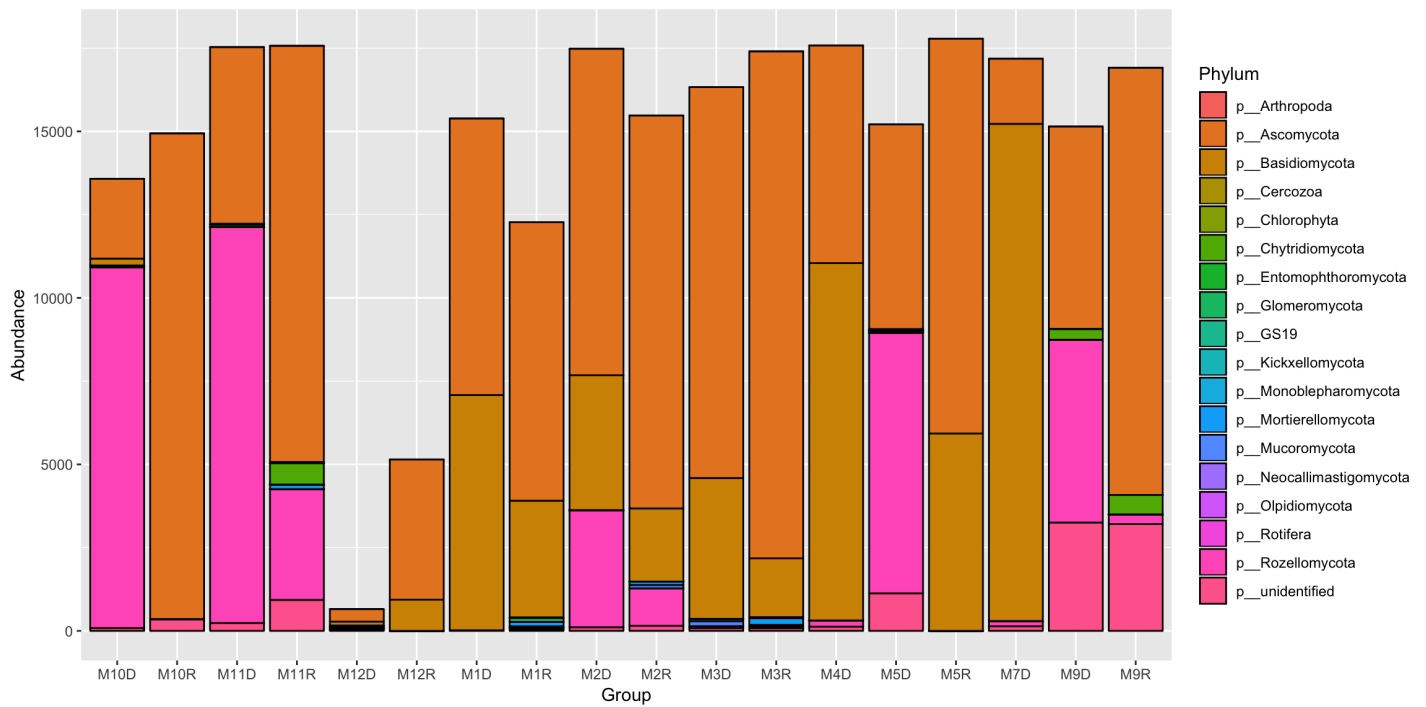


```
#Plot by family
SH_ITS.fam <- tax_glom(SH_ITS_data, "Family")
plot_bar(SH_ITS.fam, fill = "Family", x = "Group") + theme_gray()
```

Relative abudance of genus and class in BGM soil and root samples

```
TopNOTUs <- function(sample,N) {
  names(sort(taxa_sums(sample), TRUE)[1:N])
}
#Creating data frame from phyloseq object
top.SH_ITS <- TopNOTUs(SH_ITS_data, 50)
SH_ITS.df <- prune_taxa(top.SH_ITS, SH_ITS_data) %>% psmelt()
#Sumarize data by site
#test <- BGM.df %>% group_by(Genus) %>% summarise(sum(Abundance))
#plot by relative abundance
#Plot
pal <- colorRampPalette((brewer.pal(10, "Paired")))
SH_ITS.genus <- ggplot(data = SH_ITS.df, aes(Group, Abundance, fill = Genus)) +
  geom_bar(stat = "identity", position = position_fill()) + coord_flip() +
  scale_fill_manual(values = (rev(pal(24)))) +
  guides(fill = guide_legend(reverse = TRUE, ncol = 1, keyheight = 0.8)) +
  theme(text = element_text(size = 15)) + theme_gray()

SH_ITS.genus
```