rm(list = ls())

#install.packages("ggalluvial")

#install.packages("ggh4x")

library(MicrobiotaProcess)

library(ggplot2)

library(ggalluvial)

library(ggh4x)

library(phyloseq)

library(openxlsx)

library(readxl)

library(tibble)

####加载数据，包括OTU特征表、样本信息以及物种分类表

OTU <- read\_excel("OTU-MPs.xlsx", sheet = "otu")

Tax <- read\_excel("OTU-MPs.xlsx", sheet = "tax")

sample <- read\_excel("OTU-MPs.xlsx", sheet = "sample")

sample <- column\_to\_rownames(sample, var = colnames(sample)[1])

## 构造microtable

ps <- phyloseq(sample\_data(sample),

otu\_table(as.matrix(OTU), taxa\_are\_rows=TRUE),

tax\_table(as.matrix(Tax)))

#转换数据格式

df<-ps%>%as.MPSE()

df

df %<>%

mp\_cal\_abundance( # for each samples

.abundance = RareAbundance

) %>%

mp\_cal\_abundance( # for each groups

.abundance=RareAbundance,

.group=group

)

p1 <- df %>% mp\_plot\_abundance(

.abundance=RareAbundance,

.group=group, #指定分组以分面

taxa.class = Phylum, #指定分类水平

topn = 10,#可视化物种的数量

relative = TRUE#相对丰度

)+

theme(legend.position = "none")

p1

p3 <- df %>%

mp\_plot\_abundance(

.abundance = RareAbundance,

.group = group,

taxa.class = Phylum,

topn = 10,

plot.group = TRUE

) +

theme\_minimal() +

theme(

legend.position = "right",

text = element\_text(family = "serif", size = 14, face = "bold"), # 字体加粗

panel.border = element\_rect(color = "black", fill = NA, size = 1) # 外边框

) +

scale\_fill\_manual(values = c("#E3F2FD", "#A0D8F1", "#6BCDF2", "#87CEEB", "#5AB3F0", "#FFD97D", "#FFDC70", "#F9D29B", "#F8C58C", "#F6B680", "#F4A261")) +

scale\_x\_discrete(limits = c("Control", "PP", "PLA"))

p3

ggsave("Phylum\_堆积.pdf", p3, width = 5, height = 7, dpi = 300)