library(vegan)

data <- read.csv("./group2.csv",header = T, check.names = F)

data$Treatment%>% as.factor() %>% as.numeric()

data = data.frame(row.names = row.names(map),

species = map$Group %>% as.factor() %>% as.numeric())

data <- data[which(rowSums(data) > 0),]

data <- t(data)

s.dist <- vegdist(data,method = "euclidean")

data1 <- read.csv("./all\_pcoa.csv",row.names = 1)%>%t()

r.dist <- vegdist(data1)

set.seed(520)

mantel(s.dist,r.dist)

mantel(s.dist,r.dist,method = "spearman")

mds.s <- monoMDS(s.dist)

mds.r <- monoMDS(r.dist)

pro.s.r <- procrustes(mds.s,mds.r)

protest(mds.s,mds.r)

library(ggplot2)

Y <- cbind(data.frame(pro.s.r$Yrot), data.frame(pro.s.r$X))

X <- data.frame(pro.s.r$rotation)

Y$ID <- rownames(Y)

p <- ggplot(Y) +

geom\_segment(aes(x = X1, y = X2, xend = (X1 + MDS1)/2, yend = (X2 + MDS2)/2),

arrow = arrow(length = unit(0, 'cm')),

color = "#B2182B", size = 1) +

geom\_segment(aes(x = (X1 + MDS1)/2, y = (X2 + MDS2)/2, xend = MDS1, yend = MDS2),

arrow = arrow(length = unit(0, 'cm')),

color = "#56B4E9", size = 1) +

geom\_point(aes(X1, X2), fill = "#B2182B", size = 4, shape = 21) +

geom\_point(aes(MDS1, MDS2), fill = "#56B4E9", size = 4, shape = 21) +

theme(panel.grid = element\_blank(),

panel.background = element\_rect(color = 'black', fill = 'transparent'),

legend.key = element\_rect(fill = 'transparent'),

axis.ticks.length = unit(0.4,"lines"), axis.ticks = element\_line(color='black'),

axis.line = element\_line(colour = "black"),

axis.title.x=element\_text(colour='black', size=14),

axis.title.y=element\_text(colour='black', size=14),

axis.text=element\_text(colour='black',size=12)) +

labs(x = 'Dimension 1', y = 'Dimension 2', color = '') +

labs(title=" Treatment and mtabolites") +

geom\_vline(xintercept = 0, color = 'gray', linetype = 2, size = 0.3) +

geom\_hline(yintercept = 0, color = 'gray', linetype = 2, size = 0.3) +

geom\_abline(intercept = 0, slope = X[1,2]/X[1,1], size = 0.3) +

geom\_abline(intercept = 0, slope = X[2,2]/X[2,1], size = 0.3) +

annotate('text', label = 'Procrustes analysis:\nM2 = 0.8041, p-value = 0.001',

x = -1.5, y = 1.2, size = 4,hjust = 0) +

theme(plot.title = element\_text(size=16,colour = "black",hjust = 0,face = "bold"))

p

pdf(p,file = "prco.pdf",width = 6,height = 5.4)

dev.off()