title: " microbial data analysis"

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library(vegan)

data("varespec")

df<-varespec

rownames(df)<-paste0("site",1:24)

bray\_dist<-vegdist(df,method = "bray")

library(ape)

df.pcoa<-pcoa(bray\_dist,correction = "cailliez")

df.pcoa$vectors

df.pcoa$values

df.plot<-data.frame(df.pcoa$vectors)

head(df.plot)

library(ggplot2)

x\_label<-round(df.pcoa$values$Rel\_corr\_eig[1]\*100,2)

y\_label<-round(df.pcoa$values$Rel\_corr\_eig[2]\*100,2)

x\_label

y\_label

ggplot(data=df.plot,aes(x=Axis.1,y=Axis.2))+

geom\_point()+

theme\_bw()+

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

geom\_vline(xintercept = 0,lty="dashed")+

geom\_hline(yintercept = 0,lty="dashed")+

labs(x=paste0("PCoA1 ",x\_label,"%"),

y=paste0("PCoA2 ",y\_label,"%"))

df.plot$group<-ifelse(df.plot$Axis.1<0,"AAA","BBB")

ggplot(data=df.plot,aes(x=Axis.1,y=Axis.2,

color=group,shape=group))+

geom\_point(size=5)+

theme\_bw()+

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

geom\_vline(xintercept = 0,lty="dashed")+

geom\_hline(yintercept = 0,lty="dashed")+

labs(x=paste0("PCoA1 ",x\_label,"%"),

y=paste0("PCoA2 ",y\_label,"%"))+

stat\_ellipse(data=df.plot,

geom = "polygon",

aes(fill=group),

alpha=0.3)+

scale\_fill\_manual(values = c("#e31a1c","#1f78b4"))