### During re-run of the tutorial provided on https://benjjneb.github.io/LRASManuscript/LRASms\_fecal.html, I have found one small error in the ordination step. Here, I have used bold font and red font to show the code and there replacement code is shown in green color##############

library(dada2)

library(Biostrings)

library(ShortRead)

library(ggplot2)

library(reshape2)

library(RColorBrewer)

library(gridExtra)

library('phyloseq')

st2 <- readRDS(file.path("/Users/DELL/Desktop/LRASManuscript-master/LRASManuscript-master/RDS/", "Fecal\_st2.rds"))

tax2 <- readRDS(file.path("/Users/DELL/Desktop/LRASManuscript-master/LRASManuscript-master/RDS/", "Fecal\_tax2\_Silva128.rds"))

#Import the metadata for these samples, which is just the #subject and the time ordering of the sample from that subject #(only relevant for the two subjects with multiple samples).

ft2 <- sweep(st2, 1, rowSums(st2), "/")

df <- read.table("/Users/DELL/Desktop/LRASManuscript-master/LRASManuscript-master/Docs/Fecal\_Metadata.csv", header=TRUE, sep="\t", stringsAsFactors=FALSE)

df$SampleID <- gsub("\_", ".", df$X)

df$SampleID <- gsub("^D", "D\_", df$SampleID)

df$SampleID <- gsub("^R", "R\_", df$SampleID)

#Create an ordination.

ps2 <- phyloseq(otu\_table(ft2, taxa\_are\_rows=FALSE), sample\_names(df))

ord2 <- ordinate(ps2, method="MDS", distance="bray")

**#dford2 <- cbind(df, ord2$vectors)**

**#Error in data.frame(..., check.names = FALSE) :**

**# arguments imply differing number of rows: 12, 9**

#dford2 <- cbind(df[c(12, 1, 3, 4, 5, 7, 9, 10 , 11),], ord2$vectors)

dford2 <- cbind(df[match(row.names(ord2$vectors),df$SampleID),], ord2$vectors)

ggplot(data=dford2, aes(x=Axis.1, y=Axis.2, color=Subject)) + geom\_text(aes(label=SampleID))