require("vegan"); library(ggplot2); library(ggpubr); library (readr); library(reshape2); library(car); library (dplyr)

myData <- read.table("PseAbundance.BareSoil.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

myData$Pse <- log10(myData$Pse)

p.PseAb <- **ggplot**(myData, aes(x=Trt, y= Pse, fill=Trt)) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=0, geom="bar")+

**stat\_summary**(fun.data=mean\_se, geom="errorbar", position=position\_dodge(0.70),

width=0.40, linewidth=0.75, colour="black") +

scale\_fill\_manual(values = c("dodgerblue", "darkorange")) +

scale\_y\_continuous (limits=c(0, 10), expand=c(0, 0.0001)) +

labs(x=NULL, y="Pseudomonas sp. (log10 copies g−1 soil)") +

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), axis.title=element\_text(size=12) )

p.PseAb

( p.PseAb.0 <- p.PseAb +coord\_cartesian(ylim = c(6, 8)) )

myData$Bacillus <- log10(myData$Bacillus)

p.BacAb <- **ggplot**(myData, aes(x=Trt, y= Bacillus, fill=Trt)) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=0, geom="bar")+

**stat\_summary**(fun.data=mean\_se, geom="errorbar", position=position\_dodge(0.70),

width=0.40, linewidth=0.75, colour="black") +

scale\_fill\_manual(values = c("dodgerblue", "darkorange")) +

scale\_y\_continuous (limits=c(0, 10), expand=c(0, 0.0001)) +

labs(x=NULL, y="Bacillus sp. (log10 copies g−1 soil)") +

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), axis.title=element\_text(size=12) )

p.BacAb

( p.BacAb.0 <- p.BacAb +coord\_cartesian(ylim = c(6, 8)) )

p.Biomass <- **ggplot**(myData, aes(x=Trt, y= Biomass, fill=Trt)) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=0, geom="bar")+

**stat\_summary**(fun.data=mean\_se, geom="errorbar", position=position\_dodge(0.70),

width=0.40, linewidth=0.75, colour="black") +

scale\_fill\_manual(values = c("dodgerblue", "darkorange")) +

scale\_y\_continuous (limits=c(0, 4.5), expand=c(0, 0.0001))+

labs(x=NULL, y="Plant dry biomass (g/plant)")+theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), axis.title=element\_text(size=12) )

p.Biomass

**stats::t.test**(myData $ Pse ~ myData $Trt, p.adj="BH", var.equal=F) #Welch’s T test

**stats::t.test**(myData $ Bacillus ~ myData $Trt, p.adj="BH", var.equal=F) #Welch’s T test

**stats::t.test**(myData $ Biomass ~ myData $Trt, p.adj="BH", var.equal=F) #Welch’s T test

**ggarrange**(p.PseAb.0, p.BacAb.0, p.Biomass, ncol=3, nrow=1, align="hv", legend="none" )