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

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

pGrowth33 <- **ggplot**(Data, aes(x= **factor**(Compounds, levels=c('Control', 'Glutaricacid', 'Malicacid', 'Fructose', 'Riboflavin', 'Rutin', 'Hydroxyacetophenone', 'Fumaricacid', 'Lysine', 'Phenylalanine', 'Glutamine')), y= Biomass33 )) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, geom="bar", fill="grey50") +

**stat\_summary**(fun.data = mean\_se, geom="errorbar", width=0.40, linewidth =0.75, colour="black") +

scale\_y\_continuous (limits=c(0, 2), expand=c(0, 0.0001) ) + # , breaks=seq(0, 9, 2)

labs(x=NULL, y="Bacteria growth (OD600)")+

theme\_bw() +

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

axis.text.x = element\_text(angle = 90, hjust = 1, vjust = 0.5) )

pGrowth33

library(car); library(lsmeans); library(multcomp)

mydata <- Data

model<-lm(Biomass33 ~ Compounds, data= mydata); #summary(model);

Anova(model, type="II")

marginal=lsmeans(model, ~ Compounds); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

pGrowth57 <- **ggplot**(Data, aes(x= **factor**(Compounds, levels=c('Control', 'Glutaricacid', 'Malicacid', 'Fructose', 'Riboflavin', 'Rutin', 'Hydroxyacetophenone', 'Fumaricacid', 'Lysine', 'Phenylalanine', 'Glutamine')), y= Biomass57 )) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, geom="bar", fill="grey50") +

**stat\_summary**(fun.data = mean\_se, geom="errorbar", width=0.40, linewidth =0.75, colour="black") +

scale\_y\_continuous (limits=c(0, 2), expand=c(0, 0.0001) ) + # , breaks=seq(0, 9, 2)

labs(x=NULL, y="Bacteria growth (OD600)")+

theme\_bw() +

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

axis.text.x = element\_text(angle = 90, hjust = 1, vjust = 0.5) )

pGrowth57

library(car); library(lsmeans); library(multcomp)

mydata <- Data

model<-lm(Biomass57 ~ Compounds, data= mydata); #summary(model);

Anova(model, type="II")

marginal=lsmeans(model, ~ Compounds); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

############################################################################

pBiofilm33 <- **ggplot**(Data, aes(x= **factor**(Compounds, levels=c('Control', 'Glutaricacid', 'Malicacid', 'Fructose', 'Riboflavin', 'Rutin', 'Hydroxyacetophenone', 'Fumaricacid', 'Lysine', 'Phenylalanine', 'Glutamine')), y= Biofilm33 )) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, geom="bar", fill="grey50") +

**stat\_summary**(fun.data = mean\_se, geom="errorbar", width=0.40, linewidth =0.75, colour="black") +

scale\_y\_continuous (limits=c(0, 1.8), expand=c(0, 0.0001) ) + # , breaks=seq(0, 9, 2)

labs(x=NULL, y="Biofilm formation (OD600)")+

theme\_bw() +

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

axis.text.x = element\_text(angle = 90, hjust = 1, vjust = 0.5) )

pBiofilm33

library(car); library(lsmeans); library(multcomp)

mydata <- Data

model<-lm(Biofilm33 ~ Compounds, data= mydata); #summary(model);

Anova(model, type="II")

marginal=lsmeans(model, ~ Compounds); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

pBiofilm57 <- **ggplot**(Data, aes(x= **factor**(Compounds, levels=c('Control', 'Glutaricacid', 'Malicacid', 'Fructose', 'Riboflavin', 'Rutin', 'Hydroxyacetophenone', 'Fumaricacid', 'Lysine', 'Phenylalanine', 'Glutamine')), y= Biofilm57)) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, geom="bar", fill="grey50") +

**stat\_summary**(fun.data = mean\_se, geom="errorbar", width=0.40, linewidth =0.75, colour="black") +

scale\_y\_continuous (limits=c(0, 1.8), expand=c(0, 0.0001) ) + # , breaks=seq(0, 9, 2)

labs(x=NULL, y="Biofilm formation (OD600)")+

theme\_bw() +

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

axis.text.x = element\_text(angle = 90, hjust = 1, vjust = 0.5) )

pBiofilm57

library(car); library(lsmeans); library(multcomp)

mydata <- Data

model<-lm(Biofilm57 ~ Compounds, data= mydata); #summary(model);

Anova(model, type="II")

marginal=lsmeans(model, ~ Compounds); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

( pGrowth33.0 <- pGrowth33 +coord\_cartesian(ylim = c(0.80, 2.2)) )

( pGrowth57.0 <- pGrowth57 +coord\_cartesian(ylim = c(0.60, 1.87)) )

**ggarrange**(pGrowth33.0, pGrowth57.0, ncol=2, nrow=1, align="hv", legend="none" )

( pBiofilm33.0 <- pBiofilm33 +coord\_cartesian(ylim = c(0.6, 1.8)) )

( pBiofilm57.0 <- pBiofilm57 +coord\_cartesian(ylim = c(0.4, 1.65)) )