###Plotting data of the root colonization of each bacterial strain as affected by FOL####

**###########Inoculated individually##########**

library(ggplot2); library(ggpubr)

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

Recruit$CFU <- log10(Recruit$CFU)

pRecruit.split <- **ggplot**(Recruit, aes(x= Cultivar, y= CFU, fill = **factor**(Trt, levels= c('CK', 'FOL') ) )) + #

**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") +

facet\_wrap ( .~ **factor**(Strain, levels=c('Fl79', 'Ar03', 'St81', 'Ly56', 'Sb87', 'Sm12')), scales = "free", nrow =1) +

labs(x=NULL, y="Abundance (log10 copies/g soil)")+

theme\_bw() +

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

legend.position="none",

axis.title=element\_text(size=12) )

pRecruit.split

(pRecruit.split.0 <- pRecruit.split +coord\_cartesian(ylim = c(5.5, 7.5)) )

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

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

mydata <- Recruit

mydata.1 <- **filter**(Recruit, Strain == "Fl79")

model<-lm(CFU ~ Trt.Cul, data= mydata.1); #summary(model); # Anova(model, type="II")

marginal=lsmeans(model, ~ Trt.Cul); #pairs(marginal, adjust="fdr")

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

**##################Syn community#####################**

Recruit$Syn <- log10(Recruit$Syn)

pSyn.split <- **ggplot**(Recruit, aes(x= **factor** (Strain, levels= c('Fl79', 'Ar03', 'St81', 'Ly56', 'Sb87', 'Sm12')), y= Syn, fill = **factor**(Trt.Cul, levels= c('CK.D72', 'FOL.D72', 'CK.Z19', 'FOL.Z19') ) )) + #

**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") +

labs(x=NULL, y="Abundance (log10 copies/g soil)")+

theme\_bw() +

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

legend.position="none",

axis.title=element\_text(size=12) )

pSyn.split

(pSyn.split.0 <- pSyn.split +coord\_cartesian(ylim = c(5.5, 7.5)) )

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

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

mydata <- Recruit

mydata.1 <- **filter**(Recruit, Strain == "Fl79")

model<-lm(Syn ~ Trt.Cul, data= mydata.1); #summary(model); # Anova(model, type="II")

marginal=lsmeans(model, ~ Trt.Cul); #pairs(marginal, adjust="fdr")

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