**“Glmer\_Richness\_Greenhouse”**

library(lme4)

library(lsmeans)

library(MuMIn)

library(ggplot2)

library(multcomp)

#####Input data ###

data=read.table("greenhouse condition\_data.txt",header=T,sep="\t")

LOGP=log(data$weight)

Animal=data$Animal

site=data$Site

Season=data$Season

rep=data$Site.name

################################# FUL MODLE ###############################

m.nb3 <- glmer(Frequency ~ Animal\*site+Animal\*Season+(1|rep), family = poisson, na.action = na.fail, data=data)

################################# Model validation ###############################

E2 <- resid(m.nb3 , type = "pearson")

N <- nrow(data)

p1 <- length(coef(m.nb3))

sum(E2^2) / (N - p1)

################################# Model selection ###############################

options(na.action = "na.fail")

dreABUN <- dredge(m.nb3)

dreABUN

################################### BEST MODEL#############################

m.nb4 <- glmer(Frequency ~ Animal+(1|rep), family = poisson, na.action = na.fail, data=data)

summary(m.nb4)

################################### Model validation ##########################

E2 <- resid(m.nb4 , type = "pearson")

N <- nrow(data)

p1 <- length(coef(m.nb4))

sum(E2^2) / (N - p1)

################################ Tukey-adjusted comparisons#####################

GN1LSPAIR1=lsmeans(m.nb4,pairwise~Animal,type="response",adjust="tukey")

cold= summary(GN1LSPAIR1$lsmean)

###############################Significant letters###############################

marginal = lsmeans(m.nb4,

~ Animal,type="response",adjust="tukey")

CLD1 = cld(marginal,

alpha=0.05,

Letters=letters)

################################## Plot #######################################

### Order the levels for printing ###

CLD1$Animal = factor(CLD1$Animal,

levels=c("Red deer", "Roe deer", "Wild boar", "Brown bear"))

ggplot(CLD1,

aes(x = Animal,

y = rate,

label = .group)) +

coord\_cartesian(ylim = c(0,3))+

geom\_point(shape = 15,

size = 3) +

geom\_errorbar(aes(ymin = asymp.LCL,

ymax = asymp.UCL),

width = 0.2,

size = 0.7) +

theme\_bw() +

theme(axis.title = element\_text(face = "bold"),

axis.text = element\_text(face = "bold"),

plot.caption = element\_text(hjust = 0)) +

ylab("Least square mean") +

ggtitle ("Species richness per animal faeces")+

geom\_text(nudge\_x = c(0, 0, 0, 0),

nudge\_y = c(1, 1, 1, 1),

color = "red")

**“Glmer.nb \_Abundance\_Greenhouse”**

library(lme4)

library(lsmeans)

library(MuMIn)

library(ggplot2)

library(multcomp)

#####Input data #####

data=read.table("natural condition\_data.txt",header=T,sep="\t")

LOGP=log(data$weight)

Animal=data$Animal

site=data$Site

Season=data$Season

rep=data$Site.name

################################# FUL MODLE ###############################

m.nb1 <- glmer.nb(abundance ~Animal\*site+Animal\*Season+(1|rep), offset=LOGP, data=data)

summary(m.nb1)

################################# Model selection ###############################

options(na.action = "na.fail")

dreABUN <- dredge(m.nb1)

dreABUN

################################### BEST MODEL#############################

m.nb2 <- glmer.nb(abundance ~ Animal\*Season+(1|rep), offset=LOGP, data=data)

summary(m.nb2)

################################ Tukey-adjusted comparisons#####################

GN1LSPAIR1=lsmeans(m.nb2,pairwise~Animal\*Season, type="response",adjust="tukey")

###############################Significant letters###############################

CLD1= summary(GN1LSPAIR1$lsmean)

################################## Plot #######################################

### Order the levels for printing###

CLD1$Season = factor(CLD1$Season,

levels=c("Spring", "Summer","Fall"))

CLD1$Animal = factor(CLD1$Animal,

levels=c("Red deer", "Roe deer", "Wild boar", " Brown bear"))

pd = position\_dodge(0.5)

ggplot(CLD1,

aes(x = Season,

y = response,

color = Animal)) +

coord\_cartesian(ylim = c(0,2))+

geom\_point(shape = 15,

size = 5,

position = pd) +

geom\_errorbar(aes(ymin = asymp.LCL,

ymax = asymp.UCL),

width = 0.2,

size = 0.7,

position = pd) +

theme\_bw() +

theme(axis.title = element\_text(face = "bold"),

axis.text = element\_text(face = "bold"),

plot.caption = element\_text(hjust = 0)) +

ylab("Least square mean") +

ggtitle ("Seedling abundance per gram of each animal faeces",

subtitle = "In three seasons") +

scale\_color\_manual(values = c("blue", "red", "green", "black"))

**“GLMER\_Natural vs Greenhouse”**

library(lme4)

library(lsmeans)

library(MuMIn)

library(ggplot2)

#####Input data ###

data=read.table("total data set.txt",header=T,sep="\t")

Animal=data$Animal

condition=data$Germination.condition

rep=data$dung.number

#Seedling abundance

################################# FUL MODLE ###############################

m.nb1 <- glmer(Abundance~Animal\*condition+(1|rep), family = poisson, na.action = na.fail, data=data)

################################# Model validation ###############################

E2 <- resid(m.nb1 , type = "pearson")

N <- nrow(data)

p1 <- length(coef(m.nb1))

sum(E2^2) / (N - p1)

################################# Model selection ###############################

options(na.action = "na.fail")

dreABUN <- dredge(m.nb1)

dreABUN

################################ Tukey-adjusted comparisons#####################

GN1LSPAIR1=lsmeans(m.nb1,pairwise~Animal\*condition,type="response",adjust="tukey")

#Species richness

################################# FUL MODLE ###############################

m.nb2 <- glmer(Frequency~Animal\*condition+(1|rep), family = poisson, na.action = na.fail, data=data)

summary(m.nb2)

################################# Model validation ###############################

E2 <- resid(m.nb2 , type = "pearson")

N <- nrow(data)

p1 <- length(coef(m.nb2))

sum(E2^2) / (N - p1)

################################# Model selection ###############################

options(na.action = "na.fail")

dreABUN <- dredge(m.nb2)

dreABUN

################################ Tukey-adjusted comparisons#####################

GN1LSPAIR1=lsmeans(m.nb2,pairwise~Animal\*condition,type="response",adjust="tukey")

**“Species accumulation curves”**

library(vegan)

################################## Greenhouse##################################

brown=read.table("BBg.txt",header=T,sep="\t")

roe=read.table("ROEg.txt",header=T,sep="\t")

red=read.table("REDg.txt",header=T,sep="\t")

sus=read.table("WBg.txt",header=T,sep="\t")

specpool(brown)

specpool(roe)

specpool(red)

specpool(sus)

redc=specaccum(red,method="random",gamma="chao")

roec=specaccum(roe,method="random",gamma="chao")

susc=specaccum(sus,method="random",gamma="chao")

brownc=specaccum(brown,method="random",gamma="chao")

################################## Natural##################################

brownn=read.table("BBn.txt",header=T,sep="\t")

roen=read.table("ROEn.txt",header=T,sep="\t")

redn=read.table("REDn.txt",header=T,sep="\t")

susn=read.table("WBn.txt",header=T,sep="\t")

specpool(brownn)

specpool(roen)

specpool(redn)

specpool(susn)

redcn=specaccum(redn,method="random",gamma="chao")

roecn=specaccum(roen,method="random",gamma="chao")

suscn=specaccum(susn,method="random",gamma="chao")

browncn=specaccum(brownn,method="random",gamma="chao")

###############################Species accumulation curves Herbivores##################

par(mfrow=c(1,1))

plot(redc,ci.type="line",col="red",lwd=2,ci.lty=1,ci.col="red",

xlim=c(0,182),ylim=c(0,79),las=1,

xlab="Sampling effort (number of faeces)",ylab="Number of species",main="Herbivores")

legend("topleft",legend=c("Red deer (G)","Red deer (N)","Roe deer (G)","Roe deer (N)"),col=c("red","violetred1","slateblue1","deepskyblue"),lwd=2,bty="n",xjust=0)

plot(redcn,ci.type="line",col="violetred1",lwd=2,ci.lty=1,ci.col="violetred1",

xlim=c(0,182),ylim=c(0,25),las=1,

xlab="",ylab="",xaxt="n",yaxt="n",add=T)

plot(roec,ci.type="line",col="slateblue1",lwd=2,ci.lty=1,ci.col="slateblue1",

xlim=c(0,50),ylim=c(0,6),las=1,

xlab="",ylab="",xaxt="n",yaxt="n",add=T)

plot(roecn,ci.type="line",col="deepskyblue",lwd=2,ci.lty=1,ci.col="deepskyblue",

xlim=c(0,50),ylim=c(0,6),las=1,

xlab="",ylab="",xaxt="n",yaxt="n",add=T)

###########################Species accumulation curves omnivores#######################

par(mfrow=c(1,1))

plot(susc,ci.type="line",col="chartreuse4",lwd=2,ci.lty=1,ci.col="chartreuse4",

xlim=c(0,182),ylim=c(0,80),las=1,

xlab="Sampling effort (number of faeces)",ylab="Number of species",main="Omnivores")

legend("topleft",legend=c("Wild boar (G)","Wild boar (N)","Brown bear (G)", "Brown bear (N)"),col=c("chartreuse4", "chartreuse","deeppink4","deeppink"),lwd=2,bty="n",xjust=0)

plot(brownc, ci.type="line",col="deeppink4",lwd=2,ci.lty=1,ci.col="deeppink4",

xlim=c(0,64),ylim=c(0,33),las=1,

xlab="",ylab="",xaxt="n",yaxt="n",add=T)

plot(suscn, ci.type="line",col="chartreuse",lwd=2,ci.lty=1,ci.col="chartreuse",

xlim=c(0,149),ylim=c(0,22),las=1,

xlab="",ylab="",xaxt="n",yaxt="n",add=T)

plot(browncn, ci.type="line",col="deeppink",lwd=2,ci.lty=1,ci.col="deeppink",

xlim=c(0,64),ylim=c(0,16),las=1,

xlab="",ylab="",xaxt="n",yaxt="n",add=T)

**“CCA NG”**

library(vegan)

species=read.table("CCA data.txt",header=T,sep="\t")

factor=read.table("CCA code.txt",header=T,sep="\t")

sqrtspecies = sqrt(species)

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

#NG

mod <- cca (sqrtspecies ~ animalcondition, data= factor)

summary(mod)

anova(mod, by="term")

ord.fit <- envfit(sqrtspecies ~ animalcondition,data=factor, perm=999) #mont carlo

## species priority; which species drawn last, i.e. on top##

priSpp <- diversity(sqrtspecies, index = "invsimpson", MARGIN = 2)

## sample priority##

priSite <- diversity(sqrtspecies, index = "invsimpson", MARGIN = 1)

## scaling to use##

scl <- 1

## Species scores##

plot(mod, type = "n", scaling = -1, xlim = c(0,4), ylim = c(-3.5,2),cex.axis=0.8,cex.lab = 0.8)

orditorp(mod, display = "species", priority = priSpp, scaling = -1,

col = "blue", pch = NA, cex = 0.7)

with(factor, ordiellipse (mod,animalcondition,scaling = -1, kind = "se", conf = 0.95, col = "NA", lwd=1.9,

label = T, cex=0.9,pos=4))

## site/sample scores##

plot(mod, type = "n", scaling = -1, cex = 1)

orditorp(mod, display = "sites", priority = priSite, scaling = -1,

col = "forestgreen", cex = 1, pch = 2)

**“Anosim“**

#NG

#BROWN BEAR G & N

BBGN=read.table("BBGN.txt",header=T,sep="\t")

BBGNCOD=read.table("BBGN code.txt",header=T,sep="\t")

dune.dist <- vegdist(BBGN)

dune.ano1 <- anosim(dune.dist, BBGNCOD$animalcondition)

summary(dune.ano1)

#RED DEER G & N

RDGN=read.table("RDGN.txt",header=T,sep="\t")

RDGNCOD=read.table("RDGN code.txt",header=T,sep="\t")

dune.dist <- vegdist(RDGN)

dune.ano2 <- anosim(dune.dist, RDGNCOD$animalcondition)

summary(dune.ano2)

#ROE DEER G & N

ROGN=read.table("ROGN.txt",header=T,sep="\t")

ROGNCOD=read.table("ROGN code.txt",header=T,sep="\t")

dune.dist <- vegdist(ROGN)

dune.ano3 <- anosim(dune.dist, ROGNCOD$animalcondition)

summary(dune.ano3)

#WILD BOAR G & N

WBGN=read.table("WBGN.txt",header=T,sep="\t")

WBGNCOD=read.table("WBGN code.txt",header=T,sep="\t")

dune.dist <- vegdist(WBGN)

dune.ano4 <- anosim(dune.dist, WBGNCOD$animalcondition)

summary(dune.ano4)

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

#Anosim # N

#BROWN BEAR & ROE DEER

BBRO=read.table("BBRO.txt",header=T,sep="\t")

BBROCOD=read.table("BBROCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(BBRO)

dune.ano1 <- anosim(dune.dist, BBROCOD$animal)

summary(dune.ano1)

#BROWN BEAR & RED DEER

BBRD=read.table("BBRD.txt",header=T,sep="\t")

BBRDCOD=read.table("BBRDCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(BBRD)

dune.ano2 <- anosim(dune.dist, BBRDCOD$animal)

summary(dune.ano2)

#BROWN BEAR & WILD BOAR

BBWB=read.table("BBWB.txt",header=T,sep="\t")

BBWBCOD=read.table("BBWBCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(BBWB)

dune.ano3 <- anosim(dune.dist, BBWBCOD$animal)

summary(dune.ano3)

#RED DEER & ROE DEER

RDRO=read.table("RDRO.txt",header=T,sep="\t")

RDROCOD=read.table("RDROCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(RDRO)

dune.ano4 <- anosim(dune.dist, RDROCOD$animal)

summary(dune.ano4)

#WILD BOAR & RED DEER

WBRD=read.table("WBRD.txt",header=T,sep="\t")

WBRDCOD=read.table("WBRDCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(WBRD)

dune.ano9 <- anosim(dune.dist, WBRDCOD$animal)

summary(dune.ano9)

#WILD BOAR & ROE DEER

WBRO=read.table("WBRO.txt",header=T,sep="\t")

WBROCOD=read.table("WBROCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(WBRO)

dune.ano5 <- anosim(dune.dist, WBROCOD$animal)

summary(dune.ano5)

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

#Anosim # G

#BROWN BEAR & ROE DEER

BBRO=read.table("BBRO.txt",header=T,sep="\t")

BBROCOD=read.table("BBROCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(BBRO)

dune.ano1 <- anosim(dune.dist, BBROCOD$animal)

summary(dune.ano1)

#BROWN BEAR & RED DEER

BBRD=read.table("BBRD.txt",header=T,sep="\t")

BBRDCOD=read.table("BBRDCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(BBRD)

dune.ano2 <- anosim(dune.dist, BBRDCOD$animal)

summary(dune.ano2)

#BROWN BEAR & WILD BOAR

BBWB=read.table("BBWB.txt",header=T,sep="\t")

BBWBCOD=read.table("BBWBCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(BBWB)

dune.ano3 <- anosim(dune.dist, BBWBCOD$animal)

summary(dune.ano3)

#RED DEER & ROE DEER

RDRO=read.table("RORD.txt",header=T,sep="\t")

RDROCOD=read.table("RORDCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(RDRO)

dune.ano4 <- anosim(dune.dist, RDROCOD$animal)

summary(dune.ano4)

#WILD BOAR & RED DEER

RDWB=read.table("WBRD.txt",header=T,sep="\t")

RDWBCOD=read.table("WBRDCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(RDWB)

dune.ano5 <- anosim(dune.dist, RDWBCOD$animal)

summary(dune.ano5)

#WILD BOAR & ROE DEER

ROWB=read.table("WBRO.txt",header=T,sep="\t")

ROWBCOD=read.table("WBROCOD.txt",header=T,sep="\t")

dune.dist <- vegdist(ROWB)

dune.ano5 <- anosim(dune.dist, ROWBCOD$animal)

summary(dune.ano5)