

```
### PING small mammals - statistical analyses
```

```
#####  
#####  
##### STATS correlations between the concentrations of the 3 compounds #  
#####  
library(pgirmess)  
##### Load datas: #####
```

```
TAB<-read.delim2("PING_micromam_Final Results GLY-AMPA-  
GLUF_ALL_update.txt")  
summary(TAB)
```

```
TAB$Species_Check<-as.factor(TAB$Species_Check)  
TAB$Habitat<-as.factor(TAB$Habitat)  
TAB$T_NT<-as.factor(TAB$T_NT)  
TAB$Farming<-as.factor(TAB$Farming)  
TAB$Context<-as.factor(TAB$Context)
```

```
summary(TAB)
```

```
###----- Correlation test non paramétriques entre chaque molécule dans  
les poils -----
```

```
cor.test(TAB$GLY,TAB$AMPA, method=c("spearman"))  
cor.test(TAB$GLY,TAB$GLUF, method=c("spearman"))  
cor.test(TAB$AMPA,TAB$GLUF, method=c("spearman"))
```

```
plot(TAB$GLY,TAB$AMPA,log="xy")  
plot(TAB$GLY,TAB$GLUF,log="xy")  
plot(TAB$AMPA,TAB$GLUF,log="xy")
```

```
summary(TAB$GLY)  
summary(TAB$AMPA)  
summary(TAB$GLUF)
```

```
plot(TAB$GLY+1,TAB$AMPA+1,xaxt="n",yaxt="n",log="xy",ylim=c(1,55),xlim=c(  
1,550))  
xtick<-c(1,2,5,10,100,500,1000)  
axis(side=1, at=xtick, labels = TRUE)  
ytick<-c(1,2,5,10,20,50)  
axis(side=2, at=ytick, labels = TRUE)
```

```
plot(TAB$GLY+1,TAB$GLUF+1,xaxt="n",yaxt="n",log="xy",ylim=c(1,55),xlim=c(  
1,550))  
xtick<-c(1,2,5,10,100,500,1000)  
axis(side=1, at=xtick, labels = TRUE)  
ytick<-c(1,2,5,10,20,50)  
axis(side=2, at=ytick, labels = TRUE)
```

```
plot(TAB$GLUF+1,TAB$AMPA+1,xaxt="n",yaxt="n",log="xy",ylim=c(1,55),xlim=c(  
1,55))  
xtick<-c(1,2,5,10,20,50)  
axis(side=1, at=xtick, labels = TRUE)  
ytick<-c(1,2,5,10,20,50)  
axis(side=2, at=ytick, labels = TRUE)
```

```
#### ----- GLMs Correlation lm entre chaque molécule dans les poils
en fonction espèce -----
```

```
#Attention pb leverage cause pt numéro 20 (outlier Miar)
TAB2<-TAB[-20,]
summary(TAB2)
```

```
lmGLYAMPFull<-lm(log(TAB$AMPA+1)~TAB$Species_Check*log(TAB$GLY+1))
par(mfrow=c(2,2))
plot(lmGLYAMPFull)
```

```
# --> Modèle impliquant GLY sans outlier pour outputs et predict,
# average predict since slopes did not significantly differ
```

```
lmGLYAMPFull<-lm(log(TAB2$AMPA+1)~TAB2$Species_Check*log(TAB2$GLY+1))
summary(lmGLYAMPFull)
anova(lmGLYAMPFull) ### interaction ns différences pentes ns
par(mfrow=c(2,2))
plot(lmGLYAMPFull)
```

```
lmGLYAMPFullSP<-lm(log(TAB2$AMPA+1)~TAB2$Species_Check+log(TAB2$GLY+1))
summary(lmGLYAMPFullSP)
anova(lmGLYAMPFullSP) ### signif
# Multiple R-squared: 0.5712, Adjusted R-squared: 0.5315
20.8948/(20.8948+8.1259+21.7815)
# R2 Species 0.4112971
8.1259/(20.8948+8.1259+21.7815)
# R2 GLY 0.1599517
lmGLYAMPFullseul<-lm(log(TAB2$AMPA+1)~log(TAB2$GLY+1))
summary(lmGLYAMPFullseul)
```

```
lmAMPAGLUFfull<-lm(log(TAB$AMPA+1)~TAB$Species_Check*log(TAB$GLUF+1))
summary(lmAMPAGLUFfull)
anova(lmAMPAGLUFfull) ### interaction p=0.053 différences pentes presque
signif
# Multiple R-squared: 0.7347, Adjusted R-squared: 0.6879
21.202/(21.202+13.687+2.670+13.560)
# R2 Species 0.4147
13.687/(21.202+13.687+2.670+13.560)
# R2 GLUF 0.2677
2.670/(21.202+13.687+2.670+13.560)
# R2 interaction 0.052
```

```
lmGLYGLUFfull<-lm(log(GLUF+1)~Species_Check*log(GLY+1),data=TAB2)
summary(lmGLYGLUFfull)
anova(lmGLYGLUFfull) ### interaction p=0.027 différences pentes signif
que avec outlier!!!
### sans outlier
# Multiple R-squared: 0.6818, Adjusted R-squared: 0.6245
20.6727/(20.6727+13.8262+1.1539+16.6411)
# R2 Species 0.395
13.8262/(20.6727+13.8262+1.1539+16.6411)
# R2 GLY 0.264
```

```
lmGLYGLUF<-lm(log(GLUF+1)~log(GLY+1),data=TAB2)
```

```

summary(lmGLYGLUF)

TAB3<-TAB
TAB3$Species_Check <- relevel(TAB$Species_Check, "Mumu")
lmGLYGLUFfull3<-lm(log(GLUF+1)~Species_Check*log(GLY+1),data=TAB3)
summary(lmGLYGLUFfull3)

TAB4<-TAB
TAB4$Species_Check <- relevel(TAB$Species_Check, "Crru")
lmGLYGLUFfull4<-lm(log(GLUF+1)~Species_Check*log(GLY+1),data=TAB4)
summary(lmGLYGLUFfull4)

###----- Graphiques predict -----
summary(TAB2$GLY)
summary(TAB$AMPA)
summary(TAB$GLUF)
CGLY<-seq(0,15,length.out=2000)
CAMPAC<-seq(0,35,length.out=2000)
CGLUF<-seq(0,30,length.out=2000)
ndAll<-data.frame(GLY=CGLY,AMPA=CAMPAC,GLUF=CGLUF)

summary(TAB$GLY[TAB$Species_Check=="Apsy"])
summary(TAB$AMPA[TAB$Species_Check=="Apsy"])
summary(TAB$GLUF[TAB$Species_Check=="Apsy"])
CGLYApsy<-seq(0,6,length.out=2000)
CAMPAApsy<-seq(0,2.5,length.out=2000)
CGLUFApsy<-seq(0,30,length.out=2000)
SpApsy<-rep("Apsy",length.out=2000)
ndApsy<-
data.frame(GLY=CGLYApsy,AMPA=CAMPAApsy,GLUF=CGLUFApsy,Species_Check=SpApsy)

summary(TAB$GLY[TAB$Species_Check=="Crru"])
summary(TAB$AMPA[TAB$Species_Check=="Crru"])
summary(TAB$GLUF[TAB$Species_Check=="Crru"])
CGLYCrru<-seq(0,1.5,length.out=2000)
CAMPACrru<-seq(0,1.5,length.out=2000)
CGLUFCrru<-seq(0,1.5,length.out=2000)
SpCrru<-rep("Crru",length.out=2000)
ndCrru<-
data.frame(GLY=CGLYCrru,AMPA=CAMPACrru,GLUF=CGLUFCrru,Species_Check=SpCrru)

summary(TAB2$GLY[TAB2$Species_Check=="Miar"])
summary(TAB$AMPA[TAB$Species_Check=="Miar"])
summary(TAB$GLUF[TAB$Species_Check=="Miar"])
CGLYMiar<-seq(0,15,length.out=2000)
CAMPAMiar<-seq(0,20,length.out=2000)
CGLUFMiar<-seq(0,25,length.out=2000)
SpMiar<-rep("Miar",length.out=2000)
ndMiar<-
data.frame(GLY=CGLYMiar,AMPA=CAMPAMiar,GLUF=CGLUFMiar,Species_Check=SpMiar)

```

```

summary(TAB$GLY[TAB$Species_Check=="Mumu"])
summary(TAB$AMPA[TAB$Species_Check=="Mumu"])
summary(TAB$GLUF[TAB$Species_Check=="Mumu"])
CGLYMumu<-seq(0,4,length.out=2000)
CAMPAMumu<-seq(0,1.5,length.out=2000)
CGLUFMumu<-seq(0,10,length.out=2000)
SpMumu<-rep("Mumu",length.out=2000)
SpMumu<-rep("Mumu",length.out=20)
ndMumu<-
data.frame(GLY=CGLYMumu,AMPA=CAMPAMumu,GLUF=CGLUFMumu,Species_Check=SpMumu)

```

```

summary(TAB$GLY[TAB$Species_Check=="Mygl"])
summary(TAB$AMPA[TAB$Species_Check=="Mygl"])
summary(TAB$GLUF[TAB$Species_Check=="Mygl"])
CGLYMygl<-seq(0,8,length.out=2000)
CAMPAMygl<-seq(0,35,length.out=2000)
CGLUFMygl<-seq(0,15,length.out=2000)
SpMygl<-rep("Mygl",length.out=2000)
SpMygl<-rep("Mygl",length.out=2000)
ndMygl<-
data.frame(GLY=CGLYMygl,AMPA=CAMPAMygl,GLUF=CGLUFMygl,Species_Check=SpMygl)

```

```

lmGLYAMPA<-lm(log(AMPA+1)~log(GLY+1),data=TAB2)
lmAMPAGLUFfull<-lm(log(AMPA+1)~Species_Check*log(GLUF+1),data=TAB)
lmGLYGLUF<-lm(log(GLUF+1)~log(GLY+1),data=TAB2)

```

```

GA.pr<-predict(lmGLYAMPA,newdata=ndAll,se=TRUE,type="response")

```

```

AGF.Apsy.pr<-
predict(lmAMPAGLUFfull,newdata=ndApsy,se=FALSE,type="response")
AGF.Crru.pr<-
predict(lmAMPAGLUFfull,newdata=ndCrru,se=FALSE,type="response")
AGF.Miar.pr<-
predict(lmAMPAGLUFfull,newdata=ndMiar,se=FALSE,type="response")
AGF.Mumu.pr<-
predict(lmAMPAGLUFfull,newdata=ndMumu,se=FALSE,type="response")
AGF.Mygl.pr<-
predict(lmAMPAGLUFfull,newdata=ndMygl,se=FALSE,type="response")

```

```

GFG.pr<-predict(lmGLYGLUF,newdata=ndAll,se=TRUE,type="response")

```

```

GFG.Apsy.pr<-
predict(lmGLYGLUFfull,newdata=ndApsy,se=FALSE,type="response")
GFG.Crru.pr<-
predict(lmGLYGLUFfull,newdata=ndCrru,se=FALSE,type="response")
GFG.Miar.pr<-
predict(lmGLYGLUFfull,newdata=ndMiar,se=FALSE,type="response")
GFG.Mumu.pr<-
predict(lmGLYGLUFfull,newdata=ndMumu,se=FALSE,type="response")
GFG.Mygl.pr<-
predict(lmGLYGLUFfull,newdata=ndMygl,se=FALSE,type="response")

```

```

### AMPA GLY

```

```
plot(log(AMPA+1)~log(GLY+1),type="n",main="AMPA/GLY",ylab="log [AMPA]
+1",xlab="log [GLYPHOSATE]
+1",cex.axis=1.5,ylim=c(0,4),xlim=c(0,4),data=TAB)
```

```
points(log(TAB$GLY[TAB$Species_Check=="Crru"]+1),log(TAB$AMPA[TAB$Species
_Check=="Crru"]+1),pch=16,cex=1,col="grey50")
points(log(TAB$GLY[TAB$Species_Check=="Miar"]+1),log(TAB$AMPA[TAB$Species
_Check=="Miar"]+1),pch=16,cex=1,col="orange")
points(log(TAB$GLY[TAB$Species_Check=="Mumu"]+1),log(TAB$AMPA[TAB$Species
_Check=="Mumu"]+1),pch=16,cex=1,col="lightblue")
points(log(TAB$GLY[TAB$Species_Check=="Mygl"]+1),log(TAB$AMPA[TAB$Species
_Check=="Mygl"]+1),pch=1,cex=1,col="red4")
points(log(TAB$GLY[TAB$Species_Check=="Apsy"]+1),log(TAB$AMPA[TAB$Species
_Check=="Apsy"]+1),pch=1,cex=1,col="black")
```

```
lines(log(CGLY+1),GA.pr$fit,lwd=2,col="black")
lines(log(CGLY+1),GA.pr$fit+1.96*GA.pr$se.fit,lty=3,lwd=1)
lines(log(CGLY+1),GA.pr$fit-1.96*GA.pr$se.fit,lty=3,lwd=1)
```

```
legend(3.5,4,c("Apsy","Crru","Miar","Mumu","Mygl"),col=c("grey2","grey50"
,"orange","lightblue","red4"),pch=c(1,16,16,16,1),title="SPECIES",
cex=0.8)
```

```
### AMPA GLUF
```

```
plot(log(AMPA+1)~log(GLUF+1),type="n",main="AMPA/GLUF",ylab="log [AMPA]
+1",xlab="log [GLUFOSINATE]
+1",cex.axis=1.5,ylim=c(0,4),xlim=c(0,4),data=TAB)
```

```
points(log(TAB$GLUF[TAB$Species_Check=="Crru"]+1),log(TAB$AMPA[TAB$Specie
s_Check=="Crru"]+1),pch=16,cex=1,col="grey50")
points(log(TAB$GLUF[TAB$Species_Check=="Miar"]+1),log(TAB$AMPA[TAB$Specie
s_Check=="Miar"]+1),pch=16,cex=1,col="orange")
points(log(TAB$GLUF[TAB$Species_Check=="Mumu"]+1),log(TAB$AMPA[TAB$Specie
s_Check=="Mumu"]+1),pch=16,cex=1,col="lightblue")
points(log(TAB$GLUF[TAB$Species_Check=="Mygl"]+1),log(TAB$AMPA[TAB$Specie
s_Check=="Mygl"]+1),pch=1,cex=1,col="red4")
points(log(TAB$GLUF[TAB$Species_Check=="Apsy"]+1),log(TAB$AMPA[TAB$Specie
s_Check=="Apsy"]+1),pch=1,cex=1,col="grey2")
```

```
lines(log(CGLUF+Apsy+1),AGF.Apsy.pr,lwd=1,col="grey2")
lines(log(CGLUFCrru+1),AGF.Crru.pr,lwd=2,lty=2,col="grey50")
lines(log(CGLUFMiar+1),AGF.Miar.pr,lwd=1,col="orange")
lines(log(CGLUFMumu+1),AGF.Mumu.pr,lwd=2,lty=2,col="lightblue")
lines(log(CGLUFMygl+1),AGF.Mygl.pr,lwd=1,col="red4")
```

```
legend(3.4,4,c("Apsy","Crru","Miar","Mumu","Mygl"),col=c("grey2","grey50"
,"orange","lightblue","red4"),pch=c(1,16,16,16,1),lty=c(1,2,1,2,1),lwd=1,
title="SPECIES",cex=0.8)
```

```
### GLUF GLY
```

```
plot(log(GLUF+1)~log(GLY+1),type="n",main="GLUF/GLY",ylab="log
[GLUFOSINATE] +1",xlab="log [GLYPHOSATE]
+1",cex.axis=1.5,ylim=c(0,4),xlim=c(0,4),data=TAB)
```

```

points(log(TAB$GLY[TAB$Species_Check=="Crru"]+1),log(TAB$GLUF[TAB$Species
_Check=="Crru"]+1),pch=16,cex=1,col="grey50")
points(log(TAB$GLY[TAB$Species_Check=="Miar"]+1),log(TAB$GLUF[TAB$Species
_Check=="Miar"]+1),pch=16,cex=1,col="orange")
points(log(TAB$GLY[TAB$Species_Check=="Mumu"]+1),log(TAB$GLUF[TAB$Species
_Check=="Mumu"]+1),pch=16,cex=1,col="lightblue")
points(log(TAB$GLY[TAB$Species_Check=="Mygl"]+1),log(TAB$GLUF[TAB$Species
_Check=="Mygl"]+1),pch=1,cex=1,col="red4")
points(log(TAB$GLY[TAB$Species_Check=="Apsy"]+1),log(TAB$GLUF[TAB$Species
_Check=="Apsy"]+1),pch=1,cex=1,col="grey2")

lines(log(CGLY+1),GFG.pr$fit,lwd=2,col="black")
lines(log(CGLY+1),GFG.pr$fit+1.96*GFG.pr$se.fit,lty=3,lwd=1)
lines(log(CGLY+1),GFG.pr$fit-1.96*GFG.pr$se.fit,lty=3,lwd=1)

lines(log(CGLYApsy+1),GFG.Apsy.pr,lwd=1,col="grey2")
lines(log(CGLYCrru+1),GFG.Crru.pr,lwd=2,lty=2,col="grey50")
lines(log(CGLYMiar+1),GFG.Miar.pr,lwd=1,col="orange")
lines(log(CGLYMumu+1),GFG.Mumu.pr,lwd=2,lty=2,col="lightblue")
lines(log(CGLYMygl+1),GFG.Mygl.pr,lwd=1,col="red4")

legend(3.4,4,c("Apsy","Crru","Miar","Mumu","Mygl"),col=c("grey2","grey50"
,"orange","lightblue","red4"),pch=c(1,16,16,16,1),lty=c(1,2,1,2,1),lwd=1,
title="SPECIES",cex=0.8)

```

```

#####
#####
### STATS GLMs & non paramteric with non detect set at 0 #####
#####
#####
##### Load datas#####

```

```

TAB<-read.delim2("PING_micromam_Final Results GLY-AMPA-
GLUF_ALL_update.txt")
summary(TAB)

```

```

TAB$Species_Check<-as.factor(TAB$Species_Check)
TAB$Habitat<-as.factor(TAB$Habitat)
TAB$T_NT<-as.factor(TAB$T_NT)
TAB$Farming<-as.factor(TAB$Farming)
TAB$Context<-as.factor(TAB$Context)
TAB$gpLandAB2<-as.factor(TAB$gpLandAB2)
TAB$GLUF_CAT_TOT<-as.factor(TAB$GLUF_CAT_TOT)
TAB$GLY_CAT_TOT<-as.factor(TAB$GLY_CAT_TOT)

```

```
summary(TAB)
```

```

boxplot(TAB$GLY+1~TAB$Context,log="y")
boxplot(TAB$AMPA+1~TAB$Context,log="y")
boxplot(TAB$GLUF+1~TAB$Context,log="y")

```

```

boxplot(TAB$GLY+1~TAB$Species_Check,log="y")
boxplot(TAB$AMPA+1~TAB$Species_Check,log="y")
boxplot(TAB$GLUF+1~TAB$Species_Check,log="y")

```

```

boxplot (TAB$GLY+1~TAB$Habitat, log="y")
boxplot (TAB$AMPA+1~TAB$Habitat, log="y")
boxplot (TAB$GLUF+1~TAB$Habitat, log="y")

boxplot (TAB$GLY+1~TAB$Farming, log="y")
boxplot (TAB$AMPA+1~TAB$Farming, log="y")
boxplot (TAB$GLUF+1~TAB$Farming, log="y")

boxplot (TAB$GLY+1~TAB$gpLandAB2, log="y")
boxplot (TAB$AMPA+1~TAB$gpLandAB2, log="y")
boxplot (TAB$GLUF+1~TAB$gpLandAB2, log="y")

plot (TAB$GLY+1~TAB$LandscapeAB, log="y")
plot (TAB$AMPA+1~TAB$LandscapeAB, log="y")
plot (TAB$GLUF+1~TAB$LandscapeAB, log="y")

par (mfrow=c (2, 3))
hist (TAB$GLY)
hist (TAB$AMPA)
hist (TAB$GLUF)
hist (log10 (TAB$GLY+1))
hist (log10 (TAB$AMPA+1))
hist (log10 (TAB$GLUF+1))

hist (log10 (TAB$GLY))
hist (log10 (TAB$AMPA))
hist (log10 (TAB$GLUF))

### set exploratoire et tests non paramétriques #####

### GLY
#####
kruskal.test (TAB$GLY~TAB$Species_Check)
kruskalmc (TAB$GLY~TAB$Species_Check)

kruskal.test (TAB$GLY~TAB$Farming)

wilcox.test (TAB$GLY~TAB$Habitat)

wilcox.test (TAB$GLY~TAB$T_NT)

wilcox.test (TAB$GLY~TAB$gpLandAB2)

cor.test (TAB$LandscapeAB, TAB$GLY, method=c ("spearman"))

wilcox.test (TAB$GLY~TAB$GLY_CAT_TOT)
cor.test (TAB$GLY_TOT1718, TAB$GLY, method=c ("spearman"))

### GLUF
#####
kruskal.test (TAB$GLUF~TAB$Species_Check)
kruskalmc (TAB$GLUF~TAB$Species_Check)

kruskal.test (TAB$GLUF~TAB$Farming)

```

```

wilcox.test(TAB$GLUF~TAB$Habitat)

wilcox.test(TAB$GLUF~TAB$T_NT)

wilcox.test(TAB$GLUF~TAB$gpLandAB2)

cor.test(TAB$LandscapeAB, TAB$GLUF, method=c("spearman"))

wilcox.test(TAB$GLUF~TAB$GLUF_CAT_TOT)
cor.test(TAB$GLUF_TOT1718, TAB$GLUF, method=c("spearman"))

### AMPA #####
kruskal.test(TAB$AMPA~TAB$Species_Check)
kruskalmc(TAB$AMPA~TAB$Species_Check)

kruskal.test(TAB$AMPA~TAB$Farming)

wilcox.test(TAB$AMPA~TAB$Habitat)

wilcox.test(TAB$AMPA~TAB$T_NT)

wilcox.test(TAB$AMPA~TAB$gpLandAB2)

cor.test(TAB$LandscapeAB, TAB$AMPA, method=c("spearman"))

wilcox.test(TAB$AMPA~TAB$GLY_CAT_TOT)
cor.test(TAB$GLY_TOT1718, TAB$AMPA, method=c("spearman"))

#####
##### GLMs #####
#####

### GLY #####
lmGLY<-
lm(log10(TAB$GLY+1)~TAB$Species_Check*TAB$Habitat*TAB$Farming*TAB$LandscapeAB)
summary(lmGLY)
anova(lmGLY)
lmGLYb<-
lm(log10(TAB$GLY+1)~TAB$Species_Check*TAB$Habitat*TAB$Farming*TAB$gpLandAB2)
summary(lmGLYb)
anova(lmGLYb)

lmGLY2<-lm(log10(TAB$GLY+1)~TAB$Species_Check*TAB$T_NT*TAB$LandscapeAB)
summary(lmGLY2)
anova(lmGLY2)
lmGLY2b<-lm(log10(TAB$GLY+1)~TAB$Species_Check*TAB$T_NT*TAB$gpLandAB2)
summary(lmGLY2b)
anova(lmGLY2b)

lmGLY3<-lm(log10(TAB$GLY+1)~TAB$Species_Check*TAB$LandscapeAB)
summary(lmGLY3)
anova(lmGLY3)
lmGLY3b<-lm(log10(TAB$GLY+1)~TAB$Species_Check*TAB$gpLandAB2)
summary(lmGLY3b)

```



```

anova (lmGLY3b)

par (mfrow=c (2, 2))
plot (lmGLY)

### AMPA #####
lmAMPA<-
lm (log10 (TAB$AMPA+1) ~TAB$Species_Check*TAB$Habitat*TAB$Farming*TAB$Landsc
apeAB)
summary (lmAMPA)
anova (lmAMPA)
lmAMPAb<-
lm (log10 (TAB$AMPA+1) ~TAB$Species_Check*TAB$Habitat*TAB$Farming*TAB$gpLand
AB2)
summary (lmAMPAb)
anova (lmAMPAb)

lmAMPA2<-lm (log10 (TAB$AMPA+1) ~TAB$Species_Check*TAB$T_NT*TAB$LandscapeAB)
summary (lmAMPA2)
anova (lmAMPA2)
lmAMPA2b<-lm (log10 (TAB$AMPA+1) ~TAB$Species_Check*TAB$T_NT*TAB$gpLandAB2)
summary (lmAMPA2b)
anova (lmAMPA2b)

lmAMPA3<-lm (log10 (TAB$AMPA+1) ~TAB$Species_Check*TAB$LandscapeAB)
summary (lmAMPA3)
anova (lmAMPA3)
lmAMPA3b<-lm (log10 (TAB$AMPA+1) ~TAB$Species_Check*TAB$gpLandAB2)
summary (lmAMPA3b)
anova (lmAMPA3b)

par (mfrow=c (2, 2))
plot (lmAMPA)

### GLUF #####
lmGLUF<-
lm (log10 (TAB$GLUF+1) ~TAB$Species_Check*TAB$Habitat*TAB$Farming*TAB$Landsc
apeAB)
summary (lmGLUF)
anova (lmGLUF)
lmGLUFb<-
lm (log10 (TAB$GLUF+1) ~TAB$Species_Check*TAB$Habitat*TAB$Farming*TAB$gpLand
AB2)
summary (lmGLUFb)
anova (lmGLUFb)

lmGLUF2<-lm (log10 (TAB$GLUF+1) ~TAB$Species_Check*TAB$T_NT*TAB$LandscapeAB)
summary (lmGLUF2)
anova (lmGLUF2)
lmGLUF2b<-lm (log10 (TAB$GLUF+1) ~TAB$Species_Check*TAB$T_NT*TAB$gpLandAB2)
summary (lmGLUF2b)
anova (lmGLUF2b)

lmGLUF3<-lm (log10 (TAB$GLUF+1) ~TAB$Species_Check*TAB$LandscapeAB)

```

```

summary(lmGLUF3)
anova(lmGLUF3)
lmGLUF3b<-lm(log10(TAB$GLUF+1)~TAB$Species_Check*TAB$gpLandAB2)
summary(lmGLUF3b)
anova(lmGLUF3b)

par(mfrow=c(2,2))
plot(lmGLUF)

### GRAPHIQUES
par(mfrow=c(1,3))
boxplot(TAB$GLY+1~TAB$Species_Check,log="y")
boxplot(TAB$AMPA+1~TAB$Species_Check,log="y")
boxplot(TAB$GLUF+1~TAB$Species_Check,log="y")

par(mfrow=c(1,3))
boxplot(TAB$GLY+1~TAB$Habitat,log="y")
boxplot(TAB$AMPA+1~TAB$Habitat,log="y")
boxplot(TAB$GLUF+1~TAB$Habitat,log="y")

par(mfrow=c(1,3))
boxplot(TAB$GLY+1~TAB$Farming,log="y")
boxplot(TAB$AMPA+1~TAB$Farming,log="y")
boxplot(TAB$GLUF+1~TAB$Farming,log="y")

par(mfrow=c(1,3))
boxplot(TAB$GLY+1~TAB$T_NT,log="y")
boxplot(TAB$AMPA+1~TAB$T_NT,log="y")
boxplot(TAB$GLUF+1~TAB$T_NT,log="y")

par(mfrow=c(1,3))
plot(TAB$GLY+1~TAB$LandscapeAB,log="y", xlim=c(0,100),ylim=c(1,550))
plot(TAB$AMPA+1~TAB$LandscapeAB,log="y", xlim=c(0,100),ylim=c(1,50))
plot(TAB$GLUF+1~TAB$LandscapeAB,log="y", xlim=c(0,100),ylim=c(1,50))

par(mfrow=c(1,3))
boxplot(TAB$GLY+1~TAB$gpLandAB2,log="y")
boxplot(TAB$AMPA+1~TAB$gpLandAB2,log="y")
boxplot(TAB$GLUF+1~TAB$gpLandAB2,log="y")

#####
#####
##### STATS detection frequency binomial GLMs #####
#####
#####
library(pgirmess)
##### Load datas#####
TAB<-read.delim2("PING_micromam_Final Results GLY-AMPA-
GLUF_ALL_update.txt")
TABssmyglmumu<-read.delim2("PING_micromam_Final Results GLY AMPA
GLUF_ALL_tabR_ssmymglmumu.txt")
summary(TAB)

TAB$Species_Check<-as.factor(TAB$Species_Check)
TAB$Habitat<-as.factor(TAB$Habitat)
TAB$T_NT<-as.factor(TAB$T_NT)

```

```

TAB$Farming<-as.factor(TAB$Farming)
TAB$gpLandAB2<-as.factor(TAB$gpLandAB2)

TAB$GLY_CAT_TOT<-as.factor(TAB$GLY_CAT_TOT)
TAB$GLUF_CAT_TOT<-as.factor(TAB$GLUF_CAT_TOT)

summary(TAB)
names(TAB)

TABssmyglmumu$Species_Check<-as.factor(TABssmyglmumu$Species_Check)
TABssmyglmumu$Habitat<-as.factor(TABssmyglmumu$Habitat)
TABssmyglmumu$T_NT<-as.factor(TABssmyglmumu$T_NT)
TABssmyglmumu$Farming<-as.factor(TABssmyglmumu$Farming)
TABssmyglmumu$gpLandAB2<-as.factor(TABssmyglmumu$gpLandAB2)

TABssmyglmumu$GLY_CAT_TOT<-as.factor(TABssmyglmumu$GLY_CAT_TOT)
TABssmyglmumu$GLUF_CAT_TOT<-as.factor(TABssmyglmumu$GLUF_CAT_TOT)
summary(TABssmyglmumu)

### Remarques : tests exploratoires --> ont montré catégoriser variables
nécessaires pour odd ratio
### + pas assez effectif pour utiliser landscape AB et ventes GLY en
facteurs continus
### ventes GLY et GLUF ne garder que tot car ce sont les mêmes catégories
ou bien 0 ventes de GLUF en 2017

par(mfrow=c(3,2))
plot(TAB$GLY_detect~TAB$LandscapeAB)
boxplot(TAB$GLY_detect~TAB$gpLandAB2)
plot(TAB$AMPA_detect~TAB$LandscapeAB)
boxplot(TAB$AMPA_detect~TAB$gpLandAB2)
plot(TAB$GLUF_detect~TAB$LandscapeAB)
boxplot(TAB$GLUF_detect~TAB$gpLandAB2)

par(mfrow=c(1,3))
plot(TAB$GLY+1~TAB$GLY_TOT1718,log="y")
plot(TAB$AMPA+1~TAB$GLY_TOT1718,log="y")
plot(TAB$GLUF+1~TAB$GLUF_TOT1718,log="y")

boxplot(TAB$GLY+1~TAB$GLY_CAT_TOT,log="y")
boxplot(TAB$AMPA+1~TAB$GLY_CAT_TOT,log="y")
boxplot(TAB$GLUF+1~TAB$GLUF_CAT_TOT,log="y")

par(mfrow=c(1,3))
plot(TAB$GLY_2017~TAB$GLY_2018)
plot(TAB$GLY_2017~TAB$GLY_TOT1718)
plot(TAB$GLY_2018~TAB$GLY_TOT1718)

plot(TAB$GLUF_2017~TAB$GLUF_2018)
plot(TAB$GLUF_2017~TAB$GLUF_TOT1718)
plot(TAB$GLUF_2018~TAB$GLUF_TOT1718)

par(mfrow=c(1,3))
boxplot(TAB$GLY_detect~TAB$Species_Check)
boxplot(TAB$AMPA_detect~TAB$Species_Check)

```

```

boxplot(TAB$GLUF_detect~TAB$Species_Check)

table(TAB$GLY_detect,TAB$Species_Check)

par(mfrow=c(1,3))
plot(TAB$Habitat~TAB$GLY_TOT1718)
plot(TAB$Habitat~TAB$gpLandAB2)
plot(TAB$GLY_TOT1718~TAB$gpLandAB2)

plot(TAB$Species_Check~TAB$T_NT)
plot(TAB$Species_Check~TAB$GLUF_CAT_TOT)
plot(TAB$ssmyglmumu$Species_Check~TAB$ssmyglmumu$GLUF_CAT_TOT)
table(TAB$ssmyglmumu$GLUF_detect,TAB$ssmyglmumu$GLUF_CAT_TOT)
table(TAB$ssmyglmumu$GLUF_detect,TAB$ssmyglmumu$Species_Check)

library(questionr)
library(forestmodel)
library(effects)
library(ggeffects)
library(ggplot2)
library(AICcmodavg)
library(multcomp)

library(gtsummary)

### bug redémarrage
library(GGally)
###

freq(TAB$GLY_detect)
freq(TAB$GLY_detect[TAB$Species_Check=="Crru"])
freq(TAB$GLY_detect[TAB$Species_Check=="Apsy"])
freq(TAB$GLY_detect[TAB$Species_Check=="Miar"])
freq(TAB$GLY_detect[TAB$Species_Check=="Mumu"])
freq(TAB$GLY_detect[TAB$Species_Check=="Mygl"])
freq(TAB$AMPA_detect)
freq(TAB$AMPA_detect[TAB$Species_Check=="Crru"])
freq(TAB$AMPA_detect[TAB$Species_Check=="Apsy"])
freq(TAB$AMPA_detect[TAB$Species_Check=="Miar"])
freq(TAB$AMPA_detect[TAB$Species_Check=="Mumu"])
freq(TAB$AMPA_detect[TAB$Species_Check=="Mygl"])

freq(TAB$GLUF_detect)
freq(TAB$GLUF_detect[TAB$Species_Check=="Crru"])
freq(TAB$GLUF_detect[TAB$Species_Check=="Apsy"])
freq(TAB$GLUF_detect[TAB$Species_Check=="Miar"])
freq(TAB$GLUF_detect[TAB$Species_Check=="Mumu"])
freq(TAB$GLUF_detect[TAB$Species_Check=="Mygl"])

#----- Premiers tests exploratoires toutes variables et
interactions -----

modGLYfull1 <- glm(GLY_detect ~ Species_Check + Habitat + Farming +
gpLandAB2 + GLY_CAT_TOT

```

```

+ Species_Check:Habitat + Species_Check:Farming +
Species_Check:gpLandAB2 + Species_Check:GLY_CAT_TOT
+ Habitat:Farming + Habitat:gpLandAB2 +
Habitat:GLY_CAT_TOT
+ Farming:gpLandAB2 + Farming:GLY_CAT_TOT
+ gpLandAB2:GLY_CAT_TOT
, data = TAB, family = binomial(logit))

modGLYfull1
summary(modGLYfull1) ### nombreuses modalités NA
anova(modGLYfull1, test="Chisq")
exp(cbind(coef(modGLYfull1), confint(modGLYfull1))) ### converge pas trop
de modalités en NA

### seulement espèce et interaction habitat:gly_tot signif + proche
signif habitat:landAB

modGLYfull2 <- glm(GLY_detect ~ Species_Check + T_NT + gpLandAB2 +
GLY_CAT_TOT
+ Species_Check:T_NT + Species_Check:gpLandAB2 +
Species_Check:GLY_CAT_TOT
+ T_NT:gpLandAB2 + T_NT:GLY_CAT_TOT
+ gpLandAB2:GLY_CAT_TOT
, data = TAB, family = binomial(logit))

modGLYfull2
summary(modGLYfull2) ### nombreuses modalités NA
anova(modGLYfull2, test="Chisq")
exp(cbind(coef(modGLYfull2), confint(modGLYfull2))) ### converge pas trop
de modalités en NA

tbl_regression(modGLYfull2, exponentiate = TRUE)
forest_model(modGLYfull2)

### seulement espèce signif + TNT:gly_tot + TNT:landAB + proche signif
landAB:gly_tot

modGLYfull0 <- glm(GLY_detect ~ Species_Check + Habitat + Farming +
gpLandAB2 + GLY_CAT_TOT
, data = TAB, family = binomial(logit))

modGLYfull0
summary(modGLYfull0)
anova(modGLYfull0, test="Chisq")
exp(cbind(coef(modGLYfull0), confint(modGLYfull0))) ### converge

modGLYfull0bis <- glm(GLY_detect ~ Species_Check + T_NT + gpLandAB2 +
GLY_CAT_TOT
, data = TAB, family = binomial(logit))

modGLYfull0bis
summary(modGLYfull0bis)
anova(modGLYfull0bis, test="Chisq")
exp(cbind(coef(modGLYfull0bis), confint(modGLYfull0bis))) ### converge

Cand.mod<-list(modGLYfull0,modGLYfull0bis,modGLYfull1,modGLYfull2)
Modnames <- c("full hab farming LandAB gly ss inter","full TNT LandAB gly
ss inter",
"full hab farming LandAB gly avec inter", "full TNT LandAB
gly avec inter")
aictab(Cand.mod, Modnames)

```

```

###----- conclusions tests préliminaires -----

### Gpes landAB est la variable à utiliser : seule décrite dans M&M (pas
LandAB continue)
### pas possible tester GLY année -1 vs année cause 0 en 2017 pour GLUF
et exactement même catégories en 2017/2018/total pour GLY
### attention avec interactions, converge pas toujours et bcp
singularités, pas estimation odd ratios

### -> Calcul paramètres avec modèles sans interactions car pas
convergence certaines et nb ses singularités.
### set de tests effets espèces + autres facteurs chacun isolément
(Habitat, Farming, TNT, LandAB, GLY/GLUFtot)

###-----Calculs outputs modèles GLY -----
##### MODELE GLY #####
modGLYSPFarm <- glm(GLY_detect ~ Species_Check + Farming , data = TAB,
family = binomial(logit))
summary(modGLYSPFarm)
anova(modGLYSPFarm, test="Chisq")
tbl_regression(modGLYSPFarm, exponentiate = TRUE)
forest_model(modGLYSPFarm)

modGLYSPTNT <- glm(GLY_detect ~ Species_Check + T_NT , data = TAB, family
= binomial(logit))
summary(modGLYSPTNT)
anova(modGLYSPTNT, test="Chisq")
tbl_regression(modGLYSPTNT, exponentiate = TRUE)
forest_model(modGLYSTNT)

modGLYSPHab <- glm(GLY_detect ~ Species_Check + Habitat , data = TAB,
family = binomial(logit))
summary(modGLYSPHab)
anova(modGLYSPHab, test="Chisq")
tbl_regression(modGLYSPHab, exponentiate = TRUE)
forest_model(modGLYSPHab)

modGLYSPLandAB <- glm(GLY_detect ~ Species_Check + gpLandAB2 , data =
TAB, family = binomial(logit))
summary(modGLYSPLandAB)
anova(modGLYSPLandAB, test="Chisq")
tbl_regression(modGLYSPLandAB, exponentiate = TRUE)
forest_model(modGLYSPLandAB)

modGLYSP1718 <- glm(GLY_detect ~ Species_Check + GLY_CAT_TOT , data =
TAB, family = binomial(logit))
summary(modGLYSP1718)
anova(modGLYSP1718, test="Chisq")
tbl_regression(modGLYSP1718, exponentiate = TRUE)
forest_model(modGLYSP1718)

#####-----Compute GLY comp multiples espèces

```

```

modGLYb <- glm(GLY_detect ~ Species_Check , data = TAB, family =
binomial(logit))
summary(modGLYb)
anova(modGLYb, test="Chisq")
cbind(coef(modGLYb), confint(modGLYb))
exp(cbind(coef(modGLYb), confint(modGLYb)))
odds.ratio(modGLYb)

tbl_regression(modGLYb, exponentiate = TRUE)
forest_model(modGLYb)

TAB$Species_Check <- relevel(TAB$Species_Check, "Miar")
TAB$Species_Check <- relevel(TAB$Species_Check, "Apsy")

### ----- plots ggeffects -----
par(mfrow=c(1,3))
plot(ggeffect(modGLYb, "Species_Check"))
plot(ggeffect(modGLY, "Habitat"))
plot(ggeffect(modGLY, "Farming"))
plot(ggeffect(modGLYb, "T_NT"))

### comparaisons multiples entre espèces /// préférer ODD ratio
multComp(modGLYb, factor.id = "Species_Check", correction = "none") # à
préférer même mode calcul tab odd ratio

CompMultGLYSp <- glht(modGLYb, linfct=mcp(Species_Check="Tukey"))
summary(CompMultGLYSp) ### attention légères différences cause pr > Z pas
même mode calcul

TAB$Species_Check <- relevel(TAB$Species_Check, "Miar")
TAB$Species_Check <- relevel(TAB$Species_Check, "Apsy")
modGLYb <- glm(GLY_detect ~ Species_Check , data = TAB, family =
binomial(logit))

par(mfrow=c(1,3))
plot(ggeffect(modGLYb, "Species_Check"))
plot(ggeffect(modGLY, "Habitat"))
plot(ggeffect(modGLY, "Farming"))

### attention si utilisation cowplot blocage autres fonctions autres
packages
cowplot::plot_grid(plotlist = plot(ggeffect(modGLY)))
###

#----- GLY check validation -----
-----
modGLYFarm <- glm(GLY_detect ~ Farming , data = TAB, family =
binomial(logit))
summary(modGLYFarm)
anova(modGLYFarm, test="Chisq")

modGLYTNT <- glm(GLY_detect ~ T_NT , data = TAB, family =
binomial(logit))
summary(modGLYTNT)

```

```

anova(modGLYTNT, test="Chisq")

modGLYHab <- glm(GLY_detect ~ Habitat , data = TAB, family =
binomial(logit))
summary(modGLYHab)
anova(modGLYHab, test="Chisq")

modGLYLandAB <- glm(GLY_detect ~ gpLandAB2 , data = TAB, family =
binomial(logit))
summary(modGLYLandAB)
anova(modGLYLandAB, test="Chisq")

modGLY1718 <- glm(GLY_detect ~ GLY_CAT_TOT , data = TAB, family =
binomial(logit))
summary(modGLY1718)
anova(modGLY1718, test="Chisq")

### check validation aucune variable seule signif

#---- GLY check validation -----

### check validation aucune variable Sp + seulesignif

##### TESTS SUR AMPA -----
### AMPA
###-----Calculs outputs modèles AMPA -----
### MODELE AMPA
modAMPASPFarm <- glm(AMPA_detect ~ Species_Check + Farming , data = TAB,
family = binomial(logit))
summary(modAMPASPFarm)
anova(modAMPASPFarm, test="Chisq")
tbl_regression(modAMPASPFarm, exponentiate = TRUE)
forest_model(modAMPASPFarm)

modAMPASPTNT <- glm(AMPA_detect ~ Species_Check + T_NT , data = TAB,
family = binomial(logit))
summary(modAMPASPTNT)
anova(modAMPASPTNT, test="Chisq")
tbl_regression(modAMPASPTNT, exponentiate = TRUE)
forest_model(modAMPASPTNT)

modAMPASPHab <- glm(AMPA_detect ~ Species_Check + Habitat , data = TAB,
family = binomial(logit))
summary(modAMPASPHab)
anova(modAMPASPHab, test="Chisq")
tbl_regression(modAMPASPHab, exponentiate = TRUE)
forest_model(modAMPASPHab)

modAMPASPLandAB <- glm(AMPA_detect ~ Species_Check + gpLandAB2 , data =
TAB, family = binomial(logit))
summary(modAMPASPLandAB)
anova(modAMPASPLandAB, test="Chisq")
tbl_regression(modAMPASPLandAB, exponentiate = TRUE)
forest_model(modAMPASPLandAB)

```



```

modAMPASP1718 <- glm(AMPA_detect ~ Species_Check + GLY_CAT_TOT , data =
TAB, family = binomial(logit))
summary(modAMPASP1718)
anova(modAMPASP1718, test="Chisq")
tbl_regression(modAMPASP1718, exponentiate = TRUE)
forest_model(modAMPASP1718)

```

```
#####-----Compute comp multiples espèces
```

```

modAMPAb <- glm(AMPA_detect ~ Species_Check , data = TAB, family =
binomial(logit))
summary(modAMPAb)
anova(modAMPAb, test="Chisq")
cbind(coef(modAMPAb), confint(modAMPAb))
exp(cbind(coef(modAMPAb), confint(modAMPAb)))
odds.ratio(modAMPAb)

```

```
tbl_regression(modAMPAb, exponentiate = TRUE)
forest_model(modAMPAb)
```

```
### ----- plots ggeffects -----
```

```

par(mfrow=c(1,3))
plot(ggeffect(modAMPAb, "Species_Check"))
plot(ggeffect(modAMPA, "Habitat"))
plot(ggeffect(modAMPA, "Farming"))
plot(ggeffect(modAMPAb, "T_NT"))

```

```

### comparaisons multiples entre espèces /// préférer ODD ratio
modAMPAb <- glm(AMPA_detect ~ Species_Check , data = TAB, family =
binomial(logit))
multComp(modAMPAb, factor.id = "Species_Check", correction = "none")

```

```

CompMultGLYSp <- glht(modAMPAb, linfct=mcp(Species_Check="Tukey"))
summary(CompMultGLYSp)

```

```

TAB$Species_Check <- relevel(TAB$Species_Check, "Miar")
TAB$Species_Check <- relevel(TAB$Species_Check, "Apsy")

```

```

par(mfrow=c(1,3))
plot(ggeffect(modAMPAb, "Species_Check"))
plot(ggeffect(modAMPA, "Habitat"))
plot(ggeffect(modAMPA, "Farming"))

```

```

### attention si utilisation cowplot blocage autres fonctions autres
packages

```

```

cowplot::plot_grid(plotlist = plot(ggeffect(modAMPA)))
###

```

```

#----- AMPA check validation -----
-----

```

```

modAMPAPFarm <- glm(AMPA_detect ~ Farming , data = TAB, family =
binomial(logit))

```

```

summary(modAMPAFarm)
anova(modAMPAFarm, test="Chisq")

modAMPATNT <- glm(AMPA_detect ~ T_NT , data = TAB, family =
binomial(logit))
summary(modAMPATNT)
anova(modAMPATNT, test="Chisq")

modAMPAHab <- glm(AMPA_detect ~ Habitat , data = TAB, family =
binomial(logit))
summary(modAMPAHab)
anova(modAMPAHab, test="Chisq")

modAMPALandAB <- glm(AMPA_detect ~ gpLandAB2 , data = TAB, family =
binomial(logit))
summary(modAMPALandAB)
anova(modAMPALandAB, test="Chisq")

modAMPA1718 <- glm(AMPA_detect ~ GLY_CAT_TOT , data = TAB, family =
binomial(logit))
summary(modAMPA1718)
anova(modAMPA1718, test="Chisq")

### check validation aucune variable seule signif

##### TESTS SUR GLUF -----
### GLUF
###-----Calculs outputs modèles GLUF -----
### MODELE GLUF
modGLUFSPFarm <- glm(GLUF_detect ~ Species_Check + Farming , data = TAB,
family = binomial(logit))
summary(modGLUFSPFarm)
anova(modGLUFSPFarm, test="Chisq")
tbl_regression(modGLUFSPFarm, exponentiate = TRUE)
forest_model(modGLUFSPFarm)

modGLUFSPNT <- glm(GLUF_detect ~ Species_Check + T_NT , data = TAB,
family = binomial(logit))
summary(modGLUFSPNT)
anova(modGLUFSPNT, test="Chisq")
tbl_regression(modGLUFSPNT, exponentiate = TRUE)
forest_model(modGLUFSPNT)

modGLUFSPHab <- glm(GLUF_detect ~ Species_Check + Habitat , data = TAB,
family = binomial(logit))
summary(modGLUFSPHab)
anova(modGLUFSPHab, test="Chisq")
tbl_regression(modGLUFSPHab, exponentiate = TRUE)
forest_model(modGLUFSPHab)

modGLUFSPLandAB <- glm(GLUF_detect ~ Species_Check + gpLandAB2 , data =
TAB, family = binomial(logit))
summary(modGLUFSPLandAB)
anova(modGLUFSPLandAB, test="Chisq")
tbl_regression(modGLUFSPLandAB, exponentiate = TRUE)

```

```

forest_model(modGLUFSPLandAB)

modGLUFSP1718.1 <- glm(GLUF_detect ~ Species_Check + GLUF_CAT_TOT , data
= TAB, family = binomial(logit))
summary(modGLUFSP1718.1)
anova(modGLUFSP1718.1, test="Chisq")
tbl_regression(modGLUFSP1718.1, exponentiate = TRUE)
forest_model(modGLUFSP1718.1)
cbind(coef(modGLUFSP1718.1), confint(modGLUFSP1718.1))
exp(cbind(coef(modGLUFSP1718.1), confint(modGLUFSP1718.1)))
odds.ratio(modGLUFSP1718.1)

modGLUFSP1718 <- glm(GLUF_detect ~ Species_Check + GLUF_CAT_TOT , data =
TABssmyglmumu, family = binomial(logit))
summary(modGLUFSP1718)
anova(modGLUFSP1718, test="Chisq")
tbl_regression(modGLUFSP1718, exponentiate = TRUE)
forest_model(modGLUFSP1718)

cbind(coef(modGLUFSP1718), confint(modGLUFSP1718))
exp(cbind(coef(modGLUFSP1718), confint(modGLUFSP1718)))
odds.ratio(modGLUFSP1718)
warnings()

modGLUFSP1718seul <- glm(GLUF_detect ~ GLUF_CAT_TOT , data = TAB, family
= binomial(logit))
anova(modGLUFSP1718seul, test="Chisq")
tbl_regression(modGLUFSP1718seul, exponentiate = TRUE)
forest_model(modGLUFSP1718seul)

#####-----Compute GLUF comp multiples espèces

modGLUFb <- glm(GLUF_detect ~ Species_Check , data = TAB, family =
binomial(logit))
summary(modGLUFb)
anova(modGLUFb, test="Chisq")
cbind(coef(modGLUFb), confint(modGLUFb))
exp(cbind(coef(modGLUFb), confint(modGLUFb)))
odds.ratio(modGLUFb)

tbl_regression(modGLUFb, exponentiate = TRUE)
forest_model(modGLUFb)

### ----- plots ggeffects -----
par(mfrow=c(1,3))
plot(ggeffect(modGLUFb, "Species_Check"))
plot(ggeffect(modGLUF, "Habitat"))
plot(ggeffect(modGLUF, "Farming"))
plot(ggeffect(modGLUFb, "T_NT"))

### comparaisons multiples entre espèces /// préférer ODD ratio
multComp(modGLUFb, factor.id = "Species_Check", correction = "none")

CompMultGLUFSp <- glht(modGLUF, linfct=mcp(Species_Check="Tukey"))
summary(CompMultGLUFSp)

TAB$Species_Check <- relevel(TAB$Species_Check, "Miar")
TAB$Species_Check <- relevel(TAB$Species_Check, "Apsy")

```

```

par(mfrow=c(1,3))
plot(ggeffect(modGLUFb, "Species_Check"))
plot(ggeffect(modGLUF, "Habitat"))
plot(ggeffect(modGLUF, "Farming"))

modGLUFSP1718 <- glm(GLUF_detect ~ Species_Check + GLUF_CAT_TOT , data =
TAB, family = binomial(logit))
plot(ggeffect(modGLUFSP1718, "GLUF_CAT_TOT"))

multComp(modGLUFSP1718, factor.id = "GLUF_CAT_TOT", correction = "none")

modGLUFSP1718seul <- glm(GLUF_detect ~ GLUF_CAT_TOT , data = TAB, family
= binomial(logit))
plot(ggeffect(modGLUFSP1718seul, "GLUF_CAT_TOT"))

multComp(modGLUFSP1718seul, factor.id = "GLUF_CAT_TOT", correction =
"none")

### attention si utilisation cowplot blocage autres fonctions autres
packages
cowplot::plot_grid(plotlist = plot(ggeffect(modGLUF)))
###

#---- GLUF check validation -----
-----
modGLUFFarm <- glm(GLUF_detect ~ Farming , data = TAB, family =
binomial(logit))
summary(modGLUFFarm)
anova(modGLUFFarm, test="Chisq")

modGLUFTNT <- glm(GLUF_detect ~ T_NT , data = TAB, family =
binomial(logit))
summary(modGLUFTNT)
anova(modGLUFTNT, test="Chisq")

modGLUFHab <- glm(GLUF_detect ~ Habitat , data = TAB, family =
binomial(logit))
summary(modGLUFHab)
anova(modGLUFHab, test="Chisq")

modGLUFLandAB <- glm(GLUF_detect ~ gpLandAB2 , data = TAB, family =
binomial(logit))
summary(modGLUFLandAB)
anova(modGLUFLandAB, test="Chisq")

modGLUF1718 <- glm(GLUF_detect ~ GLUF_CAT_TOT , data = TAB, family =
binomial(logit))
summary(modGLUF1718)
anova(modGLUF1718, test="Chisq")

### check validation aucune variable seule signif

```

```

#####
#####
### STATS GLMs quantified concentrations #####
#####
library(pgirmess)
library(AICcmodavg)
## Load datas: #####
TABGLY<-read.delim2("PING_micromam_Final Results GLY sans nd_ALL.txt")
TABAMPA<-read.delim2("PING_micromam_Final Results AMPA sans nd_ALL.txt")
TABGLUF<-read.delim2("PING_micromam_Final Results GLUF sans nd_ALL.txt")

summary(TABGLY$GLY)
summary(TABAMPA$AMPA)
summary(TABGLUF$GLUF)

TABGLY$Species_Check<-as.factor(TABGLY$Species_Check)
TABGLY$Habitat<-as.factor(TABGLY$Habitat)
TABGLY$T_NT<-as.factor(TABGLY$T_NT)
TABGLY$Farming<-as.factor(TABGLY$Farming)
TABGLY$Context<-as.factor(TABGLY$Context)
TABGLY$gpLandAB2<-as.factor(TABGLY$gpLandAB2)
TABGLY$GLY_CAT_TOT<-as.factor(TABGLY$GLY_CAT_TOT)
TABGLY$GLUF_CAT_TOT<-as.factor(TABGLY$GLUF_CAT_TOT)

TABAMPA$Species_Check<-as.factor(TABAMPA$Species_Check)
TABAMPA$Habitat<-as.factor(TABAMPA$Habitat)
TABAMPA$T_NT<-as.factor(TABAMPA$T_NT)
TABAMPA$Farming<-as.factor(TABAMPA$Farming)
TABAMPA$Context<-as.factor(TABAMPA$Context)
TABAMPA$gpLandAB2<-as.factor(TABAMPA$gpLandAB2)
TABAMPA$GLY_CAT_TOT<-as.factor(TABAMPA$GLY_CAT_TOT)
TABAMPA$GLUF_CAT_TOT<-as.factor(TABAMPA$GLUF_CAT_TOT)

TABGLUF$Species_Check<-as.factor(TABGLUF$Species_Check)
TABGLUF$Habitat<-as.factor(TABGLUF$Habitat)
TABGLUF$T_NT<-as.factor(TABGLUF$T_NT)
TABGLUF$Farming<-as.factor(TABGLUF$Farming)
TABGLUF$Context<-as.factor(TABGLUF$Context)
TABGLUF$gpLandAB2<-as.factor(TABGLUF$gpLandAB2)
TABGLUF$GLY_CAT_TOT<-as.factor(TABGLUF$GLY_CAT_TOT)
TABGLUF$GLUF_CAT_TOT<-as.factor(TABGLUF$GLUF_CAT_TOT)

summary(TABGLY)
summary(TABAMPA)
summary(TABGLUF)

table(TABGLY$Species_Check)
table(TABGLY$Habitat)
table(TABGLY$Farming)
table(TABGLY$T_NT)
table(TABGLY$gpLandAB2)
table(TABGLY$GLY_CAT_TOT)

```

```

table(TABAMPA$Species_Check)
table(TABAMPA$Habitat)
table(TABAMPA$Farming)
table(TABAMPA$T_NT)
table(TABAMPA$gpLandAB2)
table(TABAMPA$GLY_CAT_TOT)

table(TABGLUF$Species_Check)
table(TABGLUF$Habitat)
table(TABGLUF$Farming)
table(TABGLUF$T_NT)
table(TABGLUF$gpLandAB2)
table(TABGLUF$GLUF_CAT_TOT)

###-----calculs min max med etc-----
### GLY
summary(TABGLY$GLY)
sd(TABGLY$GLY)

summary(TABGLY$GLY[TABGLY$Species_Check=="Apsy"])
sd(TABGLY$GLY[TABGLY$Species_Check=="Apsy"])

summary(TABGLY$GLY[TABGLY$Species_Check=="Crru"])
sd(TABGLY$GLY[TABGLY$Species_Check=="Crru"])

summary(TABGLY$GLY[TABGLY$Species_Check=="Miar"])
sd(TABGLY$GLY[TABGLY$Species_Check=="Miar"])

summary(TABGLY$GLY[TABGLY$Species_Check=="Mumu"])
sd(TABGLY$GLY[TABGLY$Species_Check=="Mumu"])

summary(TABGLY$GLY[TABGLY$Species_Check=="Mygl"])
sd(TABGLY$GLY[TABGLY$Species_Check=="Mygl"])

### AMPA
summary(TABAMPA$AMPA)
sd(TABAMPA$AMPA)

summary(TABAMPA$AMPA[TABAMPA$Species_Check=="Apsy"])
sd(TABAMPA$AMPA[TABAMPA$Species_Check=="Apsy"])

summary(TABAMPA$AMPA[TABAMPA$Species_Check=="Crru"])
sd(TABAMPA$AMPA[TABAMPA$Species_Check=="Crru"])

summary(TABAMPA$AMPA[TABAMPA$Species_Check=="Miar"])
sd(TABAMPA$AMPA[TABAMPA$Species_Check=="Miar"])

summary(TABAMPA$AMPA[TABAMPA$Species_Check=="Mumu"])
sd(TABAMPA$AMPA[TABAMPA$Species_Check=="Mumu"])

summary(TABAMPA$AMPA[TABAMPA$Species_Check=="Mygl"])
sd(TABAMPA$AMPA[TABAMPA$Species_Check=="Mygl"])

### GLUF
summary(TABGLUF$GLUF)
sd(TABGLUF$GLUF)

summary(TABGLUF$GLUF[TABGLUF$Species_Check=="Apsy"])

```

```

sd(TABGLUF$GLUF[TABGLUF$Species_Check=="Apsy"])

summary(TABGLUF$GLUF[TABGLUF$Species_Check=="Crru"])
sd(TABGLUF$GLUF[TABGLUF$Species_Check=="Crru"])

summary(TABGLUF$GLUF[TABGLUF$Species_Check=="Miar"])
sd(TABGLUF$GLUF[TABGLUF$Species_Check=="Miar"])

summary(TABGLUF$GLUF[TABGLUF$Species_Check=="Mumu"])
sd(TABGLUF$GLUF[TABGLUF$Species_Check=="Mumu"])

summary(TABGLUF$GLUF[TABGLUF$Species_Check=="Mygl"])
sd(TABGLUF$GLUF[TABGLUF$Species_Check=="Mygl"])

###-----vérification et tests transfo-----
par(mfrow=c(1,3))
boxplot(TABGLY$GLY+0.1~TABGLY$Species_Check,log="y")
boxplot(TABAMPA$AMPA+0.1~TABAMPA$Species_Check,log="y")
boxplot(TABGLUF$GLUF+0.1~TABGLUF$Species_Check,log="y")

boxplot(TABGLY$GLY+0.1~TABGLY$Habitat,log="y")
boxplot(TABAMPA$AMPA+0.1~TABAMPA$Habitat,log="y")
boxplot(TABGLUF$GLUF+0.1~TABGLUF$Habitat,log="y")

boxplot(TABGLY$GLY+0.1~TABGLY$Farming,log="y")
boxplot(TABAMPA$AMPA+0.1~TABAMPA$Farming,log="y")
boxplot(TABGLUF$GLUF+0.1~TABGLUF$Farming,log="y")

par(mfrow=c(2,3))
hist(TABGLY$GLY)
hist(TABAMPA$AMPA)
hist(TABGLUF$GLUF)
hist(log(TABGLY$GLY+0.1))
hist(log(TABAMPA$AMPA+0.1))
hist(log(TABGLUF$GLUF+0.1))

par(mfrow=c(2,3))
hist(log10(TABGLY$GLY))
hist(log10(TABAMPA$AMPA))
hist(log10(TABGLUF$GLUF))
### mieux avec transfo, à vérifier sans ou avec +1, log ou log10

ks.gof(log(TABGLY$GLY+0.1)) # p-value = 0.4275
ks.gof(log(TABAMPA$AMPA+0.1)) # p-value = 0.322
ks.gof(log(TABGLUF$GLUF+0.1)) # p-value = 0.6959

ks.gof(log(TABGLY$GLY)) # p-value = 0.332
ks.gof(log(TABAMPA$AMPA)) # p-value = 0.3935
ks.gof(log(TABGLUF$GLUF)) # p-value = 0.7189

### --> log et pas +0.1

####----- orthogonalité effectifs espèces vs autres facteurs -----
table(TABGLY$Species_Check,TABGLY$Habitat)
table(TABGLY$Species_Check,TABGLY$Farming)
table(TABGLY$Species_Check,TABGLY$T_NT)
table(TABGLY$Species_Check,TABGLY$gpLandAB2)
table(TABGLY$Species_Check,TABGLY$GLY_CAT_TOT)

```

```
table(TABAMPA$Species_Check, TABAMPA$Habitat)
table(TABAMPA$Species_Check, TABAMPA$Farming)
table(TABAMPA$Species_Check, TABAMPA$T_NT)
table(TABAMPA$Species_Check, TABAMPA$gpLandAB2)
table(TABAMPA$Species_Check, TABAMPA$GLY_CAT_TOT)
```

```
table(TABGLUF$Species_Check, TABGLUF$Habitat)
table(TABGLUF$Species_Check, TABGLUF$Farming)
table(TABGLUF$Species_Check, TABGLUF$T_NT)
table(TABGLUF$Species_Check, TABGLUF$gpLandAB2)
table(TABGLUF$Species_Check, TABGLUF$GLUF_CAT_TOT)
```

```
###----- graphiques préliminaires avec ventes GLY -----
```

```
par(mfrow=c(1, 3))
```

```
plot(log10(TAB$GLY+1)~TAB$GLY_2017)
plot(log10(TAB$GLY+1)~TAB$GLY_2018)
plot(log10(TAB$GLY+1)~TAB$GLY_TOT1718)
```

```
plot(log10(TAB$GLY[TAB$Species_Check=="Miar")+1)~TAB$GLY_2017[TAB$Species_Check=="Miar"])
plot(log10(TAB$GLY[TAB$Species_Check=="Miar")+1)~TAB$GLY_2018[TAB$Species_Check=="Miar"])
plot(log10(TAB$GLY[TAB$Species_Check=="Miar")+1)~TAB$GLY_TOT1718[TAB$Species_Check=="Miar"])
```

```
plot(TAB$GLY[TAB$Species_Check=="Apsy"]~TAB$GLY_2017[TAB$Species_Check=="Apsy"])
plot(TAB$GLY[TAB$Species_Check=="Apsy"]~TAB$GLY_2018[TAB$Species_Check=="Apsy"])
plot(TAB$GLY[TAB$Species_Check=="Apsy"]~TAB$GLY_TOT1718[TAB$Species_Check=="Apsy"])
```

```
plot(TAB$GLY[TAB$Species_Check=="Crru"]~TAB$GLY_2017[TAB$Species_Check=="Crru"])
plot(TAB$GLY[TAB$Species_Check=="Crru"]~TAB$GLY_2018[TAB$Species_Check=="Crru"])
plot(TAB$GLY[TAB$Species_Check=="Crru"]~TAB$GLY_TOT1718[TAB$Species_Check=="Crru"])
```

```
plot(TAB$GLY[TAB$Species_Check=="Mygl"]~TAB$GLY_2017[TAB$Species_Check=="Mygl"])
plot(TAB$GLY[TAB$Species_Check=="Mygl"]~TAB$GLY_2018[TAB$Species_Check=="Mygl"])
plot(TAB$GLY[TAB$Species_Check=="Mygl"]~TAB$GLY_TOT1718[TAB$Species_Check=="Mygl"])
```

```
essai2017<-lm(log10(TAB$GLY+1)~TAB$GLY_2017)
essai2018<-lm(log10(TAB$GLY+1)~TAB$GLY_2018)
essaitot<-lm(log10(TAB$GLY+1)~TAB$GLY_TOT1718)
```

```
summary(essai2017)
summary(essai2018)
summary(essaitot)
```



```

par(mfrow=c(1,3))

plot(log10(TAB$GLUF+1)~TAB$GLUF_2017)
plot(log10(TAB$GLUF+1)~TAB$GLUF_2018)
plot(log10(TAB$GLUF+1)~TAB$GLUF_TOT1718)

plot(log10(TAB$GLUF[TAB$Species_Check=="Miar"]+1)~TAB$GLUF_2017[TAB$Species_Check=="Miar"])
plot(log10(TAB$GLUF[TAB$Species_Check=="Miar"]+1)~TAB$GLUF_2018[TAB$Species_Check=="Miar"])
plot(log10(TAB$GLUF[TAB$Species_Check=="Miar"]+1)~TAB$GLUF_TOT1718[TAB$Species_Check=="Miar"])

plot(TAB$GLUF[TAB$Species_Check=="Apsy"]~TAB$GLUF_2017[TAB$Species_Check=="Apsy"])
plot(TAB$GLUF[TAB$Species_Check=="Apsy"]~TAB$GLUF_2018[TAB$Species_Check=="Apsy"])
plot(TAB$GLUF[TAB$Species_Check=="Apsy"]~TAB$GLUF_TOT1718[TAB$Species_Check=="Apsy"])

plot(TAB$GLUF[TAB$Species_Check=="Crru"]~TAB$GLUF_2017[TAB$Species_Check=="Crru"])
plot(TAB$GLUF[TAB$Species_Check=="Crru"]~TAB$GLUF_2018[TAB$Species_Check=="Crru"])
plot(TAB$GLUF[TAB$Species_Check=="Crru"]~TAB$GLUF_TOT1718[TAB$Species_Check=="Crru"])

plot(TAB$GLUF[TAB$Species_Check=="Mygl"]~TAB$GLUF_2017[TAB$Species_Check=="Mygl"])
plot(TAB$GLUF[TAB$Species_Check=="Mygl"]~TAB$GLUF_2018[TAB$Species_Check=="Mygl"])
plot(TAB$GLUF[TAB$Species_Check=="Mygl"]~TAB$GLUF_TOT1718[TAB$Species_Check=="Mygl"])

essai2017<-lm(log10(TAB$GLUF+1)~TAB$GLUF_2017)
essai2018<-lm(log10(TAB$GLUF+1)~TAB$GLUF_2018)
essaitot<-lm(log10(TAB$GLUF+1)~TAB$GLUF_TOT1718)

summary(essai2017)
summary(essai2018)
summary(essaitot)

par(mfrow=c(1,3))

plot(log10(TAB$AMPA+1)~TAB$GLY_2017)
plot(log10(TAB$AMPA+1)~TAB$GLY_2018)
plot(log10(TAB$AMPA+1)~TAB$GLY_TOT1718)

plot(log10(TAB$AMPA[TAB$Species_Check=="Miar"]+1)~TAB$GLY_2017[TAB$Species_Check=="Miar"])
plot(log10(TAB$AMPA[TAB$Species_Check=="Miar"]+1)~TAB$GLY_2018[TAB$Species_Check=="Miar"])
plot(log10(TAB$AMPA[TAB$Species_Check=="Miar"]+1)~TAB$GLY_TOT1718[TAB$Species_Check=="Miar"])

plot(TAB$AMPA[TAB$Species_Check=="Apsy"]~TAB$GLY_2017[TAB$Species_Check=="Apsy"])

```

```

plot(TAB$AMPA[TAB$Species_Check=="Apsy"]~TAB$GLY_2018[TAB$Species_Check=="Apsy"])
plot(TAB$AMPA[TAB$Species_Check=="Apsy"]~TAB$GLY_TOT1718[TAB$Species_Check=="Apsy"])

plot(TAB$AMPA[TAB$Species_Check=="Crru"]~TAB$GLY_2017[TAB$Species_Check=="Crru"])
plot(TAB$AMPA[TAB$Species_Check=="Crru"]~TAB$GLY_2018[TAB$Species_Check=="Crru"])
plot(TAB$AMPA[TAB$Species_Check=="Crru"]~TAB$GLY_TOT1718[TAB$Species_Check=="Crru"])

plot(TAB$AMPA[TAB$Species_Check=="Mygl"]~TAB$GLY_2017[TAB$Species_Check=="Mygl"])
plot(TAB$AMPA[TAB$Species_Check=="Mygl"]~TAB$GLY_2018[TAB$Species_Check=="Mygl"])
plot(TAB$AMPA[TAB$Species_Check=="Mygl"]~TAB$GLY_TOT1718[TAB$Species_Check=="Mygl"])

essai2017<-lm(log10(TAB$AMPA+1)~TAB$GLY_2017)
essai2018<-lm(log10(TAB$AMPA+1)~TAB$GLY_2018)
essaitot<-lm(log10(TAB$AMPA+1)~TAB$GLY_TOT1718)

summary(essai2017)
summary(essai2018)
summary(essaitot)

### ----- tests préliminaires avec ou sans interaction
### GLY

### GLY #####
###----- analyses selmod exploratoires-----

modGLYfull1 <- lm(log(GLY) ~ Species_Check + Habitat + Farming +
gpLandAB2 + GLY_CAT_TOT
+ Species_Check:Habitat + Species_Check:Farming +
Species_Check:gpLandAB2 + Species_Check:GLY_CAT_TOT
+ Habitat:Farming + Habitat:gpLandAB2 +
Habitat:GLY_CAT_TOT
+ Farming:gpLandAB2 + Farming:GLY_CAT_TOT
+ gpLandAB2:GLY_CAT_TOT
, data = TABGLY)

modGLYfull1
summary(modGLYfull1) ### nombreuses modalités NA
anova(modGLYfull1)

### habitat et interaction habitat:farming , espèce et land AB proche
signif
# Multiple R-squared: 0.6919, Adjusted R-squared: 0.3495

modGLYfull2 <- lm(log(GLY) ~ Species_Check + T_NT + gpLandAB2 +
GLY_CAT_TOT
+ Species_Check:T_NT + Species_Check:gpLandAB2 +
Species_Check:GLY_CAT_TOT

```

```

+ T_NT:gpLandAB2 + T_NT:GLY_CAT_TOT
+ gpLandAB2:GLY_CAT_TOT
, data = TABGLY)

modGLYfull12
summary(modGLYfull12) ### nombreuses modalités NA
anova(modGLYfull12)

### tous NS
# Multiple R-squared:  0.2177,    Adjusted R-squared:  -0.4156

modGLYfull10 <- lm(log(GLY) ~ Species_Check + Habitat + Farming +
gpLandAB2 + GLY_CAT_TOT
, data = TABGLY)

modGLYfull10
summary(modGLYfull10)
anova(modGLYfull10) # Habitat significatif
# Multiple R-squared:  0.3379,    Adjusted R-squared:  0.1324

modGLYfull10bis <- lm(log(GLY) ~ Species_Check + T_NT + gpLandAB2 +
GLY_CAT_TOT
, data = TABGLY)

modGLYfull10bis
summary(modGLYfull10bis)
anova(modGLYfull10bis) # tous NS
# Multiple R-squared:  0.1747,    Adjusted R-squared:  -0.01169

Cand.mod<-list(modGLYfull10,modGLYfull10bis,modGLYfull11,modGLYfull12)
Modnames <- c("full hab farming LandAB gly ss inter","full TNT LandAB gly
ss inter",
"full hab farming LandAB gly avec inter", "full TNT LandAB
gly avec inter")
aictab(Cand.mod, Modnames)
#Model selection based on AICc:
##### K    AICc Delta_AICc  AICcWt
Cum.Wt    LL
#full hab farming LandAB gly ss inter    11 157.65      0.00    0.63
0.63 -62.94
#full TNT LandAB gly ss inter            9 158.67      1.02    0.37
1.00 -67.23
#full hab farming LandAB gly avec inter  22 203.29     45.64    0.00
1.00 -48.02
#full TNT LandAB gly avec inter          19 210.38     52.73    0.00
1.00 -66.19

#-----Modèles GLY -----

modGLYSP <- lm(log(GLY) ~ Species_Check , data = TABGLY)
summary(modGLYSP)
anova(modGLYSP)

TABGLY$Species_Check <- relevel(TABGLY$Species_Check, "Miar")

plot(modGLYSP)

TukeyHSD(aov(log(GLY) ~ Species_Check , data = TABGLY)) # ns

```

```

modGLYSPHab <- lm(log(GLY) ~ Species_Check * Habitat , data = TABGLY) #
hab mais pas interaction
modGLYSPHab <- lm(log(GLY) ~ Habitat , data = TABGLY) # ns
modGLYSPHab <- lm(log(GLY) ~ Species_Check + Habitat , data = TABGLY) #
habitat si espèce en premier
summary(modGLYSPHab)
anova(modGLYSPHab)

plot(modGLYSPHab)

### lm(formula = log(GLY) ~ Habitat, data = TABGLY)
#Coefficients:
# Estimate Std. Error t value Pr(>|t|)
#(Intercept)      0.5501      0.4023   1.367   0.180
#HabitatHedgerow  0.5896      0.5025   1.173   0.248

summary(TABGLY$GLY)
par(mfrow=c(2,3))
plot(TABGLY$GLY[TABGLY$Species_Check=="Apsy"]+1 ~
TABGLY$Habitat[TABGLY$Species_Check=="Apsy"],ylim=c(1,550),log="y")
plot(TABGLY$GLY[TABGLY$Species_Check=="Crru"]+1 ~
TABGLY$Habitat[TABGLY$Species_Check=="Crru"],ylim=c(1,550),log="y")
plot(TABGLY$GLY[TABGLY$Species_Check=="Miar"]+1 ~
TABGLY$Habitat[TABGLY$Species_Check=="Miar"],ylim=c(1,550),log="y")
plot(TABGLY$GLY[TABGLY$Species_Check=="Mumu"]+1 ~
TABGLY$Habitat[TABGLY$Species_Check=="Mumu"],ylim=c(1,550),log="y")
plot(TABGLY$GLY[TABGLY$Species_Check=="Mygl"]+1 ~
TABGLY$Habitat[TABGLY$Species_Check=="Mygl"],ylim=c(1,550),log="y")
plot(TABGLY$GLY+1 ~ TABGLY$Habitat,ylim=c(1,550),log="y")

plot(modGLYSP$residuals~TABGLY$Habitat)

modGLYSPFarm <- lm(log(GLY) ~ Species_Check * Farming , data = TABGLY)
### interaction ns, nbx NA
modGLYSPFarm <- lm(log(GLY) ~ Farming , data = TABGLY) # ns
modGLYSPFarm <- lm(log(GLY) ~ Species_Check + Farming , data = TABGLY)
summary(modGLYSPFarm)
anova(modGLYSPFarm)
plot(modGLYSPFarm)

modGLYSPTNT <- lm(log(GLY) ~ Species_Check * T_NT , data = TABGLY) ###
interaction ns, nbx NA
modGLYSPTNT <- lm(log(GLY) ~ T_NT , data = TABGLY) # ns
modGLYSPTNT <- lm(log(GLY) ~ Species_Check + T_NT , data = TABGLY)
summary(modGLYSPTNT)
anova(modGLYSPTNT)
plot(modGLYSPTNT)

modGLYSPLandAB <- lm(log(GLY) ~ Species_Check * gpLandAB2 , data =
TABGLY) ### interaction ns, nbx NA
modGLYSPLandAB <- lm(log(GLY) ~ gpLandAB2 , data = TABGLY) # ns
modGLYSPLandAB <- lm(log(GLY) ~ Species_Check + gpLandAB2 , data =
TABGLY)

```

```

summary(modGLYSPLandAB)
anova(modGLYSPLandAB)
plot(modGLYSPLandAB)

modGLYSP1718 <- lm(log(GLY) ~ Species_Check * GLY_CAT_TOT , data =
TABGLY) ### interaction ns, nbx NA
modGLYSP1718 <- lm(log(GLY) ~ GLY_CAT_TOT , data = TABGLY) # ns
modGLYSP1718 <- lm(log(GLY) ~ Species_Check + GLY_CAT_TOT , data =
TABGLY)
summary(modGLYSP1718)
anova(modGLYSP1718)
plot(modGLYSP1718)

modGLYnull <- lm(log(GLY) ~ 1 , data = TABGLY)
modGLYSP <- lm(log(GLY) ~ Species_Check , data = TABGLY)
modGLYSPHab <- lm(log(GLY) ~ Species_Check + Habitat , data = TABGLY)
modGLYSPFarm <- lm(log(GLY) ~ Species_Check + Farming , data = TABGLY)
modGLYSPTNT <- lm(log(GLY) ~ Species_Check + T_NT , data = TABGLY)
modGLYSPLandAB <- lm(log(GLY) ~ Species_Check + gpLandAB2 , data =
TABGLY)
modGLYSP1718 <- lm(log(GLY) ~ Species_Check + GLY_CAT_TOT , data =
TABGLY)

Cand.mod<-
list(modGLYSP,modGLYSPHab,modGLYSPFarm,modGLYSPTNT,modGLYSPLandAB,modGLYS
P1718,modGLYnull)
Modnames <-
c("modGLYSP","modGLYSPHab","modGLYSPFarm","modGLYSPTNT","modGLYSPLandAB",
"modGLYSP1718","modGLYnull")
aictab(Cand.mod, Modnames)

#           K      AICc Delta_AICc AICcWt Cum.Wt      LL
#modGLYnull      2 146.29      0.00  0.56  0.56 -70.98
#modGLYSPHab      7 147.82      1.53  0.26  0.82 -65.10
#modGLYSP         6 149.68      3.40  0.10  0.92 -67.53
#modGLYSPTNT      7 152.40      6.11  0.03  0.95 -67.39
#modGLYSPLandAB  7 152.49      6.21  0.03  0.97 -67.44
#modGLYSP1718    7 152.55      6.27  0.02  1.00 -67.47
#modGLYSPFarm     8 155.82      9.53  0.00  1.00 -67.51

### AMPA #####
###----- Analyses selmod exploratoires -----

modAMPAfull1 <- lm(log(AMPA) ~ Species_Check + Habitat + Farming +
gpLandAB2 + GLY_CAT_TOT
+ Species_Check:Habitat + Species_Check:Farming +
Species_Check:gpLandAB2 + Species_Check:GLY_CAT_TOT
+ Habitat:Farming + Habitat:gpLandAB2 +
Habitat:GLY_CAT_TOT
+ Farming:gpLandAB2 + Farming:GLY_CAT_TOT
+ gpLandAB2:GLY_CAT_TOT
, data = TABAMPA)

modAMPAfull1
summary(modAMPAfull1) ### nombreuses modalités NA
anova(modAMPAfull1)

### tous NS

```

```

# Multiple R-squared:  0.3623,    Adjusted R-squared:  -0.2754

modAMPFull12 <- lm(log(AMPA) ~ Species_Check + T_NT + gpLandAB2 +
  GLY_CAT_TOT
                + Species_Check:T_NT + Species_Check:gpLandAB2 +
  Species_Check:GLY_CAT_TOT
                + T_NT:gpLandAB2 + T_NT:GLY_CAT_TOT
                + gpLandAB2:GLY_CAT_TOT
                , data = TABAMPA)

modAMPFull12
summary(modAMPFull12) ### nombreuses modalités NA
anova(modAMPFull12)

### tous NS
# Multiple R-squared:  0.348,    Adjusted R-squared:  -0.2225

modAMPFull10 <- lm(log(AMPA) ~ Species_Check + Habitat + Farming +
  gpLandAB2 + GLY_CAT_TOT
                , data = TABAMPA)

modAMPFull10
summary(modAMPFull10)
anova(modAMPFull10) # tous NS
# Multiple R-squared:  Multiple R-squared:  0.2437,    Adjusted R-
squared:  -0.08039

modAMPFull10bis <- lm(log(AMPA) ~ Species_Check + T_NT + gpLandAB2 +
  GLY_CAT_TOT
                    , data = TABAMPA)

modAMPFull10bis
summary(modAMPFull10bis)
anova(modAMPFull10bis) # tous NS
# Multiple R-squared:  0.2223,    Adjusted R-squared:  -0.01444

Cand.mod<-list(modAMPFull10,modAMPFull10bis,modAMPFull11,modAMPFull12)
Modnames <- c("full hab farming LandAB AMPA ss inter","full TNT LandAB
AMPA ss inter",
              "full hab farming LandAB AMPA avec inter", "full TNT LandAB
AMPA avec inter")
aictab(Cand.mod, Modnames)
#Model selection based on AICc:
##
Cum.Wt      LL
#full TNT LandAB AMPA ss inter      9 120.54      0.00  0.99
0.99 -46.99
#full hab farming LandAB AMPA ss inter 11 129.00      8.46  0.01
1.00 -46.55
#full TNT LandAB AMPA avec inter      16 159.36     38.82  0.00
1.00 -44.25
#full hab farming LandAB AMPA avec inter 17 168.89     48.35  0.00
1.00 -43.91

#-----Modèles AMPA -----

modAMPASP <- lm(log(AMPA) ~ Species_Check , data = TABAMPA)
summary(modAMPASP)
anova(modAMPASP)

```

```

TABAMPA$Species_Check <- relevel(TABAMPA$Species_Check, "Miar")

plot(modAMPASP)
TukeyHSD(aov(log(AMPA) ~ Species_Check , data = TABAMPA)) # ns

modAMPASPHab <- lm(log(AMPA) ~ Species_Check * Habitat , data = TABAMPA)
# hab mais pas interaction
modAMPASPHab <- lm(log(AMPA) ~ Habitat , data = TABAMPA) # ns
modAMPASPHab <- lm(log(AMPA) ~ Species_Check + Habitat , data = TABAMPA)
# habitat si espèce en premier
summary(modAMPASPHab)
anova(modAMPASPHab)
plot(modAMPASPHab)

modAMPASPFarm <- lm(log(AMPA) ~ Species_Check * Farming , data = TABAMPA)
### interaction ns, nbx NA
modAMPASPFarm <- lm(log(AMPA) ~ Farming , data = TABAMPA) # ns
modAMPASPFarm <- lm(log(AMPA) ~ Species_Check + Farming , data = TABAMPA)
summary(modAMPASPFarm)
anova(modAMPASPFarm)
plot(modAMPASPFarm)

modAMPASPTNT <- lm(log(AMPA) ~ Species_Check * T_NT , data = TABAMPA)
### interaction ns, nbx NA
modAMPASPTNT <- lm(log(AMPA) ~ T_NT , data = TABAMPA) # ns
modAMPASPTNT <- lm(log(AMPA) ~ Species_Check + T_NT , data = TABAMPA)
summary(modAMPASPTNT)
anova(modAMPASPTNT)
plot(modAMPASPTNT)

modAMPASPLandAB <- lm(log(AMPA) ~ Species_Check * gpLandAB2 , data =
TABAMPA) ### interaction ns, nbx NA
modAMPASPLandAB <- lm(log(AMPA) ~ gpLandAB2 , data = TABAMPA) # ns
modAMPASPLandAB <- lm(log(AMPA) ~ Species_Check + gpLandAB2 , data =
TABAMPA)
summary(modAMPASPLandAB)
anova(modAMPASPLandAB)
plot(modAMPASPLandAB)

modAMPASP1718 <- lm(log(AMPA) ~ Species_Check * GLY_CAT_TOT , data =
TABAMPA) ### interaction ns, nbx NA
modAMPASP1718 <- lm(log(AMPA) ~ GLY_CAT_TOT , data = TABAMPA) # ns
modAMPASP1718 <- lm(log(AMPA) ~ Species_Check + GLY_CAT_TOT , data =
TABAMPA)
summary(modAMPASP1718)
anova(modAMPASP1718)
plot(modAMPASP1718)

modAMPAnull <- lm(log(AMPA) ~ 1 , data = TABAMPA)
modAMPASP <- lm(log(AMPA) ~ Species_Check , data = TABAMPA)
modAMPASPHab <- lm(log(AMPA) ~ Species_Check + Habitat , data = TABAMPA)
modAMPASPFarm <- lm(log(AMPA) ~ Species_Check + Farming , data = TABAMPA)
modAMPASPTNT <- lm(log(AMPA) ~ Species_Check + T_NT , data = TABAMPA)
modAMPASPLandAB <- lm(log(AMPA) ~ Species_Check + gpLandAB2 , data =
TABAMPA)

```

```
modAMPASP1718 <- lm(log(AMPA) ~ Species_Check + GLY_CAT_TOT , data =
TABAMPA)
```

```
Cand.mod<-
```

```
list(modAMPASP,modAMPASPHab,modAMPASPFarm,modAMPASPTNT,modAMPASPLandAB,mo
dAMPASP1718,modAMPAnull)
```

```
Modnames <-
```

```
c("modAMPASP","modAMPASPHab","modAMPASPFarm","modAMPASPTNT","modAMPASPLan
dAB","modAMPASP1718","modAMPAnull")
```

```
aictab(Cand.mod, Modnames)
```

#	K	AICc	Delta_AICc	AICcWt	Cum.Wt	LL
#modAMPAnull	2	106.19	0.00	0.91	0.91	-50.88
#modAMPASP	6	112.38	6.18	0.04	0.95	-48.44
#modAMPASPLandAB	7	114.82	8.63	0.01	0.96	-47.98
#modAMPASPHab	7	114.83	8.64	0.01	0.97	-47.98
#modAMPASPTNT	7	114.83	8.64	0.01	0.99	-47.98
#modAMPASP1718	7	115.02	8.82	0.01	1.00	-48.07
#modAMPASPFarm	8	117.60	11.41	0.00	1.00	-47.53

```
####----- GLUF -----
```

```
###-----Analyses selmod exploratoires -----
```

```
modGLUFfull1 <- lm(log(GLUF) ~ Species_Check + Habitat + Farming +
gpLandAB2 + GLUF_CAT_TOT
+ Species_Check:Habitat + Species_Check:Farming +
Species_Check:gpLandAB2 + Species_Check:GLUF_CAT_TOT
+ Habitat:Farming + Habitat:gpLandAB2 +
Habitat:GLUF_CAT_TOT
+ Farming:gpLandAB2 + Farming:GLUF_CAT_TOT
+ gpLandAB2:GLUF_CAT_TOT
, data = TABGLUF)
```

```
modGLUFfull1
```

```
summary(modGLUFfull1) ### très nombreuses modalités NA
```

```
anova(modGLUFfull1)
```

```
### tous NS
```

```
# Multiple R-squared: 0.4558, Adjusted R-squared: -0.01069
```

```
modGLUFfull2 <- lm(log(GLUF) ~ Species_Check + T_NT + gpLandAB2 +
GLUF_CAT_TOT
```

```
+ Species_Check:T_NT + Species_Check:gpLandAB2 +
Species_Check:GLUF_CAT_TOT
+ T_NT:gpLandAB2 + T_NT:GLUF_CAT_TOT
+ gpLandAB2:GLUF_CAT_TOT
, data = TABGLUF)
```

```
modGLUFfull2
```

```
summary(modGLUFfull2) ### très nombreuses modalités NA
```

```
anova(modGLUFfull2)
```

```
### tous NS
```

```
# Multiple R-squared: 0.4423, Adjusted R-squared: 0.0938
```

```
modGLUFfull0 <- lm(log(GLUF) ~ Species_Check + Habitat + Farming +
gpLandAB2 + GLUF_CAT_TOT
```



```

, data = TABGLUF)
modGLUFfull0
summary(modGLUFfull0)
anova(modGLUFfull0) # tous NS
# Multiple R-squared: 0.3754, Adjusted R-squared: 0.04476

modGLUFfull0bis <- lm(log(GLUF) ~ Species_Check + T_NT + gpLandAB2 +
GLUF_CAT_TOT
, data = TABGLUF)
modGLUFfull0bis
summary(modGLUFfull0bis)
anova(modGLUFfull0bis) # tous NS mais landAB proche signif
# Multiple R-squared: 0.3585, Adjusted R-squared: 0.1222

Cand.mod<-list(modGLUFfull0,modGLUFfull0bis,modGLUFfull1,modGLUFfull2)
Modnames <- c("full hab farming LandAB GLUF ss inter","full TNT LandAB
GLUF ss inter",
"full hab farming LandAB GLUF avec inter", "full TNT LandAB
GLUF avec inter")
aictab(Cand.mod, Modnames)
#Model selection based on AICc:
##### K AICc Delta_AICc AICcWt
Cum.Wt LL
#full TNT LandAB GLUF ss inter 9 84.41 0.00 0.99
0.99 -27.91
#full hab farming LandAB GLUF ss inter 11 94.71 10.29 0.01
1.00 -27.55
#full TNT LandAB GLUF avec inter 12 98.33 13.92 0.00
1.00 -26.02
#full hab farming LandAB GLUF avec inter 14 114.39 29.97 0.00
1.00 -25.69

#-----Modèles GLUF -----

modGLUFSP <- lm(log(GLUF) ~ Species_Check , data = TABGLUF)
summary(modGLUFSP)
anova(modGLUFSP)
plot(modGLUFSP)

TABGLUF$Species_Check <- relevel(TABGLUF$Species_Check, "Miar")

TukeyHSD(aov(log(GLUF) ~ Species_Check , data = TABGLUF)) # ns

modGLUFSPHab <- lm(log(GLUF) ~ Species_Check * Habitat , data = TABGLUF)
# ns mais hab et interaction proche
modGLUFSPHab <- lm(log(GLUF) ~ Habitat , data = TABGLUF) # signif
modGLUFSPHab <- lm(log(GLUF) ~ Species_Check + Habitat , data = TABGLUF)
# habitat pas signif si espèce en premier
summary(modGLUFSPHab)
anova(modGLUFSPHab)
plot(modGLUFSPHab)

#lm(formula = log(GLUF) ~ Habitat, data = TABGLUF)
#Coefficients:
# Estimate Std. Error t value Pr(>|t|)
#(Intercept) 1.8736 0.2653 7.062 2.11e-07 ***
# HabitatHedgerow -0.7793 0.3250 -2.398 0.0243 *

```

```

modGLUFSPFarm <- lm(log(GLUF) ~ Species_Check * Farming , data = TABGLUF)
### interaction ns, nbx NA
modGLUFSPFarm <- lm(log(GLUF) ~ Farming , data = TABGLUF) # ns
modGLUFSPFarm <- lm(log(GLUF) ~ Species_Check + Farming , data = TABGLUF)
summary(modGLUFSPFarm)
anova(modGLUFSPFarm)
plot(modGLUFSPFarm)

modGLUFSPNTNT <- lm(log(GLUF) ~ Species_Check * T_NT , data = TABGLUF)
### i # ns mais TNT et interaction proche
modGLUFSPNTNT <- lm(log(GLUF) ~ T_NT , data = TABGLUF) # proche signif
modGLUFSPNTNT <- lm(log(GLUF) ~ Species_Check + T_NT , data = TABGLUF)
summary(modGLUFSPNTNT)
anova(modGLUFSPNTNT)
plot(modGLUFSPNTNT)

#lm(formula = log(GLUF) ~ T_NT, data = TABGLUF)
#Coefficients:
#             Estimate Std. Error t value Pr(>|t|)
# (Intercept)  1.1566      0.1891   6.117 2.15e-06 ***
#   T_NT      0.6666      0.3474   1.919  0.0665 .

modGLUFSPLandAB <- lm(log(GLUF) ~ Species_Check * gpLandAB2 , data =
TABGLUF) ### interaction ns, landAB proche, nbx NA
modGLUFSPLandAB <- lm(log(GLUF) ~ gpLandAB2 , data = TABGLUF) #
significatif
modGLUFSPLandAB <- lm(log(GLUF) ~ Species_Check + gpLandAB2 , data =
TABGLUF)
summary(modGLUFSPLandAB)
anova(modGLUFSPLandAB)
plot(modGLUFSPLandAB)

# lm(formula = log(GLUF) ~ gpLandAB2, data = TABGLUF)
#Coefficients:
#             Estimate Std. Error t value Pr(>|t|)
# (Intercept)  1.0971      0.1792   6.123 2.12e-06 ***
# gpLandAB240-80  0.8675      0.3291   2.636  0.0142 *

modGLUFSP1718 <- lm(log(GLUF) ~ Species_Check * GLUF_CAT_TOT , data =
TABGLUF) ### interaction ns, nbx NA
modGLUFSP1718 <- lm(log(GLUF) ~ GLUF_CAT_TOT , data = TABGLUF) # ns
modGLUFSP1718 <- lm(log(GLUF) ~ Species_Check + GLUF_CAT_TOT , data =
TABGLUF)
summary(modGLUFSP1718)
anova(modGLUFSP1718)
plot(modGLUFSP1718)

modGLUFnull <- lm(log(GLUF) ~ 1 , data = TABGLUF)
modGLUFSP <- lm(log(GLUF) ~ Species_Check , data = TABGLUF)
modGLUFSPHab <- lm(log(GLUF) ~ Species_Check + Habitat , data = TABGLUF)
modGLUFSPHabseul <- lm(log(GLUF) ~ Habitat , data = TABGLUF)
modGLUFSPFarm <- lm(log(GLUF) ~ Species_Check + Farming , data = TABGLUF)
modGLUFSPNTNT <- lm(log(GLUF) ~ Species_Check + T_NT , data = TABGLUF)
modGLUFSPLandAB <- lm(log(GLUF) ~ Species_Check + gpLandAB2 , data =
TABGLUF)
modGLUFSPLandABseul <- lm(log(GLUF) ~ gpLandAB2 , data = TABGLUF)
modGLUFSP1718 <- lm(log(GLUF) ~ Species_Check + GLUF_CAT_TOT , data =
TABGLUF)

```

```

Cand.mod<-
list(modGLUFSP,modGLUFSPHab,modGLUFSPHabseul,modGLUFSPFarm,modGLUFSPPTNT
,modGLUFSPLandAB,modGLUFSPLandABseul,modGLUFSP1718,modGLUFnull)
Modnames <-
c("modGLUFSP","modGLUFSPHab","modGLUFSPHabseul","modGLUFSPFarm","modGLUFSP
PTNT"
,"modGLUFSPLandAB","modGLUFSPLandABseul","modGLUFSP1718","modGLUFnull")
aictab(Cand.mod, Modnames)

```

#	K	AICc	Delta_AICc	AICcWt	Cum.Wt	LL
#modGLUFSPLandABseul	3	68.24	0.00	0.57	0.57	-30.60
#modGLUFSPHabseul	3	69.27	1.03	0.34	0.92	-31.11
#modGLUFnull	2	72.31	4.08	0.07	0.99	-33.91
#modGLUFSPLandAB	7	79.05	10.82	0.00	0.99	-29.58
#modGLUFSP	6	79.47	11.23	0.00	1.00	-31.64
#modGLUFSPHab	7	79.83	11.60	0.00	1.00	-29.97
#modGLUFSPPTNT	7	79.83	11.60	0.00	1.00	-29.97
#modGLUFSP1718	7	82.05	13.81	0.00	1.00	-31.08
#modGLUFSPFarm	8	87.04	18.80	0.00	1.00	-31.52