

## Agressivité en fonction de l'âge

```
{r setup, include=FALSE} knitr::opts_chunk$set(echo = TRUE)
```

### R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
{r cars} summary(cars)
```

### Including Plots

You can also embed plots, for example:

```
{r pressure, echo=FALSE} plot(pressure)
```

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

```
if (!require("pacman")) install.packages("pacman") pacman::p_load(ade4, Hmisc, tidyverse, data.table, lubridate, kableExtra, corrplot, PerformanceAnalytics, factoextra, FactoMineR, ggpubr, png, knitr)
```

```
library(tidyverse) library(data.table) library(lubridate) library(kableExtra) library(corrplot) library(PerformanceAnalytics) library(factoextra) library(FactoMineR) library(ggpubr) library(ggplot2) library(png) library(knitr) library(car) library(lme4) library(nlme) library(bestNormalize) library(sjstats) library(sjPlot) library(sjmisc) library(sjlabelled)
```

```
setwd("C:/Users/boule/OneDrive/Bureau/Mémoire/Stat mémoire")
```

```
allData <- fread("ComportementsansS21.csv", header = T, dec=",")
```

```
allData <- rename(allData, c("Temp"="Température", "Sal"="µS", "Zeloign"="Zéloignée", "LFB"="LatencetoFirstBite"))
```

```
allData View(allData) summary(allData) str(allData)
```

```
allData$`Fishnumber`=as.factor(allData$Fishnumber) allData$timepoint =  
as.factor(allData$timepoint) allData$`Bite`=as.numeric(allData$Bite)  
allData$`Sal`=as.numeric(allData$Sal) allData$`Zproche`=as.numeric(allData$Zproche)  
allData$`Zinterm`=as.numeric(allData$Zinterm)  
allData$`Zeloign`=as.numeric(allData$Zeloign)
```

```

allData$`Zrefuge`=as.numeric(allData$Zrefuge)
allData$`Taille`=as.numeric(allData$Taille)

allData <- na.omit(allData) #delete the rows with NA in all the columns

#change Distmov in relative Distmov allData <- mutate(allData,
RTDM=Distmov/Taille)#add a new column with a calculation

#Test correlation and PCA between all response variables (behavior)

allData <- mutate(allData, PZproche=Zproche/(Zproche+Zinterm+Zeloign+Zrefuge))
allData <- mutate(allData, PZinterm=Zinterm/(Zproche+Zinterm+Zeloign+Zrefuge)) allData
<- mutate(allData, PZeloign=Zeloign/(Zproche+Zinterm+Zeloign+Zrefuge)) allData <-
mutate(allData, PZrefuge=Zrefuge/(Zproche+Zinterm+Zeloign+Zrefuge))

test1 <- allData[,c("RTDM", "Velocity max", "Bite", "PZproche", "PZinterm", "PZeloign",
"PZrefuge", "LFB")] #subset only the columns of interest for response var

correlation <- rcorr(as.matrix(test1), type = "spearman")

corrplot(correlation$r, type="upper", order="hclust", p.mat=correlation$P, sig.level=0.01,
insig="blank", tl.cex=0.7 ,tl.col="black",tl.srt=45)

acp <- dudi.pca(df = test1, center = TRUE, scale = TRUE, scannf = FALSE, nf=3) varcont <-
fviz_pca_var(acp, col.var = "contrib", # Color by the contribution gradient.cols =
c("#00AFBB", "#E7B800", "#FC4E07"), repel = T,# Avoid text overlapping ) varcont

res.var <- get_pca_var(acp) varcoord <- res.var$coord # Coordinates varcontrib <-
res.var$contrib varcontrib corrplotvar <- corrplot(res.var$contrib, is.corr=F, sig.level=0.01,
tl.cex=0.7)

chart.Correlation(as.matrix(test1[,1:8]), histogram = T,pch=19) # LFB and bite are not
correlated ! 2 different features for aggressivity > analyse both ; but thy are opposite in PCA
# > I would take RTDM, Bite, PZeloign, LFB to analyse

```

## Search for correlations between all explanatory variables

```

test2 <- allData[,c("timepoint", "Sal", "Temp", "Taille")] #subset only the columns of interest
test2

correlation2 <- rcorr(as.matrix(test2[,2:4]), type = "spearman") correlation2

chart.Correlation(as.matrix(test2[,2:4]), histogram = T,pch=19)

ggplot(test2) + aes(x = timepoint, y = Taille) + geom_boxplot(shape = "circle", fill =
"#112446") + theme_minimal()

ggplot(test2) + aes(x = timepoint, y = Temp) + geom_boxplot(shape = "circle", fill =
"#112446") + theme_minimal()

```

```
ggplot(test2) + aes(x = timepoint, y = Sal) + geom_boxplot(shape = "circle", fill = "#112446")
+ theme_minimal()
```

## Temp is much lower at S17

## Taille et timepoint sont corrélés > ne garder que timepoint

### > timepoint, Temp, Sal

#### search for extreme values

```
test3 <- allData[,c("RTDM", "PZeloign", "Bite", "LFB", "Sal", "Temp", "timepoint",
"Fishnumber")] #subset only the columns of interest
```

```
dotchart(test3$RTDM, main="RTDM") # > il y a des valeurs extrêmes > check si c'est
correct ; should be discussed dotchart(test3$PZeloign, main="PZeloign") # ok
dotchart(test3$Bite, main="Bite") # ok dotchart(test3$LFB, main="LFB") # few extreme
values to be checked
```

#### variables transformation

```
hist(test3$RTDM) # normal shapiro.test(test3$RTDM)
```

```
hist(test3$PZeloign) # normality ok shapiro.test(test3$PZeloign)
```

```
bestNormalize(allData$Zeloign) # > orderNorm PZeloign <- orderNorm(test3$PZeloign) x2
<- predict(test3$PZeloign) test3$PZeloign <- x2
```

```
hist(test3$PZeloign) shapiro.test(test3$PZeloign) # ok
```

```
hist(test3$LFB) # normality not ok hist(test3$Bite) # Poisson car comptage
```

```
hist(test3$Sal) # normality not ok hist(test3$Temp) # normality not ok
shapiro.test(test3$Temp)
```

```
library(bestNormalize)
```

```
bestNormalize(test3$LFB) # > log10 test3$LFB <- log10(test3$LFB) x2 <-
predict(LFB) test3$LFB <- x2 hist(test3$LFB) #ok shapiro.test(test3$LFB)
```

```
bestNormalize(test3$Sal) # > ordernorm Sal <- orderNorm(test3$Sal) x2 <- predict(Sal)
test3$Sal <- x2 hist(test3$Sal) shapiro.test(test3$Sal) # ok
```

```
bestNormalize(test3$Temp) # > log10 test3$Temp <- log10(test3$Temp) x2 <-
predict(Temp) test3$Temp <- x2 hist(test3$Temp) #ok shapiro.test(test3$Temp)
```

test3

```
#1Â° RTDM !!!! we must work with relative distmov to distinguish effect of size and of age #  
Build the beyond model M1 <-  
lmer(RTDM~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, REML=T) summary(M1) Anova(M1) ranova(M1) # it's to check the random  
effect with the likelihood ratio test ; if the random variable is significant, it means that the  
model is worse without the random effect > keep the random effect.
```

## test for the best random structure with nlme > we don't have enough data to do that

```
M1 <- lme(RTDMtimepoint+Temp+Sal+Temp:timepoint+Sal:timepoint,random=1|Fishnumber, data=test3,  
method="REML") M12 <-  
lme(RTDMtimepoint+Temp+Sal+Temp:timepoint+Sal:timepoint,random=1+timepoint|Fishnumber, data=test3,  
method="REML") # best AIC(M1, M12) # keep M1: not enough observations to support  
M12
```

## test for the best fixed effects

```
M1 <- lmer(RTDM~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, REML=F) Anova(M1) M2 <-  
lmer(RTDM~timepoint+Temp+Sal+Temp:timepoint+(1|Fishnumber), data=test3, REML=F)  
Anova(M2) M3 <- lmer(RTDM~timepoint+Temp+Sal+(1|Fishnumber), data=test3,  
REML=F) Anova(M3) M4 <- lmer(RTDM~timepoint+Temp+(1|Fishnumber), data=test3,  
REML=F) Anova(M4) M5 <- lmer(RTDM~timepoint+(1|Fishnumber), data=test3, REML=F)  
Anova(M5) M6 <- lmer(RTDM~(1|Fishnumber), data=test3, REML=F)  
  
anova(M6,M5,M4,M3,M2,M1)  
  
#Best model M4 M5 <- lmer(RTDM~timepoint+(1|Fishnumber), data=test3, REML=T)  
Anova(M5) summary(M5) ranova(M5)  
  
tab <- tab_model(M5, p.val="kr", show.df=T, show.reflvl=T, p.style="stars") tab  
  
ggplot(data = test3, aes(x = timepoint, y = RTDM)) + stat_boxplot(geom = "errorbar", #  
Boxplot with error bars width = 0.2) + geom_boxplot(fill = "#4271AE", colour = "#1F3552",  
# Colors alpha = 0.9, outlier.colour = "red") + ggtitle("Distance parcourue relative en  
fonction de l'âge") + geom_jitter(alpha = 0.25, width = 0.2) + theme(axis.line =  
element_line(colour = "black", # Theme customization size = 0.25))  
  
library(emmeans) emmeans(M5, list(pairwise ~ timepoint), adjust = "Tukey")  
  
#S13 differences et S09 et S21
```

## Model validation

```
plot(resid(M5)~fitted(M5), xlab="Predicted values", ylab="Normalized residuals")+  
abline(h=0, lty=2)
```

```
op <- par(mfrow=c(1,3), mar=c(4,4,.5,.5)) plot(resid(M5)~test3$timepoint,  
xlab="Timepoint", ylab="Normalized residuals")+ abline(h=0, lty=2)  
plot(resid(M5)~test3$Temp, xlab="Temp", ylab="Normalized residuals")+ abline(h=0,  
lty=2) plot(resid(M5)~test3$Sal, xlab="Sal", ylab="Normalized residuals")+ abline(h=0,  
lty=2)
```

```
hist(resid(M5)) par(op)
```

```
#Calculate conditional (adjusted) repeatability for each population #https://cran.r-project.org/web/packages/rptR/vignettes/rptR.html library(rptR) rpt <-  
rpt(RTDM~timepoint+(1|Fishnumber),grname=c("Fishnumber", "Fixed"), data= test3,  
datatype="Gaussian", nboot=1000, npermut=0) print(rpt) # > R de 0.339 pour RTDM  
(p=0.000412 ) > the R is significant > fish are different to each other compared to replicate  
of the same fish, here the age effect
```

```
#2Â° LFB
```

## Build the beyond model

```
M3B <- lmer(LFB~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, REML=T) summary(M3B) Anova(M3B) # > Temp Sal, timepoint effect  
ranova(M3B) # it's to check the random effect with the likelihood ratio test ; if the random  
variable is significant, it means that the model is worse without the random effect > keep  
the random effect.
```

## test for the best random structure with nlme > we don't have enough data to do that

```
M3B <- lme(LFBtimepoint+Temp+Sal+Temp:timepoint+Sal:timepoint,random=1|Fishnumber, data=test3,  
method="REML") M32B <-  
lme(LFBtimepoint+Temp+Sal+Temp:timepoint+Sal:timepoint,random=1+timepoint|Fishnumber, data=test3,  
method="REML") AIC(M3B, M32B) # keep M3b
```

## test for the best fixed effects

```
M3B <- lmer(LFB~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, REML=T) Anova(M3B) M31B <-  
lmer(LFB~timepoint+Temp+Sal+Temp:timepoint+(1|Fishnumber), data=test3, REML=T)  
Anova(M31B) M32B <- lmer(LFB~timepoint+Temp+Sal+(1|Fishnumber), data=test3,  
REML=T) Anova(M32B) M33B <- lmer(LFB~timepoint+Temp+(1|Fishnumber), data=test3,
```

```
REML=T) Anova(M33B) M34B <- lmer(LFB~timepoint+(1|Fishnumber), data=test3,
REML=T) Anova(M34B) M35B <- lmer(LFB~(1|Fishnumber), data=test3, REML=T)
```

```
anova(M35B,M34B,M33B,M32B,M31B,M3B)
```

```
M34B <- lmer(LFB~timepoint+(1|Fishnumber), data=test3, REML=T) Anova(M34B)
summary(M34B) ranova(M34B)
```

```
tab <- tab_model(M34B, p.val="kr", show.df=T, show.reflvl=T, p.style="stars") tab
```

```
ggplot(data = test3, aes(x = timepoint, y = LFB)) + stat_boxplot(geom = "errorbar", #
Boxplot with error bars width = 0.2) + geom_boxplot(fill = "#4271AE", colour = "#1F3552",
# Colors alpha = 0.9, outlier.colour = "red") + ggtitle("Latence avant la première morsure en
fonction de l'âge") + geom_jitter(alpha = 0.25, width = 0.2) + theme(axis.line =
element_line(colour = "black", # Theme customization size = 0.25))
```

```
library(emmeans) emmeans(M34B, list(pairwise ~ timepoint), adjust = "Tukey")
```

```
ggplot(test3) + aes(x = timepoint, y = LFB) + ggtitle("Latence de la première morsure en
fonction de l'Age") + geom_point(shape = "circle", size = 3L, colour = "#112446") +
theme_minimal()
```

## Model validation

```
plot(resid(M34B)~fitted(M34B), xlab="Predicted values", ylab="Normalized residuals")+
abline(h=0, lty=2)
```

```
op2 <- par(mfrow=c(1,3), mar=c(4,4,.5,.5)) plot(resid(M34B)~test3$timepoint,
xlab="Timepoint", ylab="Normalized residuals")+ abline(h=0, lty=2)
plot(resid(M34B)~test3$Temp, xlab="Temp", ylab="Normalized residuals")+ abline(h=0,
lty=2) plot(resid(M34B)~test3$Sal, xlab="Sal", ylab="Normalized residuals")+ abline(h=0,
lty=2)
```

```
hist(resid(M34B)) par(op2)
```

```
rpt3 <- rpt(LFB~timepoint+(1|Fishnumber),grname=c("Fishnumber"), data= test3,
datatype="Gaussian", nboot=1000, npermut=0) print(rpt3) #0.019 avec p val de 0.037
```

```
ggplot(test3) + aes(x = timepoint, y = LFB) + ggtitle("Latence de la première morsure en
fonction de l'Age") + geom_point(shape = "circle", size = 3L, colour = "#112446") +
theme_minimal()
```

```
#3Â° Bite (GLMM)
```

```
str(test3)
```

```
ggplot(test3) + aes(x = timepoint, y = Bite) + geom_boxplot(shape = "circle", fill = "red") +
theme_minimal()
```

```
dotchart(test1$Bite, main="Number of attack", group=test1$timepoint, ylab = "timepoint")
```

```
hist(test1$Bite, xlab = "Number of attack", main = "Histogram of attack")
```

```
M21 <- glmer(Bite~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, family="poisson") Anova(M21) M22 <-  
glmer(Bite~timepoint+Temp+Sal+Temp:timepoint+(1|Fishnumber), data=test3,  
family="poisson") Anova(M22) M23 <- glmer(Bite~timepoint+Temp+Sal+(1|Fishnumber),  
data=test3, family="poisson") Anova(M23) M24 <-  
glmer(Bite~timepoint+Temp+(1|Fishnumber), data=test3, family="poisson") Anova(M24)  
M25 <- glmer(Bite~timepoint+(1|Fishnumber), data=test3, family="poisson") Anova(M25)  
M26 <- glmer(Bite~(1|Fishnumber), data=test3, family="poisson") Anova(M26)  
  
anova(M26,M25,M24,M23,M22,M21)
```

## timepoint effect

```
ggplot(test3) + aes(x = timepoint, y = Bite) + geom_boxplot(shape = "circle", fill = "red") +  
theme_minimal()
```

## Temp and Sal effects

```
ggplot(test3) + aes(x = Temp, y = Bite) + geom_point(shape = "circle", size = 1.5, colour =  
"#112446") + theme_minimal()
```

```
ggplot(test3) + aes(x = Sal, y = Bite) + geom_point(shape = "circle", size = 1.5, colour =  
"#112446") + theme_minimal()
```

## validation: check for overdispersion

```
install.packages("devtools") library("devtools")
```

```
install_github("markushuff/PsychHelperFunctions") library(PsychHelperFunctions)  
overdisp_fun(M22) # overdispersion
```

#if overdispersion > quasipoisson (not for GLMM) or negative binomial

```
mnb1 <-  
glmer.nb(Bite~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, control=glmerControl(optimizer="bobyqa")) overdisp_fun(mnb1) # no  
overdispersion anymore
```

```
summary(mnb1) Anova(mnb1)
```

```
mnb1 <-  
glmer.nb(Bite~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, control=glmerControl(optimizer="bobyqa")) Anova(mnb1) mnb11 <-  
glmer.nb(Bite~timepoint+Temp+Sal+Temp:timepoint+(1|Fishnumber), data=test3,
```

```
control=glmerControl(optimizer="bobyqa")) Anova(mnb11) mnb12 <-
glmer.nb(Bite~timepoint+Temp+Sal+(1|Fishnumber), data=test3,
control=glmerControl(optimizer="bobyqa")) Anova(mnb12) mnb13 <-
glmer.nb(Bite~timepoint+Temp+(1|Fishnumber), data=test3,
control=glmerControl(optimizer="bobyqa")) Anova(mnb13) mnb14 <-
glmer.nb(Bite~timepoint+(1|Fishnumber), data=test3,
control=glmerControl(optimizer="bobyqa")) Anova(mnb14) mnb15 <-
glmer.nb(Bite~(1|Fishnumber), data=test3, control=glmerControl(optimizer="bobyqa"))
anova(mnb15,mnb14,mnb13,mnb12,mnb11,mnb1)
```

## > best= mnb14 > timepoint effect

```
mnb14 <- glmer.nb(Bite~timepoint+(1|Fishnumber), data=test3,
control=glmerControl(optimizer="bobyqa")) overdisp_fun(mnb14) summary(mnb14)
Anova(mnb14)
```

**there's only a timepoint effect: S13 is higher (and weakly S17) > fish are more aggressive at S13 (and maybe S17) > age effect**

## timepoint effect

```
ggplot(test3) + aes(x = timepoint, y = Bite) + geom_boxplot(shape = "circle", fill = "red") +
theme_minimal() library(dunn.test) Bite1 <-
as.vector(test3Bite)dunn.test(Bite1, test3timepoint)
```

## Model validation

```
plot(resid(mnb14)~fitted(mnb14), xlab="Predicted values", ylab="Normalized residuals")+
abline(h=0, lty=2)
```

```
op2 <- par(mfrow=c(1,3), mar=c(4,4,.5,.5)) plot(resid(mnb14)~test3$timepoint,
xlab="Timepoint", ylab="Normalized residuals")+ abline(h=0, lty=2)
plot(resid(mnb14)~test3$Temp, xlab="Temp", ylab="Normalized residuals")+ abline(h=0,
lty=2) plot(resid(mnb14)~test3$Sal, xlab="Sal", ylab="Normalized residuals")+ abline(h=0,
lty=2)
```

```
hist(resid(mnb14)) par(op2)
```

```
rpt4 <- rpt(Bite~timepoint+(1|Fishnumber),grname=c("Fishnumber", "Fixed"), data= test3,
datatype="Poisson", nboot=1000, npermut=0) print(rpt4) # R 0.147 (p=0.0636) > there is
no individuality for Bite > variability is higher within fish (depending on age)
```

```
#4 Zeloign
```

## Build the beyond model

```
M5A <-  
lmer(PZeloign~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, REML=T) summary(M5A) Anova(M5A) ranova(M5A) # it's to check the random  
effect with the likelihood ratio test ; if the random variable is significant, it means that the  
model is worse without the random effect > keep the random effect.
```

## test for the best random structure with nlme > we don't have enough data to do that

```
M5A <- lme(PZeloign~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint,random=1|Fishnumber, data=test3,  
method="REML") M55A <-  
lme(PZeloign~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint,random=1+timepoint|Fishnumber,  
data=test3, method="REML") # best AIC(M5A, M55A) # keep M2
```

## test for the best fixed effects

```
M5A <-  
lmer(PZeloign~timepoint+Temp+Sal+Temp:timepoint+Sal:timepoint+(1|Fishnumber),  
data=test3, REML=F) Anova(M5A) M6A <-  
lmer(PZeloign~timepoint+Temp+Sal+Temp:timepoint+(1|Fishnumber), data=test3,  
REML=F) Anova(M6A) M7A <- lmer(PZeloign~timepoint+Temp+Sal+(1|Fishnumber),  
data=test3, REML=F) Anova(M7A) M8A <-  
lmer(PZeloign~timepoint+Temp+(1|Fishnumber), data=test3, REML=F) Anova(M8A) M9A  
<- lmer(PZeloign~timepoint+(1|Fishnumber), data=test3, REML=F) Anova(M9A) M10A <-  
lmer(PZeloign~(1|Fishnumber), data=test3, REML=F)
```

```
anova(M10A,M9A,M8A,M7A,M6A,M5A)
```

```
M7A <- lmer(PZeloign~timepoint+Temp+Sal+(1|Fishnumber), data=test3, REML=T)  
summary(M7A) ranova(M7A)
```

```
ggplot(test3) + aes(x = timepoint, y = PZeloign) + geom_point(shape = "circle", fill = "red") +  
theme_minimal()
```

```
ggplot(test3) + aes(x = timepoint, y = Sal) + geom_point(shape = "circle", fill = "red") +  
theme_minimal()
```

```
ggplot(test3) + aes(x = timepoint, y = Temp) + geom_point(shape = "circle", fill = "red") +  
theme_minimal()
```

```
ggplot(data = test3, aes(x = timepoint, y = PZeloign)) + stat_boxplot(geom = "errorbar", #  
Boxplot with error bars width = 0.2) + geom_boxplot(fill = "#4271AE", colour = "#1F3552",  
# Colors alpha = 0.9, outlier.colour = "red") + ggtitle("Latence avant la première morsure en
```

```
fonction de l'âge") +geom_jitter(alpha = 0.25, width = 0.2)+ theme(axis.line =
element_line(colour = "black", # Theme customization size = 0.25))
```

```
tab5 <- tab_model(M7A, p.val="kr", show.df=T, show.refl=1=T, p.style="stars") tab5
Anova(M7A) emmeans(M7A, list(pairwise ~ timepoint), adjust = "Tukey")
```

## Model validation

```
plot(resid(M6A)~fitted(M6A), xlab="Predicted values", ylab="Normalized residuals")+
abline(h=0, lty=2)
```

```
op2 <- par(mfrow=c(1,3), mar=c(4,4,.5,.5)) plot(resid(M6A)~test3$timepoint,
xlab="Timepoint", ylab="Normalized residuals")+ abline(h=0, lty=2)
plot(resid(M6A)~test3$Temp, xlab="Temp", ylab="Normalized residuals")+ abline(h=0,
lty=2) plot(resid(M6A)~test3$Sal, xlab="Sal", ylab="Normalized residuals")+ abline(h=0,
lty=2)
```

```
hist(resid(M6A)) par(op2)
```

## >Temp et timepoint effect

```
rpt5 <- rpt(PZeloign~timepoint+Temp+Sal+(1|Fishnumber),grname=c("Fishnumber"),
data= test3, datatype="Gaussian", nboot=1000, npermut=0) print(rpt5) #R de 0.235 avec p
valeur de 0.00785 the R is weakly significant > fish are a bit different each other compared
to replicate of the same fish, here no age effect and a temp effect
```

### Summary

```
#RTDM M5 <- lmer(RTDM~timepoint+(1|Fishnumber), data=test3, REML=T) # RTDM
increases at S13 : higher than other weeks and also S09-S21 difference > effect of age on
activity # R de 0.339 pour RTDM (p=0.000412 ) > the R is significant > fish are different to
each other compared to replicate of the same fish, here the age effect
```

```
#Zeloign M7A <- lmer(PZeloign~timepoint+Temp+Sal+(1|Fishnumber), data=test3,
REML=T) # Temp et timepoint effect but no timepoint effect after contrast #R de 0.235 avec
p valeur de 0.00785 the R is weakly significant > fish are a bit different each other
compared to replicate of the same fish, here age effect and a temp effect
```

```
#LFB M34B <- lmer(LFB~timepoint+(1|Fishnumber), data=test3, REML=T) # No age effect
# 0.019 avec p val de 0.037 > there is no individuality for LFB > variability is higher within
fish depending not on age
```

```
#Bite mnb14 <- glmer.nb(Bite~timepoint+(1|Fishnumber), data=test3,
control=glmerControl(optimizer="bobyqa")) # there's only a timepoint effect: S13 is higher
(and weakly S17) > fish are more aggressive at S13 (and maybe S17) > age effect # R 0.147
(p=0.0636) > there is no individuality for Bite > variability is higher within fish (depending
on age)
```

Age effect at S13 (and S17) > fish are more active and aggressive (Bite)  
; then it's decreasing with age

> LFB and Bite should be considered different parameters for  
aggressivity

There is individuality for RTDM , but not for BITE and LFB > not a  
personality trait here