**Social foraging between Little Egrets (*Egretta garzetta*) and Crested Ibises (*Nipponia nippon*)**

**Electronic Supplementary Materials**

**Appendix S1 - R Code of the statistical analyses.**

library (afex)

library (lme4)

library(lmerTest)

library (emmeans)

library (tidyverse)

library (ggpubr)

library(mvtnorm)

library(survival)

library(dplyr)

library(MASS)

library(TH.data)

library (multcomp)

library(ggplot2)

library (ggbeeswarm)

library(Rcpp)

library (summarytools)

library (interactions)

library (jtools)

library(descr)

rm(list = ls ())

setwd("D:/xxx")

flock <- read.csv("vigilancedata.csv", na.strings = c("","NA"), header=TRUE)

str(flock)

flock$Habitats <- as.factor(flock$Habitats)

flock$Group\_types <- as.factor(flock$Group\_types)

flock$year <- as.factor(flock$year)

flock$day\_of\_study <- as.factor(flock$day\_of\_study)

flock$period <- as.factor(flock$period)

flock$location <- as.factor(flock$location)

#we check for the types of variables

str(flock)

set\_sum\_contrasts()

###### proportion scanning

propscan <- mixed(proportion\_scan ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(propscan$full\_model)

# normality of the residuals

qqnorm(residuals(propscan$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, arc\_proportion\_scan = asin(sqrt(proportion\_scan)))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$proportion\_scan, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$arc\_proportion\_scan, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# new model with transformed variables

propscant1 <- mixed(arc\_proportion\_scan ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

anova(propscant1)

#checking assumptions

# homogeneity of variance

plot(propscant1$full\_model)

# normality of the residuals

qqnorm(residuals(propscant1$full\_model))

# assumptions fitting improved, so we keep this model

# plotting the significant effect

interact\_plot(propscant1$full\_model, pred = Total\_number\_birds, modx = Group\_types, plot.points = TRUE, interval = TRUE, int.width = 0.95,

line.thickness = 1, x.label = "Flock size",

y.label = "Proportion time vigilant (arcsin)", modx.labels = c("single-species", "mixed-species"), legend.main = "Flock type") +

theme\_apa(legend.pos = "topmiddle") +

theme (axis.title.y = element\_text(size=16), axis.text.y = element\_text(size=13),

axis.title.x = element\_text(size=16), axis.text.x = element\_text(size=13),

legend.title = element\_text(size=14), legend.text = element\_text(size=14))

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(propscant1, "Group\_types")

emm\_gt

emm\_h <- emmeans(propscant1, "Habitats")

emm\_h

######proportion\_foraging

propfor <- mixed(proportion\_foraging ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(propfor$full\_model)

# normality of the residuals

qqnorm(residuals(propfor$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, arc\_proportion\_for = asin(sqrt(proportion\_foraging)))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$proportion\_foraging, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$arc\_proportion\_for, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# we use the transformed dependent for the new model

propfort1 <- mixed(arc\_proportion\_for ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(propfort1$full\_model)

# normality of the residuals

qqnorm(residuals(propfort1$full\_model))

# assumptions improved, so we use the model with the transformed variable

anova (propfort1)

# plotting the significant effect

interact\_plot(propfort1$full\_model, pred = Total\_number\_birds, modx = Group\_types, plot.points = TRUE, interval = TRUE, int.width = 0.95,

line.thickness = 1, x.label = "Flock size",

y.label = "Proportion time foraging (arcsin)", modx.labels = c("single-species", "mixed-species"), legend.main = "Flock type") +

theme\_apa(legend.pos = "topleft") +

theme (axis.title.y = element\_text(size=16), axis.text.y = element\_text(size=13),

axis.title.x = element\_text(size=16), axis.text.x = element\_text(size=13),

legend.title = element\_text(size=14), legend.text = element\_text(size=14))

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(propfort1, "Group\_types")

emm\_gt

emm\_h <- emmeans(propfort1, "Habitats")

emm\_h

###### searching rate

searchrate <- mixed(Rate\_searching ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(searchrate$full\_model)

# normality of the residuals

qqnorm(residuals(searchrate$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, log\_Rate\_searching = log(Rate\_searching))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$Rate\_searching, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$log\_Rate\_searching, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# we use the transformed dependent for the new model

searchratet1 <- mixed(log\_Rate\_searching ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(searchratet1$full\_model)

# normality of the residuals

qqnorm(residuals(searchratet1$full\_model))

# assumptions improved, so we use the model with the transformed variable

anova (searchratet1)

# plotting the significant effect

interact\_plot(searchratet1$full\_model, pred = Total\_number\_birds, modx = Group\_types, plot.points = TRUE, interval = TRUE, int.width = 0.95,

line.thickness = 1, x.label = "Flock size",

y.label = "Searching rate (log)", modx.labels = c("single-species", "mixed-species"), legend.main = "Flock type") +

theme\_apa(legend.pos = "bottomleft") +

theme (axis.title.y = element\_text(size=16), axis.text.y = element\_text(size=13),

axis.title.x = element\_text(size=16), axis.text.x = element\_text(size=13),

legend.title = element\_text(size=14), legend.text = element\_text(size=14))

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(searchratet1, "Group\_types")

emm\_gt

emm\_h <- emmeans(searchratet1, "Habitats")

emm\_h

###### pecking rate

peckrate <- mixed(Rate\_peck ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(searchrate$full\_model)

# normality of the residuals

qqnorm(residuals(searchrate$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, log\_Rate\_peck = log(Rate\_peck+1))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$Rate\_peck, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$log\_Rate\_peck, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# we use the transformed dependent for the new model

peckratet1 <- mixed(log\_Rate\_peck ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(peckratet1$full\_model)

# normality of the residuals

qqnorm(residuals(peckratet1$full\_model))

# assumptions improved, so we use the model with the transformed variable

anova (peckratet1)

# plotting the significant effect

afex\_plot(peckratet1, x = "Habitats", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Habitats = c("Winter-flooded rice paddies", "Riverbanks "))) + labs(y = "Pecking rate (log)", x = "Habitat type") + theme\_pubr(16)

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(peckratet1, "Group\_types")

emm\_gt

emm\_h <- emmeans(peckratet1, "Habitats")

emm\_h

###### Finding food rate (Rate\_found\_food)

foodfoundrate <- mixed(Rate\_found\_food ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(foodfoundrate$full\_model)

# normality of the residuals

qqnorm(residuals(foodfoundrate$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, log\_Rate\_found\_food = log(Rate\_found\_food+1))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$Rate\_found\_food, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$log\_Rate\_found\_food, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# we use the transformed dependent for the new model

foodfoundratet1 <- mixed(log\_Rate\_found\_food ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(foodfoundratet1$full\_model)

# normality of the residuals

qqnorm(residuals(foodfoundratet1$full\_model))

# assumptions improved, so we use the model with the transformed variable

anova (foodfoundratet1)

# plotting the significant effect

afex\_plot(foodfoundratet1, x = "Habitats", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Habitats = c("Winter-flooded rice paddies", "Riverbanks"))) + labs(y = "Intake rate (log)", x = "Habitat type") + theme\_pubr(16)

afex\_plot(foodfoundratet1, x = "Habitats", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Habitats = c("Winter-flooded rice paddies", "Riverbanks "))) + labs(y = "Pecking rate (log)", x = "Habitat type") + theme\_pubr(16)

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(foodfoundratet1, "Group\_types")

emm\_gt

emm\_h <- emmeans(foodfoundratet1, "Habitats")

emm\_h

###### moving rate

movingrate <- mixed(step\_egrets ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(movingrate$full\_model)

# normality of the residuals

qqnorm(residuals(movingrate$full\_model))

# assumptions are met, so we use this model

anova (movingrate)

# plotting the significant effect

afex\_plot(movingrate, x = "Group\_types", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Group\_types = c("Single-species", "Mixed-species"))) + labs(y = "Moving rate", x = "Flock type") + theme\_pubr(16)

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(movingrate, "Group\_types")

emm\_gt

emm\_h <- emmeans(movingrate, "Habitats")

emm\_h

######## number of moving steps per attempted capture

movstepspcapt <- mixed(pecking\_steps ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(movstepspcapt$full\_model)

# normality of the residuals

qqnorm(residuals(movstepspcapt$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, log\_pecking\_steps = log(pecking\_steps))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$pecking\_steps, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$log\_pecking\_steps, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# we use the transformed dependent for the new model

movstepspcaptt1 <- mixed(log\_pecking\_steps ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(movstepspcaptt1$full\_model)

# normality of the residuals

qqnorm(residuals(movstepspcaptt1$full\_model))

# assumptions improved, so we use the model with the transformed variable

anova (movstepspcaptt1)

summary (movstepspcaptt1)

# we use the transformed dependent for the new model

movstepspcaptt2 <- mixed(log\_pecking\_steps ~ Group\_types + Habitats + Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

anova (movstepspcaptt1,movstepspcaptt2 )

anova (movstepspcaptt2,movstepspcaptt1 )

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(movstepspcaptt1, "Group\_types")

emm\_gt

emm\_h <- emmeans(movstepspcaptt1, "Habitats")

emm\_h

#back transforming means and SEs

exp(2.68)

exp(0.291)

exp(2.26)

exp(0.349)

exp(1.83)

exp(0.386)

exp(3.11)

exp(0.291)

# plotting the significant effects

afex\_plot(movstepspcaptt1, x = "Group\_types", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Group\_types = c("Single-species", "Mixed-species"))) + labs(y = "Moving steps per attempted capture (log)", x = "Flock type") + theme\_pubr(16)

afex\_plot(movstepspcaptt1, x = "Habitats", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Habitats = c("Paddy field", "River"))) + labs(y = "Moving steps per attempted capture (log)", x = "Habitat type") + theme\_pubr(16)

interact\_plot(movstepspcaptt1$full\_model, pred = Total\_number\_birds, modx = Group\_types, plot.points = TRUE, interval = TRUE, int.width = 0.95,

line.thickness = 1, x.label = "Flock size",

y.label = "Moving steps per attempted capture (log)", modx.labels = c("single-species", "mixed-species"), legend.main = "Flock type") +

theme\_apa(legend.pos = "topmiddle") +

theme (axis.title.y = element\_text(size=16), axis.text.y = element\_text(size=13),

axis.title.x = element\_text(size=16), axis.text.x = element\_text(size=13),

legend.title = element\_text(size=14), legend.text = element\_text(size=14))

interact\_plot(movstepspcaptt1$full\_model, pred = Total\_number\_birds, modx = Habitats, plot.points = TRUE, interval = TRUE, int.width = 0.95,

line.thickness = 1, x.label = "Flock size",

y.label = "Moving steps per attempted capture (log)", modx.labels = c("winter-flooded rice paddies", "riverbanks"), legend.main = "Habitat type") +

theme\_apa(legend.pos = "bottomleft") +

theme (axis.title.y = element\_text(size=16), axis.text.y = element\_text(size=13),

axis.title.x = element\_text(size=16), axis.text.x = element\_text(size=13),

legend.title = element\_text(size=14), legend.text = element\_text(size=14))

######number of moving steps per capture

mvstcapt <- mixed(capture\_foods\_steps ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(mvstcapt$full\_model)

# normality of the residuals

qqnorm(residuals(mvstcapt$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, log\_capture\_foods\_steps = log(capture\_foods\_steps+1))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$capture\_foods\_steps, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$log\_capture\_foods\_steps, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# we use the transformed dependent for the new model

mvstcaptt1 <- mixed(log\_capture\_foods\_steps ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(mvstcaptt1$full\_model)

# normality of the residuals

qqnorm(residuals(mvstcaptt1$full\_model))

# assumptions improved, so we use the model with the transformed variable

anova (mvstcaptt1)

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(mvstcaptt1, "Group\_types")

emm\_gt

emm\_h <- emmeans(mvstcaptt1, "Habitats")

emm\_h

# plotting the significant effect

afex\_plot(mvstcaptt1, x = "Habitats", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Habitats = c("Winter-flooded rice paddies", "Riverbanks"))) + labs(y = "Number of moving steps per capture (log)", x = "Habitat type") + theme\_pubr(16)

####### avg\_searching\_boutdur

searchboutdur <- mixed(average\_searching\_boudur ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

anova(searchboutdur)

#checking assumptions

# homogeneity of variance

plot(searchboutdur$full\_model)

# normality of the residuals

qqnorm(residuals(searchboutdur$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, log\_average\_searching\_boudur = log(average\_searching\_boudur))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$average\_searching\_boudur, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$log\_average\_searching\_boudur, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# we use the transformed dependent for the new model

searchboutdurt1 <- mixed(log\_average\_searching\_boudur ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(searchboutdurt1$full\_model)

# normality of the residuals

qqnorm(residuals(searchboutdurt1$full\_model))

# assumptions improved, so we use the model with the transformed variable

anova (searchboutdurt1)

# plotting the significant effect

interact\_plot(searchboutdurt1$full\_model, pred = Total\_number\_birds, modx = Group\_types, plot.points = TRUE, interval = TRUE, int.width = 0.95,

line.thickness = 1, x.label = "Flock size",

y.label = "Search bout duration (log)", modx.labels = c("single-species", "mixed-species"), legend.main = "Flock type") +

theme\_apa(legend.pos = "topmiddle") +

theme (axis.title.y = element\_text(size=16), axis.text.y = element\_text(size=13),

axis.title.x = element\_text(size=16), axis.text.x = element\_text(size=13),

legend.title = element\_text(size=14), legend.text = element\_text(size=14))

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(searchboutdurt1, "Group\_types")

emm\_gt

emm\_h <- emmeans(searchboutdurt1, "Habitats")

emm\_h

######### distance to the nearest flock mate

nd <- mixed(distance\_nearest.\_flock\_mate ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

anova(nd)

#checking assumptions

# homogeneity of variance

plot(nd$full\_model)

# normality of the residuals

qqnorm(residuals(nd$full\_model))

# assumptions not met, so we use transformed values

flock <- mutate(flock, log\_distance\_nearest.\_flock\_mate = log(distance\_nearest.\_flock\_mate))

# checking skewness and kurtosis of continous variables (untransformed vs transformed)

descr(flock$distance\_nearest.\_flock\_mate, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

descr(flock$log\_distance\_nearest.\_flock\_mate, stats = c("Skewness", "Kurtosis"), style="rmarkdown")

# we use the transformed dependent for the new model

ndt1 <- mixed(log\_distance\_nearest.\_flock\_mate ~ Group\_types + Habitats + Total\_number\_birds + Group\_types:Total\_number\_birds + Habitats:Total\_number\_birds + year +

(1|location) + (1|day\_of\_study) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(ndt1$full\_model)

# normality of the residuals

qqnorm(residuals(ndt1$full\_model))

# assumptions improved, so we use the model with the transformed variable

anova (ndt1)

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(ndt1, "Group\_types")

emm\_gt

emm\_h <- emmeans(ndt1, "Habitats")

emm\_h

rm(list = ls ())

setwd("C:/xxx")

flock <- read.csv("ADFIDdata.csv", na.strings = c("","NA"), header=TRUE)

#we check for the types of variables

str(flock)

#assigning categorical factors

flock$year <- as.factor(flock$year)

flock$day\_of\_January <- as.factor(flock$day\_of\_January)

flock$period <- as.factor(flock$period)

flock$location <- as.factor(flock$location)

flock$Flock\_types <- as.factor(flock$Flock\_types)

#we check for the types of variables

str(flock)

# this line of code is important for afex to run in a reproducible manner

set\_sum\_contrasts()

###### AD

ADm <- mixed(AD ~ Flock\_types + Total\_number\_birds + Flock\_types:Total\_number\_birds + Start\_distance +

(1|location) + (1|day\_of\_January) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(ADm$full\_model)

# normality of the residuals

qqnorm(residuals(ADm$full\_model))

# assumptions are met, so no need of transformation

anova (ADm)

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(ADm, "Flock\_types")

emm\_gt

# plotting the significant effect

afex\_plot(ADm, x = "Flock\_types", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Flock\_types = c("Single-species", "Mixed species"))) + labs(y = "Alert distance", x = "Flock type") + theme\_pubr(16)

###### FID

FIDm <- mixed(FID ~ Flock\_types + Total\_number\_birds + Flock\_types:Total\_number\_birds + Start\_distance +

(1|location) + (1|day\_of\_January) + (1|period), data = flock, method = "KR",

control=lmerControl(optimizer="bobyqa",optCtrl=list(maxfun=1e9)), expand\_re = TRUE)

#checking assumptions

# homogeneity of variance

plot(FIDm$full\_model)

# normality of the residuals

qqnorm(residuals(FIDm$full\_model))

# assumptions are met, so no need of transformation

anova (FIDm)

# means of main factors

emm\_options(lmer.df = "kenward-roger")

emm\_gt <- emmeans(FIDm, "Flock\_types")

emm\_gt

# plotting the significant effect

afex\_plot(FIDm, x = "Flock\_types", dodge = 0.4, point\_arg = list(size = 4), factor\_levels = list(Flock\_types = c("Single-species", "Mixed species"))) + labs(y = "Flight initiation distance", x = "Flock type") + theme\_pubr(16)