

SUPPLEMENTARY ELECTRONIC MATERIAL (APPENDIX 2)

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LOW REPEATABILITY OF BREEDING EVENTS REFLECTS FLEXIBILITY IN REPRODUCTIVE TIMING IN THE PIED FLYCATCHER *FICEDULA HYPOLEUCA* IN SPAIN

LAS BAJAS REPETIBILIDADES DE LOS EVENTOS DE CRÍA REFLEJAN FLEXIBILIDAD EN EL AJUSTE TEMPORAL DE LA REPRODUCCIÓN EN EL PAPAMOSCAS CERROJILLO EN ESPAÑA

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R script for analyses / *Guión en R de los análisis*

```
# Analysis with repeatability
setwd("C:/Users/Justine/Desktop/PhD/Analysis/Variability")
LAY<-read.csv("Individual Laying Analysis.csv",header=T,sep=";",dec=".")
nrow(LAY) #n=2103 for 776 females

library(nlme) #provide SD + function lme
library(rptR) #Repeatability package

# Repeatability estimation using the glmm method and log link
##Both habitat
rep1<-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year),
grname=c("Female","Year"),CI= 0.84| data=LAY,link="log")
print(rep1)
summary(rep1)
par(mfrow=c(1, 2))
plot(rep1,grname="Year",scale="link", cex.main=0.8,main="Year
variance",las=1)
plot(rep1,grname="Female",scale="link", cex.main=0.8,main="Female
variance",las=1)

###In different habitat
oak<-LAY[which(LAY$Habitat==1),] #1460 for 560 females
pine<-LAY[which(LAY$Habitat==2),] #640 for 249 females
repoak<-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year),
grname=c("Female","Year"), data=oak,link="log")
reppine<-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year),
grname=c("Female","Year"), data=pine,link="log")
summary(repoak)
summary(reppine)
par(mfrow=c(2, 2))
plot(repoak,grname="Year",scale="link", cex.main=0.8,main="Year
variance",las=1)
plot(repoak,grname="Female",scale="link", cex.main=0.8,main="Female
variance",las=1)
plot(reppine,grname="Year",scale="link", cex.main=0.8,main="Year
variance",las=1)
plot(reppine,grname="Female",scale="link", cex.main=0.8,main="Female
variance",las=1)

####With others traits
rep2<-rptPoisson(MatingDate ~ 1+(1 | Female)+(1 | Year),
grname=c("Female","Year"),CI= 0.84, data=LAY,link="log")
rep3<-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year),
grname=c("Female","Year"), CI= 0.84, data=LAY,link="log")
rep5<-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year),
grname=c("Female","Year"),CI= 0.84, data=LAY,link="log")
```

#Within habitat

```
repoakM<-rptPoisson(MatingDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=oak,link="log",CI= 0.84)  
reppineM<-rptPoisson(MatingDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=pine,link="log",CI= 0.84)  
repoakP<-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=oak,link="log",CI= 0.84)  
reppineP<-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=pine,link="log",CI= 0.84)  
repoakH<-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=oak,link="log",CI= 0.84)  
reppineH<-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=pine,link="log",CI= 0.84)
```

#####Same analysis with only 2 year-old or older female
LAYa<-LAY[which(LAY\$Age!=1),] #332 age 1

##With Both Habitats

```
rep1a<-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=LAYa,link="log", CI= 0.84)  
rep2a<-rptPoisson(MatingDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=LAYa,link="log", CI= 0.84)  
rep3a<-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=LAYa,link="log", CI= 0.84)  
rep4a<-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=LAYa,link="log", CI= 0.84)
```

##Within Habitats

```
oakA<-LAYa[which(LAYa$Habitat==1),] #1237 for 556 females  
pineA<-LAYa[which(LAYa$Habitat==2),] #527 for 240 females  
repoakA<-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=oakA,link="log", CI= 0.84)  
reppineA<-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=pineA,link="log", CI= 0.84)  
repoakA2<-rptPoisson(MatingDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=oakA,link="log", CI= 0.84)  
reppineA2<-rptPoisson(MatingDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=pineA,link="log", CI= 0.84)  
repoakA3<-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=oakA,link="log", CI= 0.84)  
reppineA3<-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=pineA,link="log", CI= 0.84)  
repoakA4<-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=oakA,link="log", CI= 0.84)  
reppineA4<-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year),  
grname=c("Female","Year"), data=pineA,link="log", CI= 0.84)
```

Same with Mate as random factor

##For all age

```
rep1m<-rptPoisson(LayingDate ~ 1+(1 |Female)+(1 | Year)+(1 | Male),  
grname=c("Female","Year"), data=LAY,link="log", CI= 0.84)
```

```
rep2m<-rptPoisson(MatingDate ~ 1+(1 |Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=LAY,link="log", CI= 0.84)
rep3m<-rptPoisson(Prelaying ~ 1+(1 |Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=LAY,link="log", CI= 0.84)
rep4m<-rptPoisson(HatchDate ~ 1+(1 |Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=LAY,link="log", CI= 0.84)
```

##Within habitat

```
oak<-LAY[which(LAY$Habitat==1),] #1460 for 560 females
pine<-LAY[which(LAY$Habitat==2),] #640 for 249 females
repoakM <-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=oak,link="log", CI= 0.84)
reppineM<-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=pine,link="log", CI= 0.84)
repoakM2 <-rptPoisson(MatingDate~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=oak,link="log", CI= 0.84)
reppineM2<-rptPoisson(MatingDate~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=pine,link="log", CI= 0.84)
repoakM3 <-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=oak,link="log", CI= 0.84)
reppineM3<-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=pine,link="log", CI= 0.84)
repoakM4 <-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=oak,link="log", CI= 0.84)
reppineM4<-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=pine,link="log", CI= 0.84)
```

##For female of 2 year-old or older

```
rep1am<-rptPoisson(LayingDate ~ 1+(1 |Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=LAYa,link="log", CI= 0.84)
rep2am<-rptPoisson(MatingDate ~ 1+(1 |Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=LAYa,link="log", CI= 0.84)
rep3am<-rptPoisson(Prelaying ~ 1+(1 |Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=LAYa,link="log", CI= 0.84)
rep4am<-rptPoisson(HatchDate ~ 1+(1 |Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=LAYa,link="log", CI= 0.84)
```

##with both habitat

```
oaka<-LAY[which(LAYa$Habitat==1),] # 1237 for 492 females
pinea<-LAY[which(LAYa$Habitat==2),] # 527 for 222 females
#
repoakaaM <-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=oaka,link="log", CI= 0.84)
reppineaM<-rptPoisson(LayingDate ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=pinea,link="log", CI= 0.84)
repoakaaM2 <-rptPoisson(MatingDate~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=oaka,link="log", CI= 0.84)
reppineaM2<-rptPoisson(MatingDate~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=pinea,link="log", CI= 0.84)
```

```

repoakaaM3 <-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=oaka,link="log", CI= 0.84)
reppineaaM3<-rptPoisson(Prelaying ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=pinea,link="log", CI= 0.84)
repoakaaM4 <-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=oaka,link="log", CI= 0.84)
reppineaaM4<-rptPoisson(HatchDate ~ 1+(1 | Female)+(1 | Year)+(1 | Male),
grname=c("Female","Year"), data=pinea,link="log", CI= 0.84)

```

```

##### Graphs with the 84% confidence interval
library(ggplot2)
library(gridExtra)

```

```

#Put results in the same table
RR<-read.table("Repeatability.txt",header=T,sep="\t",dec=".")

```

```

RR[, "Variable"] <- factor(RR[, "Variable"] , levels=c("Mating Date", "Pre
Laying", "Laying Date", "Hatching Date"))

```

```

# for years

```

```

plotY<- ggplot(RR[which(RR$Group=="Year"),], aes(x=Variable,
y=Repeatability, group=Habitat, colour=Habitat)) + theme_classic() +
  geom_point(shape=19, size=4, position=position_dodge(width=0.5)) +
  ylim(0,0.5) +
  geom_errorbar(width=.05, aes(ymin=ci8, ymax=ci92),
position=position_dodge(width=0.5)) +
  scale_color_manual(values=c("#999999", "#E69F00", "forestgreen"))+
  theme(legend.position='none', axis.text=element_text(size=14,
face="bold"),axis.title=element_text(size=14,face="bold"))

```

```

# for females

```

```

plotF<-ggplot(RR[which(RR$Group=="Females"),], aes(x=Variable,
y=Repeatability, group=Habitat, colour=Habitat)) + theme_classic() +
  geom_point(shape=19, size=4,position=position_dodge(width=0.5) ) +
  ylim(0,0.25) +
  geom_errorbar(width=.05, aes(ymin=ci8,
ymax=ci92),position=position_dodge(width=0.5)) +
  scale_color_manual(values=c("#999999", "#E69F00", "forestgreen"))+
  theme(legend.position = c(0.9, 0.9), axis.text=element_text(size=14,
face="bold"),axis.title=element_text(size=14,face="bold"), legend.title =
element_text(size=14),legend.text = element_text(size=12))

```