Figure S1 - Time line of the experimental cross-fostering and supplementary feeding events in relation to the age of juvenile little owls.
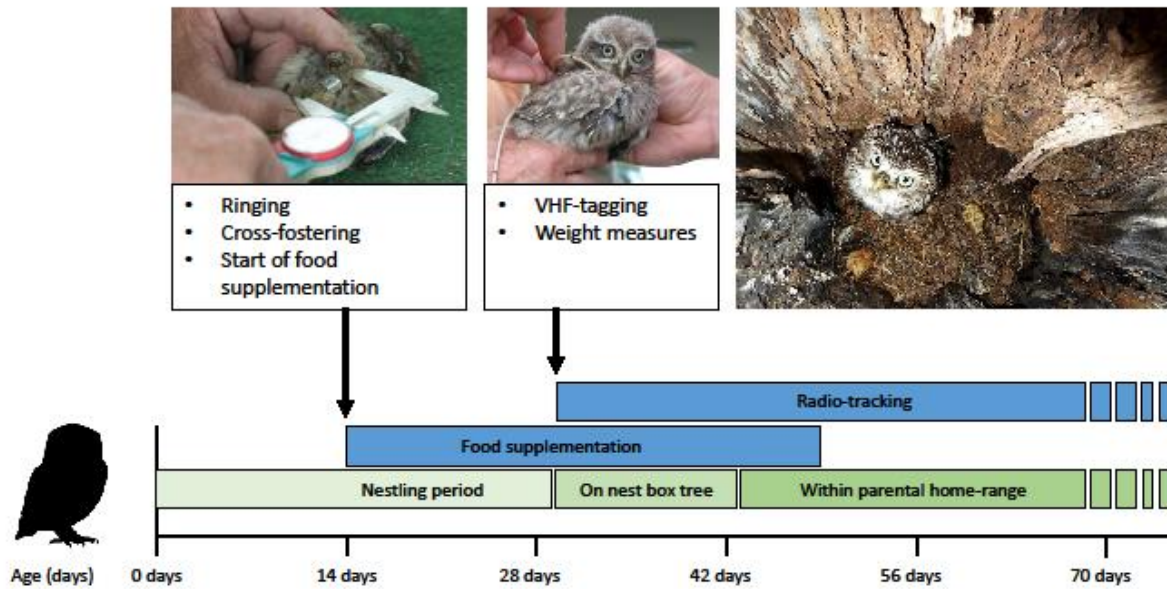
Supplementary Material for the manuscript
EXPERIMENTALLY DISENTANGLING INTRINSIC AND EXTRINSIC DRIVERS OF NATAL DISPERSAL IN A NOCTURNAL RAPTOR
By Julien Fattebert, Marco Perrig, Beat Naef-Daenzer, Martin U. Grüebler
Published in Proceedings B, doi 10.1098/rspb.2019.1537

Supplement S2 - R script for the analysis of the owl trajectory and segmentation, and R script for the Linear Mixed Modelling of the dispersal parameters

###--------------------------

#'R script for the analysis of the owl trajectory and segementation for the manuscript

#'EXPERIMENTALLY DISENTANGLING INTRINSIC AND EXTRINSIC DRIVERS OF NATAL DISPERSAL IN A NOCTURNAL RAPTOR

#'by Fattebert Julien, Marco Perrig, Beat Naef-Daenzer & Martin U. Grüebler

#'Proceedings B doi 10.1098/rspb.2019.157

###--------------------------

#'import the telemetry data----

data <- read.csv(paste0(getwd(),"/Fattebert et al dispersal_S2_little_owl_telemetry_data.csv"))

names(data)

data$CRS[1]

#spatialise the data

require(sp)

coordinates(data) <- c("x","y")

projection(data) <- CRS("+init=epsg:31466")

#'---

#HMM model

#'---

require(moveHMM)

trackData <- data[, c("ring", "x", "y", "loc_age", "DATETIMEn", "sex", "fed", "crossF", "phase")]

colnames(trackData)[1] <- "ID"

trackData <- trackData[order(trackData$loc_age),]

```
trackData <- trackData[order(trackData$ID),]
```

```
trackData.1 <- droplevels(subset(trackData,phase!="forays")) #all data excluding data during forays phase
```

```
trackData.2 <- droplevels(subset(trackData,phase=="dispersal")) #data excluding forays, and within natal range data
```

```
natal <- droplevels(subset(trackData,phase=="natal")) #data in the natal range
```

```
natal.last <- natal[ natal$DATETIMEn == ave(natal$DATETIMEn, natal$ID, FUN=max), ] #last location in the natal range
```

```
trackData <- rbind(natal.last, trackData.2) #data excluding forays, and within natal range data, but including the very last relocation within the natal range
```

```
#'function 'preData()' takes "ID" into account
```

```
hmm.data <- prepData(trackData,type="UTM",coordNames=c("x","y"))
```

```
#'3 stage model HHMM----
```

```
#'initial parameters for gamma and von Mises distributions----
```

```
mu0 <- c(0.1,0.5,3)
```

```
sigma0 <- c(0.05,0.5,1)
```

```
zeromass0 <- c(0.05,0.0001,0.0001)
```

```
stepPar0 <- c(mu0,sigma0,zeromass0)
```

```
angleMean0 <- c(pi,pi,0)
```

```
kappa0 <- c(1,1,1)
```

```
anglePar0 <- c(angleMean0,kappa0)
```

```
#fitting function----
```

```
data.3modes <- fitHMM(data=hmm.data,nbStates=3, stepPar0=stepPar0,
  anglePar0=anglePar0, stationary=T)
```

```
data.3modes_states <- viterbi(data.3modes)



#'-----------------------------------------------

#'plot 3-stage model

#'-----------------------------------------------

model_data <- cbind(hmm.data, data.3modes_states)

names(model_data)

model_times <- list()

breaks <- data.frame()

unique_id <- levels(model_data$ID)

for(i in 1:nlevels(model_data$ID))

{

  model_times[[i]]  <- droplevels(subset(model_data, ID == unique_id[i]))

  model_times[[i]]$dx <- model_times[[i]]$x - model_times[[i]][1,]$x

  model_times[[i]]$dy <-  model_times[[i]]$y - model_times[[i]][1,]$y

  model_times[[i]]$NSD <-  sqrt( model_times[[i]]$dx^2 +  model_times[[i]]$dy^2)

  model_times[[i]]$switch <- c(NA, diff(model_times[[i]]$data.3modes_states)) #this identifies when
breaks happen

}


#identify the movement mode and break points to indentify timing----

transfers <- do.call(rbind.data.frame, model_times)

transfers.3 <- droplevels(subset(transfers, data.3modes_states == 3)) #transfer is mode 3


transfers.2 <- droplevels(subset(transfers, data.3modes_states == 2 & switch == -1)) #switch from 3 to 2

transfers.1 <- droplevels(subset(transfers, data.3modes_states == 1 & switch == -2)) #switch from 3 to 1

settle.n <- rbind(transfers.2, transfers.1)
```

```
transf <- rbind(transfers.3, transfers.2, transfers.1)

transf <- transf[order(transf$ID),]

transf <- transf[order(transf$loc_age),]


xmin <- min(do.call("rbind", model_times)$dx)

xmax <- max(do.call("rbind", model_times)$dx)

ymin <- min(do.call("rbind", model_times)$dy)

ymax <- max(do.call("rbind", model_times)$dy)


for(i in 1:nlevels(model_data$ID))

{

  gender <- unique(model_times[[i]]$sex)

  eqscplot(model_times[[i]]$dx, model_times[[i]]$dy, type="l",
col="lightgrey",main=unique(model_times[[i]]$ID))

  points(model_times[[i]]$dx, model_times[[i]]$dy, col=model_times[[i]]$data.3modes_states,
pch=model_times[[i]]$data.3modes_states)

  plot(model_times[[i]]$NSD*1000 ~ model_times[[i]]$loc_age, col="lightgrey",type="l", main=paste(i))

  points(model_times[[i]]$NSD*1000 ~ model_times[[i]]$loc_age,
col=model_times[[i]]$data.3modes_states, pch=model_times[[i]]$data.3modes_states)

  switches <- subset(model_times[[i]], switch!=0)

  abline(v=c(switches$loc_age), lty=2, lwd=2, col="blue")

  breaks <- rbind(breaks, switches)

}


#all switches to settlement

settle <- droplevels(subset(transf, switch<(0)))

#identify age at first settlement
```

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```
settle_1 <- as.data.frame(setDT(settle)[, .SD[which.min(loc_age)], by=ID])
```

```
###-------------------------
```

#'R script for the analysis of the dispersal parameters for the manuscript

#'EXPERIMENTALLY DISENTANGLING INTRINSIC AND EXTRINSIC DRIVERS OF NATAL DISPERSAL IN A
NOCTURNAL RAPTOR

#'by Fattebert Julien, Marco Perrig, Beat Naef-Daenzer & Martin U. Grüebler

#'Proceedings B doi 10.1098/rspb.2019.157

```
###-------------------------
```

```
owl.160 < -
read.csv(paste0(getwd(),"/Fattebert_little_owl_variables_data_ESM3_10.1098rspb.2019.1537.csv"))
```

```
owl.89 <- droplevels(subset(owl.160, transfer=="completed"))
```

```
###summary statistics----
```

#date hatch----

```
mean((owl.160$JulianD_hatch))
```

```
sd((owl.160$JulianD_hatch))
```

```
median(owl.160$JulianD_hatch)
```

```
range((owl.160$JulianD_hatch))
```

```
###HSI----
```

```
mean((owl.160$HSI_foster))
```

```
sd((owl.160$HSI_foster))
```

```
median(owl.160$HSI_foster)
```

```
range((owl.160$HSI_foster))
```

#age at 1st foray----

mean((owl.160$ageforay))

sd((owl.160$ageforay))

median(owl.160$ageforay)

range((owl.160$ageforay))

#foray duration-----

mean((owl.160$duraforay))

sd((owl.160$duraforay))

median(owl.160$duraforay)

range((owl.160$duraforay))

#age emigration----

mean((owl.160$ageemigr))

sd((owl.160$ageemigr))

median(owl.160$ageemigr)

range((owl.160$ageemigr))

##duration transfer----

mean((owl.89$duratrans))

sd((owl.89$duratrans))

median((owl.89$duratrans))

range((owl.89$duratrans))

names(stats)

#net dispersal distance

```
mean((owl.89$net_dist))/1000

sd((owl.89$net_dist))/1000

median((owl.89$net_dist))/1000

range((owl.89$net_dist))/1000
```

```
###Statistical modelling----

require(rstanarm)
```

```
###

#age at first foray----

###

lmm.ageforay <- stan_lmer(sqrt(ageforay) ~ sex +JulianD_hatch +fed*HSI_foster

    +(1 | year_hatch) +(1 | fam_foster) +(1 | fam_hatch), data=owl.160, REML=F,

    prior_intercept=normal(9, 2),

    prior=normal(0,5))
```

```
summary(lmm.ageforay)

qqnorm(resid(lmm.ageforay))

qqline(resid(lmm.ageforay))
```

```
#bayesian simulations----

bsim <- as.matrix(lmm.ageforay)

dimnames(bsim)$parameters
```

```
#fixed effects----

round(mean(bsim[,1]), 3) #intercept

round(quantile(bsim[,1], c(0.025, 0.975)), 3)
```

```
round(mean(bsim[,2]), 3) #sex

round(quantile(bsim[,2], c(0.025, 0.975)), 3)


round(mean(bsim[,3]), 3) #JulianD_hatch

round(quantile(bsim[,3], c(0.025, 0.975)), 3)


round(mean(bsim[,4]), 3) #fed

round(quantile(bsim[,4], c(0.025, 0.975)), 3)


round(mean(bsim[,5]), 3) #HSI_foster

round(quantile(bsim[,5], c(0.025, 0.975)), 3)


round(mean(bsim[,6]), 3) #fedxHSI_foster

round(quantile(bsim[,6], c(0.025, 0.975)), 3)


#random effects----

round(mean(bsim[,163]), 3)

round(quantile(bsim[,163], c(0.025, 0.975)), 3)


round(mean(bsim[,164]), 3)

round(quantile(bsim[,164], c(0.025, 0.975)), 3)


round(mean(bsim[,165]), 3)

round(quantile(bsim[,165], c(0.025, 0.975)), 3)


####
```

```
###plot Fig. 2----

newHSI_foster <- seq(min(owl.160$HSI_foster),max(owl.160$HSI_foster), length.out=100)

newdat <- expand.grid(sex = factor("f", levels=levels(as.factor(owl.160$sex))),

  JulianD_hatch = mean(owl.160$JulianD_hatch),

  fed = c("fed","unfed"),

  HSI_foster = newHSI_foster)

newdat <- newdat[order(newdat$fed), ]; newdat


Xmat <- model.matrix(~ sex +JulianD_hatch +fed *HSI_foster, data = newdat)

b <- apply(bsim[,1:6],2,mean)  ### what is this?

newdat$fit <- Xmat%*% b

nsim <- nrow(bsim[,1:6])

predmat <- matrix(ncol=nsim, nrow = nrow(newdat))

for (i in 1:nsim){

  predmat[ , i] <- Xmat %*% bsim[i,1:6]

}


owl.160.u <- droplevels(subset(owl.160, fed=='unfed'))

owl.160.s <- droplevels(subset(owl.160, fed=='fed'))


pdf("Fig2-HSI-R2.pdf", height=4.4, width=5.4)

op <- par(mfrow=c(1,1), tcl=0.2, oma = c (0,0,1,1), mar=c(4,4,0.5,0.5))

plot(NA, NA, las = 1, type = "n", ylim=c(20,140), xlim = c(min(newHSI_foster),

        max(newHSI_foster)), xlab = "Habitat Suitability Index", ylab = "Age (day)", cex.lab = 1,
bty="n", xaxt="n")

axis(1,at=seq(0.55, 1.0, 0.05),labels=Cs(, 0.60, , 0.70, , 0.80, , 0.90, , "1.0"), pos=20)
```

```
polygon (c(newHSI_foster,rev(newHSI_foster)), c((apply(predmat [1:length(newHSI_foster), ], 1,
quantile, prob = 0.025))^2, rev((apply(predmat [1:length(newHSI_foster), ], 1, quantile, prob =
0.975)))^2), border=NA, col=rgb(19,27,29,67,maxColorValue = 255))

lines(newHSI_foster,  ((Xmat %*% fixef(lmm.ageforay))[1:length(newHSI_foster)])^2, col="black", lwd=2)

polygon (c(newHSI_foster,rev(newHSI_foster)), c((apply(predmat
[(length(newHSI_foster)+1):(2*length(newHSI_foster)), ], 1, quantile, prob = 0.025))^2,
rev((apply(predmat [(length(newHSI_foster)+1):(2*length(newHSI_foster)), ], 1, quantile, prob =
0.975)))^2), border=NA, col=rgb(19,27,29,33,maxColorValue = 255))

lines(newHSI_foster,  ((Xmat %*%
fixef(lmm.ageforay))[(length(newHSI_foster)+1):(2*length(newHSI_foster))])^2, col="black",

    lty=2, lwd=2)

legend(0.606,130, c("",""), fill=c(rgb(19,27,29,67,maxColorValue = 255),

        rgb(19,27,29,33,maxColorValue = 255)),

    bty = "n", cex=1)

legend(0.6,130, c("fed","unfed"),bty = "n", cex=1, lty=1:2)

points(owl.160.u$ageforay ~ owl.160.u$HSI_foster)

points(owl.160.s$ageforay ~ owl.160.s$HSI_foster, pch=20)

par(op)


dev.off()

#dev.off()----


#random effect variance (same additive fixed structure for all models)----

lmm.ageforay.var <- stan_lmer(sqrt(ageforay) ~ sex +JulianD_hatch +fed +HSI_foster

    +(1 | year_hatch) +(1 | fam_foster) +(1 | fam_hatch), data=owl.160, REML=F,

    prior_intercept=normal(9, 2),

    prior=normal(0,5))


bsim <- as.matrix(lmm.ageforay.var)
```

```
dimnames(bsim)$parameters


round(mean(bsim[,162]), 3) #year_hatch

round(quantile(bsim[,162], c(0.025, 0.975)), 3)


round(mean(bsim[,163]), 3) #fam_foster

round(quantile(bsim[,163], c(0.025, 0.975)), 3)


round(mean(bsim[,164]), 3) #fam_hatch

round(quantile(bsim[,164], c(0.025, 0.975)), 3)



###
#duration foray----
###
lmm.duraforay <- stan_lmer(sqrt(duraforay) ~ sex +JulianD_hatch +fed +HSI_foster  +ageforay
    +(1 | year_hatch) +(1 | fam_foster) +(1 | fam_hatch), data=owl.160, REML=F,
    prior_intercept=normal(4, 3),
    prior=normal(0,5))



summary(lmm.duraforay)

qqnorm(resid(lmm.duraforay))

qqline(resid(lmm.duraforay))


#bayesian simulations----

bsim <- as.matrix(lmm.duraforay)
```

```
dimnames(bsim)$parameters


#fixed effects----

round(mean(bsim[,1]), 3) #intercept

round(quantile(bsim[,1], c(0.025, 0.975)), 3)


round(mean(bsim[,2]), 3) #sex

round(quantile(bsim[,2], c(0.025, 0.975)), 3)


round(mean(bsim[,3]), 3) #JulianD_hatch

round(quantile(bsim[,3], c(0.025, 0.975)), 3)


round(mean(bsim[,4]), 3) #fed

round(quantile(bsim[,4], c(0.025, 0.975)), 3)


round(mean(bsim[,5]), 3) #HSI_foster

round(quantile(bsim[,5], c(0.025, 0.975)), 3)


round(mean(bsim[,6]), 3) #ageforay

round(quantile(bsim[,6], c(0.025, 0.975)), 3)


#random effects----

round(mean(bsim[,163]), 3) #bYY

round(quantile(bsim[,163], c(0.025, 0.975)), 3)


round(mean(bsim[,164]), 3) #fam_foster

round(quantile(bsim[,164], c(0.025, 0.975)), 3)
```

```
round(mean(bsim[,165]), 3) #fam_hatch

round(quantile(bsim[,165], c(0.025, 0.975)), 3)


#random effect variance (same additive fixed structure for all models)----

lmm.duraforay.var <- stan_lmer(sqrt(duraforay) ~ sex +JulianD_hatch +fed +HSI_foster

      +(1 | year_hatch) +(1 | fam_foster) +(1 | fam_hatch), data=owl.160, REML=F,

      prior_intercept=normal(4, 3),

      prior=normal(0,5))


bsim <- as.matrix(lmm.duraforay.var)

dimnames(bsim)$parameters


round(mean(bsim[,162]), 3)

round(quantile(bsim[,162], c(0.025, 0.975)), 3)


round(mean(bsim[,163]), 3)

round(quantile(bsim[,163], c(0.025, 0.975)), 3)


round(mean(bsim[,164]), 3)

round(quantile(bsim[,164], c(0.025, 0.975)), 3)


###
#age emigration----
###

lmm.ageemirg <- stan_lmer(sqrt(ageemigr) ~ sex +JulianD_hatch +fed +HSI_foster  +ageforay +duraforay

    +(1 | year_hatch) +(1 | fam_foster) +(1 | fam_hatch), data=owl.160, REML=F,
```

```
    prior_intercept=normal(10, 4),

    prior=normal(0,5))


summary(lmm.ageemirg)

qqnorm(resid(lmm.ageemirg))

qqline(resid(lmm.ageemirg))


#bayesian simulations----

bsim <- as.matrix(lmm.emi160)

dimnames(bsim)$parameters


#fixed effects

round(mean(bsim[,1]), 3) #intercept

round(quantile(bsim[,1], c(0.025, 0.975)), 3)


round(mean(bsim[,2]), 3) #sex

round(quantile(bsim[,2], c(0.025, 0.975)), 3)


round(mean(bsim[,3]), 3) #JulianD_hatch

round(quantile(bsim[,3], c(0.025, 0.975)), 3)


round(mean(bsim[,4]), 3) #fed

round(quantile(bsim[,4], c(0.025, 0.975)), 3)


round(mean(bsim[,5]), 3) #HSI_foster

round(quantile(bsim[,5], c(0.025, 0.975)), 3)
```

```
round(mean(bsim[,6]), 3) #age foray

round(quantile(bsim[,6], c(0.025, 0.975)), 3)


round(mean(bsim[,7]), 3) #duration foray

round(quantile(bsim[,7], c(0.025, 0.975)), 3)


#random effects----

round(mean(bsim[,164]), 3)

round(quantile(bsim[,164], c(0.025, 0.975)), 3)


round(mean(bsim[,165]), 3)

round(quantile(bsim[,165], c(0.025, 0.975)), 3)


round(mean(bsim[,166]), 3)

round(quantile(bsim[,166], c(0.025, 0.975)), 3)


#random effect variance (same additive fixed structure for all models)----

lmm.ageemirg.var <- stan_lmer(sqrt(ageemigr) ~ sex +JulianD_hatch +fed +HSI_foster

    +(1 | year_hatch) +(1 | fam_foster) +(1 | fam_hatch), data=owl.160, REML=F,

    prior_intercept=normal(10, 4),

    prior=normal(0,5))



bsim <- as.matrix(lmm.ageemirg.var)

dimnames(bsim)$parameters


round(mean(bsim[,162]), 3)
```

```
round(quantile(bsim[,162], c(0.025, 0.975)), 3)


round(mean(bsim[,163]), 3)

round(quantile(bsim[,163], c(0.025, 0.975)), 3)


round(mean(bsim[,164]), 3)

round(quantile(bsim[,164], c(0.025, 0.975)), 3)


###

##duration transfer----

####

lmm.duratrans <- stan_lmer(sqrt(duratrans) ~ sex +JulianD_hatch +fed +HSI_foster +ageemigr

    +(1 | year_hatch) +(1 | fam_hatch) +(1 | fam_foster), data=owl.89, REML=F,

    prior_intercept=normal(4, 2),

    prior=normal(0,5))


summary(lmm.duratrans)

qqnorm(resid(lmm.duratrans))

qqline(resid(lmm.duratrans))


#bayesian simulations----

bsim <- as.matrix(lmm.duratrans)

dimnames(bsim)$parameters


#fixed effects----

round(mean(bsim[,1]), 3) #intercept

round(quantile(bsim[,1], c(0.025, 0.975)), 3)
```

```
round(mean(bsim[,2]), 3) #sex

round(quantile(bsim[,2], c(0.025, 0.975)), 3)


round(mean(bsim[,3]), 3) #JulianD_hatch

round(quantile(bsim[,3], c(0.025, 0.975)), 3)


round(mean(bsim[,4]), 3) #fed

round(quantile(bsim[,4], c(0.025, 0.975)), 3)


round(mean(bsim[,5]), 3) #HSI_foster

round(quantile(bsim[,5], c(0.025, 0.975)), 3)


round(mean(bsim[,6]), 3) #age emigration

round(quantile(bsim[,6], c(0.025, 0.975)), 3)



#random effects----

(mean(bsim[,120]))

(quantile(bsim[,120], c(0.025, 0.975)))


(mean(bsim[,121]))

(quantile(bsim[,121], c(0.025, 0.975)))


(mean(bsim[,122]))

(quantile(bsim[,122], c(0.025, 0.975)))
```

```
#random effect variance (same additive fixed structure for all models)----

lmm.duratrans.var <- stan_lmer(sqrt(duratrans) ~ sex +JulianD_hatch +fed +HSI_foster

    +(1 | year_hatch) +(1 | fam_hatch) +(1 | fam_foster), data=owl.89, REML=F,

    prior_intercept=normal(4, 2),

    prior=normal(0,5))


bsim <- as.matrix(lmm.duratrans.var)

dimnames(bsim)$parameters


(mean(bsim[,119]))

(quantile(bsim[,119], c(0.025, 0.975)))


(mean(bsim[,120]))

(quantile(bsim[,120], c(0.025, 0.975)))


(mean(bsim[,121]))

(quantile(bsim[,121], c(0.025, 0.975)))



####

#dispersal distances----

####

owl.89$net_dist <- as.numeric(as.character(owl.89$net_dist))


lmm.net_dist <- stan_lmer(sqrt(net_dist) ~ sex +JulianD_hatch +fed +HSI_foster + ageemigr +duratrans

    +(1 | year_hatch) +(1 | fam_foster) +(1 | fam_hatch), data=owl.89, REML=F,
```

```
    prior_intercept=normal(3, 2),

    prior=normal(0,5))




summary(lmm.net_dist)

qqnorm(resid(lmm.duratrans))

qqline(resid(lmm.duratrans))


#bayesian simulations----

bsim <- as.matrix(lmm.net_dist)

dimnames(bsim)$parameters


#fixed effects-----

round(mean(bsim[,1]), 3) #intercept

round(quantile(bsim[,1], c(0.025, 0.975)), 3)


round(mean(bsim[,2]), 3) #sex

round(quantile(bsim[,2], c(0.025, 0.975)), 3)


round(mean(bsim[,3]), 3) #JulianD_hatch

round(quantile(bsim[,3], c(0.025, 0.975)), 3)


round(mean(bsim[,4]), 3) #fed

round(quantile(bsim[,4], c(0.025, 0.975)), 3)


round(mean(bsim[,5]), 3) #HSI_foster

round(quantile(bsim[,5], c(0.025, 0.975)), 3)
```

```
round(mean(bsim[,6]), 3) #age emigration

round(quantile(bsim[,6], c(0.025, 0.975)), 3)


round(mean(bsim[,7]), 3) #sex

round(quantile(bsim[,7], c(0.025, 0.975)), 3)


#random effects----

(mean(bsim[,121]))

(quantile(bsim[,121], c(0.025, 0.975)))


(mean(bsim[,122]))

(quantile(bsim[,122], c(0.025, 0.975)))


(mean(bsim[,123]))

(quantile(bsim[,123], c(0.025, 0.975)))



#random effect variance (same additive fixed structure for all models)----

lmm.net_dist.var <- stan_lmer(sqrt(net_dist) ~ sex +JulianD_hatch +fed +HSI_foster

     +(1 | year_hatch) +(1 | fam_foster) +(1 | fam_hatch), data=owl.89, REML=F,

     prior_intercept=normal(3, 2),

     prior=normal(0,5))


bsim <- as.matrix(lmm.net)

dimnames(bsim)$parameters
```

```
(mean(bsim[,119]))
```

```
(quantile(bsim[,119], c(0.025, 0.975)))
```

```
(mean(bsim[,120]))
```

```
(quantile(bsim[,120], c(0.025, 0.975)))
```

```
(mean(bsim[,121]))
```

```
(quantile(bsim[,121], c(0.025, 0.975)))
```

Table S3 - Fixed and random coefficients and credibility intervals of generalized linear mixed-models investigating factors affecting age at first settlement in 89 little owl fledglings. Coefficients with 95% credibility interval not overlapping zero are denoted significant effects.

Fixed-effect variables	Age at first settlement[a]		
	β	Lower 95% CrI	Upper 95% CrI
(Intercept)	6.929	-0.063	0.038
Food supplementation	0.035	-0.020	0.088
Habitat suitability index (HSI)	-0.188	-0.409	0.038
Males	-0.013	-0.063	0.038
Hatching date	-0.005	-0.008	0.002
Age at emigration	0.041	-0.039	0.042
Transfer duration	0.038	0.038	0.039

[a] Random-effect variance [95% credibility interval]: pre-exchange 0.001 [0.000, 0.005]; post-exchange 0.0008 [0.0000, 0.0040]; year 0.002 [0.000, 0.017]

Figure S4 - Predicted net dispersal distance with 95% CrI in female and male little owl fledglings (closed symbol). Grey circles are raw data of female fledglings, and grey dots are raw data of male fledglings (females: N = 52; males: N = 37).