Ecography

E7084
Papadatou, E., Pradel, R., Schaub, M., Dolch, D., Geiger, H., Ibañez, C., Kerth, G., Popa-Lisseanu, A., Schorcht, W., Teubner, J. and Gimenez, O. 2011. Comparing survival among species with imperfect detection using multilevel analysis of mark–recapture data: a case study on bats. – Ecography 34: xxx–xxx.

Supplementary material

Papadatou et al. “Comparing survival among species with imperfect detection using multilevel analysis of mark-recapture data: a case study on bats”

Appendix 1. BUGS code for fitting the multilevel formulation to data

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#### Multilevel analysis of mark-recapture data: comparing survival among species
#### BUGS code for fitting the multilevel formulation to data; model 1 (all species have
different survival)
#### E. Papadatou & O. Gimenez – January 2011

# # # # # # # # # # # MULTILEVEL MODELLING FOR MARK-RECAPTURE DATA:
# DATA
# "mbech" is Myotis bechsteinii
# "plaur" is Plecotus auritus
# "mdau" is M. daubentonii
# "nlei" is Nyctalus leisleri
# "nlas" is N. lasiopterus
# "MBCol1" is colony 1 of the species M. bechsteinii
# "MBCol2" is colony 2 of the species M. bechsteinii
# "MBCol3" is colony 3 of the species M. bechsteinii
# "MBCol4" is colony 4 of the species M. bechsteinii
# "PACol1" is colony 1 of the species P. auritus
# "PACol2" is colony 2 of the species P. auritus
# "ni" is the number of time intervals and equals the number of rows in the m-array
# "nj" is the number of columns in the m-array
# "m" is the m-array including first recaptures and individuals never seen again
# "R" is the number of releases at each capture occasion"
#
# PARAMETERS
# "overall.survival" is the overall mean survival μ across all colonies (sites) of a species
# "mu" is the mean survival of a colony (site) across all time intervals
# "var.site" is inter-colony (site) variance
# "var.eps"  is temporal variance
# "phi" is survival probability at each time interval
# "p"   is encounter probability
# # # # # # # # # # # # # # # # # # # # # # # # # # # # # # # # # # #

Model
{

################################## Mbech
####################################################

# Define model likelihood for mean survival of a colony (site)
for (s in 1:4)
{
# s = site effect
mu.mbech[s] ~ dnorm(overall.survival.mbech,tau.site.mbech)
}
```

```
# Define prior for overall mean survival
# In model 2 (all species have equal survival) this is replaced by overall.survival.mbech <-
mu.m1, where mu.m1 ~ dnorm(0,1.0E-3)
# In model 3 (species grouped in 2 groups) this is replaced by overall.survival.mbech <-
mu.m1, where mu.m1 ~ dnorm(0,1.0E-3)
overall.survival.mbech ~ dnorm(0,1.0E-3)

# Define prior for inter-colony variance (site random effect)
tau.site.mbech <- 1 / (sd.site.mbech * sd.site.mbech)
sd.site.mbech ~ dunif(0,5)

# Monitor variance
var.site.mbech <- 1/tau.site.mbech

################################## MBCol1 ##################################

# Define model likelihood for phi
for (i in 1:ni.MBCol1) {        # time dependent survival

logit(phi.MBCol1[i]) <- logitphi.MBCol1[i]
logitphi.MBCol1[i] ~ dnorm(mu.mbech[1],tau.eps.MBCol1)
}

# Define prior for variance of temporal random effect
tau.eps.MBCol1 <- 1 / (sd.eps.MBCol1*sd.eps.MBCol1)
sd.eps.MBCol1 ~ dunif(0,5)

# Monitor variance
var.eps.MBCol1 <- 1 / tau.eps.MBCol1

# Define priors for p
pt.MBCol1 ~ dunif(0,1)                  # constant detection
for (j in 1:nj.MBCol1) {
p.MBCol1[j] <- pt.MBCol1
}

######### Define Model Likelihood

# Define likelihood
for (i in 1:ni.MBCol1) {
m.MBCol1[i,1:(nj.MBCol1+1)] ~ dmulti(q.MBCol1[i,],R.MBCol1[i])
}

# Calculate the cell probabilities
for (i in 1:ni.MBCol1) {

# Calculate the diagonal
q.MBCol1[i,i]<-p.MBCol1[i]*phi.MBCol1[i]                    # T/T model

# Calculate remaining terms above diagonal
```

```
for (j in (i+1):nj.MBCol1) {
for (k in i:(j-1)) {
lq.MBCol1[i,j,k]<-log(phi.MBCol1[k+1]*(1-p.MBCol1[k]))        # T/T model
}

# Probabilities in table
q.MBCol1[i,j]<-p.MBCol1[j]*phi.MBCol1[i]*exp(sum(lq.MBCol1[i,j,i:(j-1)]))  # T/T model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.MBCol1[i,j]<-0
}

# Probability of an animal never being seen
q.MBCol1[i,nj.MBCol1+1] <- 1 - sum(q.MBCol1[i,1:nj.MBCol1])
}

################################### MBCol1 ###################################

################################### MBCol2 ###################################

# Define model likelihood for phi
for (i in 1:ni.MBCol2) {        # time dependent survival

logit(phi.MBCol2[i]) <- logitphi.MBCol2[i]
logitphi.MBCol2[i] ~ dnorm(mu.mbech[2],tau.eps.MBCol2)
}

# Define prior for variance of temporal random effect
tau.eps.MBCol2 <- 1 / (sd.eps.MBCol2*sd.eps.MBCol2)
sd.eps.MBCol2 ~ dunif(0,5)

# Monitor variance
var.eps.MBCol2 <- 1 / tau.eps.MBCol2

# Define priors for p
for (j in 1:nj.MBCol2) {        # time dependent detection
p.MBCol2[j] ~ dunif(0,1)
}

######### Define Model Likelihood

# Define likelihood
for (i in 1:ni.MBCol2) {
m.MBCol2[i,1:(nj.MBCol2+1)] ~ dmulti(q.MBCol2[i,],R.MBCol2[i])
}

# Calculate the cell probabilities
for (i in 1:ni.MBCol2) {
```

```
# Calculate the diagonal
q.MBCol2[i,i]<-p.MBCol2[i]*phi.MBCol2[i]                    # T/T model

# Calculate remaining terms above diagonal
for (j in (i+1):nj.MBCol2) {
for (k in i:(j-1)) {
lq.MBCol2[i,j,k]<-log(phi.MBCol2[k+1]*(1-p.MBCol2[k]))         # T/T model
}

# Probabilities in table
q.MBCol2[i,j]<-p.MBCol2[j]*phi.MBCol2[i]*exp(sum(lq.MBCol2[i,j,i:(j-1)]))              # T/T
model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.MBCol2[i,j]<-0
}

# Probability of an animal never being seen
q.MBCol2[i,nj.MBCol2+1] <- 1 - sum(q.MBCol2[i,1:nj.MBCol2])
}

################################## MBCol2 ##################################

################################## MBCol3 ##################################

# Define model likelihood for phi
for (i in 1:ni.MBCol3) {         # time dependent survival

logit(phi.MBCol3[i]) <- logitphi.MBCol3[i]
logitphi.MBCol3[i] ~ dnorm(mu.mbech[3],tau.eps.MBCol3)
}

# Define prior for variance of temporal random effect
tau.eps.MBCol3 <- 1 / (sd.eps.MBCol3*sd.eps.MBCol3)
sd.eps.MBCol3 ~ dunif(0,5)

# Monitor variance
var.eps.MBCol3 <- 1 / tau.eps.MBCol3

# Define priors for p
pt.MBCol3 ~ dunif(0,1)                # constant detection
for (j in 1:nj.MBCol3) {
p.MBCol3[j] <- pt.MBCol3
}

######### Define Model Likelihood
```

```
# Define model likelihood
for (i in 1:ni.MBCol3) {
m.MBCol3[i,1:(nj.MBCol3+1)] ~ dmulti(q.MBCol3[i,],R.MBCol3[i])
}

# Calculate the cell probabilities
for (i in 1:ni.MBCol3) {

# Calculate the diagonal
q.MBCol3[i,i]<-p.MBCol3[i]*phi.MBCol3[i]                    # T/T model

# Calculate remaining terms above diagonal
for (j in (i+1):nj.MBCol3) {
for (k in i:(j-1)) {
lq.MBCol3[i,j,k]<-log(phi.MBCol3[k+1]*(1-p.MBCol3[k]))        # T/T model
}

# Probabilities in table
q.MBCol3[i,j]<-p.MBCol3[j]*phi.MBCol3[i]*exp(sum(lq.MBCol3[i,j,i:(j-1)]))              # T/T
model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.MBCol3[i,j]<-0
}

# Probability of an animal never being seen
q.MBCol3[i,nj.MBCol3+1] <- 1 - sum(q.MBCol3[i,1:nj.MBCol3])
}

################################## MBCol3 ##################################

################################## MBCol4 ##################################


# Define model likelihood for phi
for (i in 1:ni.MBCol4) {        # time dependent survival

logit(phi.MBCol4[i]) <- logitphi.MBCol4[i]
logitphi.MBCol4[i] ~ dnorm(mu.mbech[4],tau.eps.MBCol4)
}

# Define prior for variance of temporal random effect
tau.eps.MBCol4 <- 1 / (sd.eps.MBCol4*sd.eps.MBCol4)
sd.eps.MBCol4 ~ dunif(0,5)

# Monitor variance
var.eps.MBCol4 <- 1 / tau.eps.MBCol4
```

```
# Define priors for p
pt.MBCol4 ~ dunif(0,1)                 # constant detection
for (j in 1:nj.MBCol4) {
p.MBCol4[j] <- pt.MBCol4
}

######### Define Model Likelihood

# Define likelihood
for (i in 1:ni.MBCol4) {
m.MBCol4[i,1:(nj.MBCol4+1)] ~ dmulti(q.MBCol4[i,],R.MBCol4[i])
}

# Calculate the cell probabilities
for (i in 1:ni.MBCol4) {

# Calculate the diagonal
q.MBCol4[i,i]<-p.MBCol4[i]*phi.MBCol4[i]                  # T/T model

# Calculate remaining terms above diagonal
for (j in (i+1):nj.MBCol4) {
for (k in i:(j-1)) {
lq.MBCol4[i,j,k]<-log(phi.MBCol4[k+1]*(1-p.MBCol4[k]))        # T/T model
}

# Probabilities in table
q.MBCol4[i,j]<-p.MBCol4[j]*phi.MBCol4[i]*exp(sum(lq.MBCol4[i,j,i:(j-1)]))  # T/T model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.MBCol4[i,j]<-0
}

# Probability of an animal never being seen
q.MBCol4[i,nj.MBCol4+1] <- 1 - sum(q.MBCol4[i,1:nj.MBCol4])
}

#################################### MBCol4 ####################################

################################ Mbech
###################################################


################################ Plaur
###################################################

for (i in 1:2)
{
# s = site effect
```

```
mu.plaur[s] ~ dnorm(overall.survival.plaur,tau.site.plaur)
}

# prior for overall mean survival
# In model 2 (all species have equal survival) this is replaced by overall.survival.plaur <-
mu.m1, where mu.m1 ~ dnorm(0,1.0E-3)
# In model 3 (species grouped in 2 groups) this is replaced by overall.survival.plaur <-
mu.m1, where mu.m1 ~ dnorm(0,1.0E-3)
overall.survival.plaur ~ dnorm(0,1.0E-3)

# prior for inter-colony variance (site random effect)
tau.site.plaur <- 1 / (sd.site.plaur * sd.site.plaur)
sd.site.plaur ~ dunif(0,5)
var.site.plaur <- 1/tau.site.plaur

################################## PACol1 ##################################

# Define model lieklihood for phi
for (i in 1:ni.PACol1) {          # time dependent survival

logit(phi.PACol1[i]) <- logitphi.PACol1[i]
logitphi.PACol1[i] ~ dnorm(mu.plaur[1],tau.eps.PACol1)
}

# Define prior for variance of temporal random effect
tau.eps.PACol1 <- 1 / (sd.eps.PACol1*sd.eps.PACol1)
sd.eps.PACol1 ~ dunif(0,5)

# Monitor variance
var.eps.PACol1 <- 1 / tau.eps.PACol1

# Define priors for p
for (j in 1:nj.PACol1) {          # time dependent detection
p.PACol1[j] ~ dunif(0,1)
}

######### Define Model Likelihood

# Define likelihood
for (i in 1:ni.PACol1) {
m.PACol1[i,1:(nj.PACol1+1)] ~ dmulti(q.PACol1[i,],R.PACol1[i])
}

# Calculate the cell probabilities
for (i in 1:ni.PACol1) {

# Calculate the diagonal
q.PACol1[i,i]<-p.PACol1[i]*phi.PACol1[i]             # T/T model

# Calculate remaining terms above diagonal
```

```
for (j in (i+1):nj.PACol1) {
for (k in i:(j-1)) {
lq.PACol1[i,j,k]<-log(phi.PACol1[k+1]*(1-p.PACol1[k]))            # T/T model
}

# Probabilities in table
q.PACol1[i,j]<-p.PACol1[j]*phi.PACol1[i]*exp(sum(lq.PACol1[i,j,i:(j-1)]))       # T/T model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.PACol1[i,j]<-0
}

# Probability of an animal never being seen
q.PACol1[i,nj.PACol1+1] <- 1 - sum(q.PACol1[i,1:nj.PACol1])
}

############################### PACol1 ###############################

############################### PACol2 ###############################

# Define model likelihood for phi
for (i in 1:ni.PACol2) {          # time dependent survival

logit(phi.PACol2[i]) <- logitphi.PACol2[i]
logitphi.PACol2[i] ~ dnorm(mu.plaur[2],tau.eps.PACol2)
}

# Define prior for variance of temporal random effect
tau.eps.PACol2 <- 1 / (sd.eps.PACol2*sd.eps.PACol2)
sd.eps.PACol2 ~ dunif(0,5)

# Monitor variance
var.eps.PACol2 <- 1 / tau.eps.PACol2

# Define priors for p
for (j in 1:nj.PACol2) {          # time dependent detection
p.PACol2[j] ~ dunif(0,1)
}


######### Define Model Likelihood

# Define likelihood
for (i in 1:ni.PACol2) {
m.PACol2[i,1:(nj.PACol2+1)] ~ dmulti(q.PACol2[i,],R.PACol2[i])
}

# Calculate the cell probabilities
```

```
for (i in 1:ni.PACol2) {

# Calculate the diagonal
q.PACol2[i,i]<-p.PACol2[i]*phi.PACol2[i]          # T/T model

# Calculate remaining terms above diagonal
for (j in (i+1):nj.PACol2) {
for (k in i:(j-1)) {
lq.PACol2[i,j,k]<-log(phi.PACol2[k+1]*(1-p.PACol2[k]))          # T/T model
}

# Probabilities in table
q.PACol2[i,j]<-p.PACol2[j]*phi.PACol2[i]*exp(sum(lq.PACol2[i,j,i:(j-1)]))      # T/T model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.PACol2[i,j]<-0
}

# Probability of an animal never being seen
q.PACol2[i,nj.PACol2+1] <- 1 - sum(q.PACol2[i,1:nj.PACol2])
}

################################## PACol2 ##################################

############################## Plaur
################################################


############################## Mdau
#################################################

# Define model likelihood for phi
for (i in 1:ni.mdau) {                    # time dependent survival
logit(phi.mdau[i]) <- logitphi.mdau[i]
logitphi.mdau[i] ~ dnorm(mu.mdau,tau.eps.mdau)
}

# Define prior for mean survival
# In model 2 (all species have equal survival) this is replaced by mu.mdau <- mu.m1, where
mu.m1 ~ dnorm(0,1.0E-3)
# In model 3 (species grouped in 2 groups) this is replaced by mu.mdau <- mu.m1, where
mu.m1 ~ dnorm(0,1.0E-3)
mu.mdau ~ dnorm(0,0.01)

# Define prior for variance of temporal random effect
tau.eps.mdau <- 1 / (sd.eps.mdau * sd.eps.mdau)
sd.eps.mdau ~dunif(0,5)
```

```
# Monitor variance
var.eps.mdau <- 1 / tau.eps.mdau

# Define priors for p
for (j in 1:nj.mdau) {          # time dependent detection
p.mdau[j] ~ dunif(0,1)
}

############# Define Model Likelihood

# Define likelihood
for (i in 1:ni.mdau) {
m.mdau[i,1:(nj.mdau+1)] ~ dmulti(q.mdau[i,],R.mdau[i])
}

# Calculate the cell probabilities
for (i in 1:ni.mdau) {

# Calculate the diagonal
q.mdau[i,i]<-p.mdau[i]*phi.mdau[i]          # T/T model

# Calculate remaining terms above diagonal
for (j in (i+1):nj.mdau) {
for (k in i:(j-1)) {
lq.mdau[i,j,k]<-log(phi.mdau[k+1]*(1-p.mdau[k]))          # T/T model
}

# Probabilities in table
q.mdau[i,j]<-p.mdau[j]*phi.mdau[i]*exp(sum(lq.mdau[i,j,i:(j-1)]))          # T/T model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.mdau[i,j]<-0
}

# Probability of an animal never being seen
q.mdau[i,nj.mdau+1] <- 1 - sum(q.mdau[i,1:nj.mdau])
}

############################## Mdau
#################################################


############################## Nlei
#################################################

# Define model likelihood for phi
for (i in 1:ni.nlei) {                 # time dependent survival
logit(phi.nlei[i]) <- logitphi.nlei[i]
```

```
logitphi.nlei[i] ~ dnorm(mu.nlei,tau.eps.nlei)
}

# Define prior for mean survival
# In model 2 (all species have equal survival) this is replaced by mu.nlei <- mu.m1, where
mu.m1 ~ dnorm(0,1.0E-3)
# In model 3 (species grouped in 2 groups) this is replaced by mu.nlei <- mu.m2, where
mu.m2 ~ dnorm(0,1.0E-3)
mu.nlei ~ dnorm(0,0.01)

# Define prior for variance of temporal random effect
tau.eps.nlei <- 1 / (sd.eps.nlei * sd.eps.nlei)
sd.eps.nlei ~ dunif(0,5)

# Monitor variance
var.eps.nlei <- 1 / tau.eps.nlei

# Define priors for p
pt.nlei ~ dunif(0,1)                    # constant detection
for (j in 1:nj.nlei) {
p.nlei[j] <- pt.nlei
}

######### Define Model Likelihood

# Define likelihood
for (i in 1:ni.nlei) {
m.nlei[i,1:(nj.nlei+1)] ~ dmulti(q.nlei[i,],R.nlei[i])
}

# Calculate the cell probabilities
for (i in 1:ni.nlei) {

# Calculate the diagonal
q.nlei[i,i]<-p.nlei[i]*phi.nlei[i]                  # T/T model

# Calculate remaining terms above diagonal
for (j in (i+1):nj.nlei) {
for (k in i:(j-1)) {
lq.nlei[i,j,k]<-log(phi.nlei[k+1]*(1-p.nlei[k]))        # T/T model
}

# Probabilities in table
q.nlei[i,j]<-p.nlei[j]*phi.nlei[i]*exp(sum(lq.nlei[i,j,i:(j-1)]))          # T/T model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.nlei[i,j]<-0
}
```

```
# Probability of an animal never being seen
q.nlei[i,nj.nlei+1] <- 1 - sum(q.nlei[i,1:nj.nlei])
}

############################## Nlei
#################################################


############################## Nlas
#################################################

# Define model likelihood for phi

logitphiissue1 ~ dnorm(mu.nlas,tau.eps.nlas)
logit(phi.nlas[3]) <- logitphiissue1
logit(phi.nlas[4]) <- logitphiissue1

for (i in 1:2) {
logit(phi.nlas[i]) <- logitphi.nlas[i]
logitphi.nlas[i] ~ dnorm(mu.nlas,tau.eps.nlas)
}

for (i in 5:ni.nlas) {                          # time dependent survival
logit(phi.nlas[i]) <- logitphi.nlas[i]
logitphi.nlas[i] ~ dnorm(mu.nlas,tau.eps.nlas)
}

# Define prior for mean survival
# In model 2 (all species have equal survival) this is replaced by mu.nlas <- mu.m1, where
mu.m1 ~ dnorm(0,1.0E-3)
# In model 3 (species grouped in 2 groups) this is replaced by mu.nlas <- mu.m2, where
mu.m2 ~ dnorm(0,1.0E-3)
mu.nlas ~ dnorm(0,0.01)

# Define prior for variance of temporal random effect
tau.eps.nlas <- 1 / (sd.eps.nlas * sd.eps.nlas)
sd.eps.nlas ~ dunif(0,5)

# Monitor variance
var.eps.nlas <- 1 / tau.eps.nlas

# Define priors for p
p.nlas[3] <- 0

pt.nlas ~ dunif(0,1)
for (j in 1:2) {
p.nlas[j] <- pt.nlas               # constant detection
}
```

```
for (j in 4:nj.nlas) {
p.nlas[j] <- pt.nlas              # constant detection
}

######### Define Model Likelihood


# Define likelihood
for (i in 1:ni.nlas) {
m.nlas[i,1:(nj.nlas+1)] ~ dmulti(q.nlas[i,],R.nlas[i])
}

# Calculate the cell probabilities
for (i in 1:ni.nlas) {

# Calculate the diagonal
q.nlas[i,i]<-p.nlas[i]*phi.nlas[i]                  # T/T model

# Calculate remaining terms above diagonal
for (j in (i+1):nj.nlas) {
for (k in i:(j-1)) {
lq.nlas[i,j,k]<-log(phi.nlas[k+1]*(1-p.nlas[k]))        # T/T model
}

# Probabilities in table
q.nlas[i,j]<-p.nlas[j]*phi.nlas[i]*exp(sum(lq.nlas[i,j,i:(j-1)]))        # T/T model

}
for (j in 1:(i-1)) {
# Zero probabilities in lower triangle of table
q.nlas[i,j]<-0
}

# Probability of an animal never being seen
q.nlas[i,nj.nlas+1] <- 1 - sum(q.nlas[i,1:nj.nlas])
}

############################## Nlas
################################################
}
```

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Appendix 2. Survival and recapture estimates

Here we present survival (φ) probability estimates from model 3 (Eq. 4 in main text; estimates are posterior means with standard deviations) which was best supported by the data (Table 2 in main text), and from separate frequentist analyses (estimates are provided with standard errors) for each species x site (colony) using program E-SURGE (Choquet et al. 2009). Recapture probabilities (p) are also showed. The “*” symbol stands for a redundant parameter and the “-” symbol stands for the SE of a boundary estimate that cannot be produced.

Myotis bechsteinii

Colony 1 (BS1):

Parameter	Model 3 Estimate (SD)	Separate analysis Estimate (SE)
φ_1	0.79 (0.06)	0.67 (0.10)
φ_2	0.85 (0.05)	1.00 (-)
φ_3	0.83 (0.05)	0.83 (0.08)
φ_4	0.85 (0.04)	0.94 (0.05)
φ_5	0.82 (0.05)	0.81 (0.09)
φ_6	0.82 (0.05)	0.78 (0.07)
φ_7	0.82 (0.05)	0.78 (0.10)
φ_8	0.82 (0.05)	0.78 (0.11)
φ_9	0.83 (0.05)	0.83 (0.11)
φ_{10}	0.83 (0.05)	0.83 (0.11)
φ_{11}	0.84 (0.05)	0.93 (0.07)
φ_{12}	0.84 (0.05)	0.88 (0.08)
φ_{13}	0.84 (0.05)	0.88 (0.07)
p	0.97 (0.01)	0.98 (0.01)

Colony 2 (GB):

Parameter	Model 3 Estimate (SD)	Separate analysis Estimate (SE)
φ_1	0.88 (0.05)	0.89 (0.02)
φ_2	0.89 (0.05)	0.94 (0.02)
φ_3	0.88 (0.05)	0.89 (0.03)
φ_4	0.88 (0.06)	0.89 (0.02)
φ_5	0.90 (0.05)	0.94 (0.02)
φ_6	0.71 (0.07)	0.67 (0.01)
φ_7	0.84 (0.06)	0.83 (0.03)
φ_8	0.87 (0.05)	0.88 (0.02)
φ_9	0.89 (0.05)	0.89 (0.02)
φ_{10}	0.65 (0.08)	0.60 (0.04)
φ_{11}	0.91 (0.04)	0.94 (0.02)
φ_{12}	0.84 (0.05)	0.83 (0.04)
φ_{13}	0.90 (0.05)	*
p_1	0.96 (0.04)	1.00 (-)
p_2	0.73 (0.09)	0.75 (0.08)
p_3	0.90 (0.06)	0.95 (0.04)
p_4	0.82 (0.08)	0.86 (0.06)
p_5	0.89 (0.06)	0.91 (0.04)
p_6	0.96 (0.04)	1.00 (-)
p_7	0.89 (0.06)	0.92 (0.03)
p_8	0.97 (0.03)	1.00 (-)

p_9	0.96 (0.04)	1.00 (-)
p_{10}	0.96 (0.04)	1.00 (-)
p_{11}	0.97 (0.03)	1.00 (-)
p_{12}	0.97 (0.03)	1.00 (-)
p_{13}	0.92 (0.06)	*

Colony 3 (HB):

Parameter	Model 3 Estimate (SD)	Separate analysis Estimate (SE)
φ_1	0.67 (0.08)	0.57 (0.08)
φ_2	0.78 (0.07)	0.76 (0.10)
φ_3	0.79 (0.07)	0.78 (0.11)
φ_4	0.81 (0.07)	0.84 (0.10)
φ_5	0.85 (0.06)	0.95 (0.06)
φ_6	0.76 (0.07)	0.72 (0.11)
φ_7	0.80 (0.07)	0.82 (0.07)
φ_8	0.84 (0.07)	0.93 (0.05)
φ_9	0.83 (0.06)	0.89 (0.08)
φ_{10}	0.79 (0.06)	0.80 (0.08)
φ_{11}	0.72 (0.07)	0.67 (0.09)
φ_{12}	0.70 (0.07)	0.63 (0.09)
φ_{13}	0.84 (0.06)	0.91 (0.07)
p	0.97 (0.01)	0.98 (0.01)

Colony 4 (UH):

Parameter	Model 3 Estimate (SD)	Separate analysis Estimate (SE)
φ_1	0.71 (0.09)	0.60 (0.05)
φ_2	0.78 (0.08)	0.74 (0.02)
φ_3	0.86 (0.06)	1.00 (-)
φ_4	0.82 (0.07)	0.83 (0.05)
φ_5	0.86 (0.06)	0.94 (0.02)
φ_6	0.81 (0.06)	0.81 (0.07)
φ_7	0.79 (0.07)	0.77 (0.03)
φ_8	0.77 (0.08)	0.71 (0.04)
φ_9	0.83 (0.06)	0.87 (0.05)
φ_{10}	0.87 (0.06)	0.95 (0.02)
φ_{11}	0.80 (0.06)	0.78 (0.05)
φ_{12}	0.72 (0.09)	0.62 (0.05)
φ_{13}	0.83 (0.07)	0.87 (0.06)
p	0.96 (0.02)	0.97 (0.01)

Plecotus auritus

Colony 1 (BS2):

Parameter	Model 3 Estimate (SD)	Separate analysis Estimate (SE)
φ_1	0.83 (0.13)	1.00 (-)
φ_2	0.70 (0.14)	0.55 (0.06)
φ_3	0.89 (0.06)	0.91 (0.05)
φ_4	0.97 (0.03)	1.00 (-)
φ_5	0.70 (0.08)	0.67 (0.05)
φ_6	0.75 (0.09)	0.71 (0.06)
φ_7	0.91 (0.07)	*
p_1	0.03 (0.03)	0.00 (0.00)
p_2	0.79 (0.09)	0.84 (0.10)
p_3	0.96 (0.04)	1.00 (0.00)

p_4	0.92 (0.05)	0.94 (0.03)
p_5	0.82 (0.08)	0.86 (0.06)
p_6	0.52 (0.09)	0.55 (0.05)
p_7	0.87 (0.09)	*

Colony 2 (KR):

Parameter	Model 3 Estimate (SD)	Separate analysis Estimate (SE)
φ_1	0.92 (0.06)	1.00 (-)
φ_2	0.93 (0.05)	1.00 (-)
φ_3	0.85 (0.07)	0.86 (0.07)
φ_4	0.88 (0.06)	0.91 (0.05)
φ_5	0.93 (0.04)	0.97 (0.03)
φ_6	0.91 (0.04)	0.92 (0.04)
φ_7	0.83 (0.05)	0.84 (0.04)
φ_8	0.80 (0.05)	0.80 (0.05)
φ_9	0.68 (0.06)	0.67 (0.05)
φ_{10}	0.76 (0.06)	0.75 (0.06)
φ_{11}	0.76 (0.06)	0.76 (0.06)
φ_{12}	0.63 (0.07)	0.61 (0.06)
φ_{13}	0.73 (0.10)	0.62 (0.07)
φ_{14}	0.61 (0.20)	1.00 (-)
φ_{15}	0.63 (0.19)	0.56 (0.14)
φ_{16}	0.55 (0.17)	0.34 (0.17)
φ_{17}	0.82 (0.10)	0.83 (0.10)
φ_{18}	0.85 (0.08)	0.88 (0.10)
φ_{19}	0.77 (0.10)	0.73 (0.11)
φ_{20}	0.86 (0.09)	1.00 (-)
φ_{21}	0.75 (0.17)	*
p_1	0.93 (0.06)	1.00 (-)
p_2	0.90 (0.07)	0.95 (0.05)
p_3	0.95 (0.05)	1.00 (-)
p_4	0.95 (0.04)	1.00 (-)
p_5	0.97 (0.03)	1.00 (-)
p_6	0.97 (0.03)	1.00 (-)
p_7	0.97 (0.03)	1.00 (-)
p_8	0.94 (0.04)	0.97 (0.03)
p_9	0.97 (0.03)	1.00 (-)
p_{10}	0.94 (0.04)	0.97 (0.03)
p_{11}	0.96 (0.04)	1.00 (-)
p_{12}	0.96 (0.04)	1.00 (-)
p_{13}	0.85 (0.11)	1.00 (-)
p_{14}	0.04 (0.05)	0.00 (-)
p_{15}	0.10 (0.08)	0.04 (0.04)
p_{16}	0.78 (0.13)	0.87 (0.13)
p_{17}	0.91 (0.08)	1.00 (-)
p_{18}	0.83 (0.10)	0.89 (0.11)
p_{19}	0.90 (0.09)	1.00 (-)
p_{20}	0.66 (0.12)	0.62 (0.01)
p_{21}	0.49 (0.17)	*

Myotis daubentonii (NH):

	Model 3	Separate analysis
Parameter	Estimate (SD)	Estimate (SE)
φ_1	0.79 (0.05)	0.79 (0.02)
φ_2	0.66 (0.04)	0.65 (0.01)
φ_3	0.74 (0.04)	0.75 (0.02)
φ_4	0.62 (0.05)	0.61 (0.01)
φ_5	0.54 (0.06)	0.53 (0.02)
φ_6	0.67 (0.08)	0.65 (0.02)
φ_7	0.73 (0.12)	0.70 (0.02)
φ_8	0.67 (0.20)	*
p_1	0.30 (0.03)	0.30 (0.03)
p_2	0.50 (0.03)	0.50 (0.03)
p_3	0.61 (0.04)	0.61 (0.03)
p_4	0.35 (0.04)	0.35 (0.02)
p_5	0.30 (0.04)	0.31 (0.02)
p_6	0.44 (0.05)	0.45 (0.03)
p_7	0.31 (0.06)	0.32 (0.02)
p_8	0.19 (0.14)	*

Nyctalus leisleri (WS):

	Model 3	Separate analysis
Parameter	Estimate (SD)	Estimate (SE)
φ_1	0.72 (0.11)	0.68 (0.11)
φ_2	0.72 (0.10)	0.71 (0.16)
φ_3	0.77 (0.09)	0.84 (0.12)
φ_4	0.76 (0.08)	0.78 (0.11)
φ_5	0.74 (0.08)	0.72 (0.04)
φ_6	0.77 (0.08)	0.84 (0.11)
φ_7	0.54 (0.09)	0.44 (0.06)
φ_8	0.73 (0.08)	0.74 (0.09)
φ_9	0.78 (0.08)	0.84 (0.09)
φ_{10}	0.76 (0.08)	0.79 (0.10)
φ_{11}	0.70 (0.09)	0.67 (0.10)
φ_{12}	0.68 (0.08)	0.65 (0.09)
φ_{13}	0.74 (0.07)	0.74 (0.08)
φ_{14}	0.84 (0.06)	0.91 (0.06)
φ_{15}	0.86 (0.06)	0.97 (-)
φ_{16}	0.70 (0.07)	0.66 (-)
φ_{17}	0.59 (0.08)	0.54 (0.07)
φ_{18}	0.66 (0.09)	0.60 (0.05)
p	0.75 (0.03)	0.75 (0.03)

N. lasiopterus (PML):

	Model 3	Separate analysis
Parameter	Estimate (SD)	Estimate (SE)
φ_1	0.28 (0.22)	0,11 (0,11)
φ_2	0.42 (0.23)	0.25 (0,17)
φ_3	0.89 (0.10)	1.00 (-)
φ_4	0.89 (0.10)	1.00 (-)
φ_5	0.57 (0.17)	0.45 (0,14)
φ_6	0.54 (0.16)	0.44 (0,12)
φ_7	0.83 (0.14)	0.86 (0,24)
φ_8	0.61 (0.19)	0.44 (0,15)
p	0.22 (0.06)	0.28 (0,07)

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