

Supplementary Materials

File S1: Visual Counts

Visual counts were performed during each sampling session, i.e. at least twice a year. Each colony was surveyed by the same person each year throughout the investigation period with two exceptions, where the investigator changed once. Altogether nine persons did the visual counts in the 16 colonies of the non-expanding population, and five persons counted individuals in the 19 colonies of the expanding population.

Synergism with ongoing monitoring performed by a bat protection NGO allowed an additional counting event in between sampling sessions in the expanding population. This count was always performed by the same person in all colonies. Adults and juveniles were thus partly counted by different surveyors in the expanding population. Counting juveniles may be challenging for various reasons like a difficult access to the roost or early breeding, and could not be performed for 12 out of 57 counts in the expanding population, and for 13 out of 72 in the non-expanding one.

File S2: Simulations

To test the reliability of models that utilize genetic data for estimating vital rates, we simulated two times 36 colonies consisting of 100 females each (representing the two different populations of our empirical data set) and tested the three different models. Mimicking the different sampling regimes in our empirical data, the life histories of each individual and the appearance of new ones (juveniles) were simulated for four years in the non-expanding, and for three years in the expanding population. We also simulated the birth of male juveniles, but they were excluded from the dataset used in CMR models. Based on previous knowledge on *R. hipposideros* and other bat species [28,29,31,36,52], we set adult survival to 0.85, juvenile survival to 0.4, and fecundity (considering only female juvenile) to 0.4 in our simulated colonies.

Simulated individuals were then sampled to create CMR data, considering two sessions each year and juveniles being captured only in post-birth sessions. Each simulated colony was sampled twice, following either the sampling procedure of the non-expanding population (i.e. the number of samples corresponding to twice the estimated the colony size in the first year and being equal to the estimated colony size in the following years), or the sampling procedure of the expanding population (i.e. the number of samples corresponding to twice the estimated colony size in all post-birth sampling sessions

and the pre-birth sampling session of the first year, and being equal to the estimated colony size for the pre-birth sampling sessions of the following years). Based on previous knowledge on detection probabilities in maternity colonies [22], detection probabilities were set depending on the reproductive status. For sessions where the number of samples was equivalent to colony size, we set detection probabilities between 0.45 and 0.55 for adults (pre-birth, no distinction of reproductive state) and non-mothers (post-birth), and between 0.65 and 0.75 for mothers (post-birth) due to higher roost fidelity of mothers in the post-reproduction phase. Juvenile detection probabilities were set relatively low, between 0.25 and 0.35, because there is only a single sampling session where a juvenile can be sampled and because juvenile mortality is expected to be particularly high in the first few weeks in European bats [19], which greatly reduces overall detection probability compared to adults. Detection probabilities (dp) were increased for sessions when the number of samples corresponded to twice the estimated colony size (Increased detection probability = $dp + (dp \cdot (1 - dp))$).

Colony size estimates were simulated including observation errors with a Poisson distribution, using the true colony size as lambda parameter of the distribution. Parentage assignment was conditional on the detection of both juvenile and mother and included a proportion of unassigned dyads between 5 and 15%.

Once the dataset was simulated, we estimated demographic parameters with three different models (see following sections for more details): One considering only the capture-recapture data to estimate adult and juvenile local survival (CMRo), a model including parentage assignment data to also estimate fecundity (CMRpa), and an IPM combining the CMRpa model with a state space model using colony size estimates (see section 'Integrated Population Model' in the main manuscript). We then estimated and compared the reliability of those models by computing their relative bias, precision (standard error) and accuracy (mean squared error), following Abadi et al. (2013).

File S3: CMRo model

This model draws exclusively on CMR data for the estimation of adult and juvenile survival (see Section 'Integrated Population Model' in the main manuscript for more details). Two observations are considered: "Possible Juveniles", which corresponds to individuals detected for the first time during a post-birth session, and "Adults". The observation process follows a multinomial distribution with cells that are a function of adult detection probability (p) and the proportion of adults only detected later, at the post-birth sampling session (IA). The state process also follows a multinomial distribution with cells that are a function of juvenile survival (ϕ_j – the probability for a Juvenile to survive and become an Adult) and adult survival (ϕ_a – the probability for an Adult to survive to the next year). Intra-annual survival, i.e. survival

between pre- and post-birth sampling was not considered, because we expect adult mortality to be negligible during the few days between sampling sessions. Survival rates and the proportion of adults detected late (i.e. post- instead of pre-reproduction) were assumed to remain constant in time. Detection probability however was considered to be specific for the sampling session to fit the varying sampling effort in our protocol. Given previous knowledge on bat survival probability, we constrained juvenile survival rates to be lower than adult survival by at least 0.1 [28–30]. The state process and the observation process are illustrated in Figure S 1. The initial state matrix, the transition matrix and the detection matrix containing the parameters of the multinomial distributions are displayed in Figure S 2. The likelihood of this model (Figure S 3) is $L_{CMRO} = (m|\phi_\alpha, \phi_j, p, lA)$.

File S4: CMRpa model

In addition to CMR data, information from parentage assignment is included in this model to estimate fecundity (see section ‘Integrated Population Model’ in the main manuscript for more details). Individuals sampled at the pre-reproduction session or already sampled in previous years were considered as adults and thus, potential parents. Individuals first sampled at the post-birth session were considered as potential juveniles. The full parentage assignment method is described by Zarzoso-Lacoste et al. [22].

In this model, all individuals sampled in pre-reproduction sessions are still considered as Adults (with their own capture probability - p_A), but three states are possible for post-birth sessions: Mother (of a female offspring), Non-mother and Juvenile (Figure S 4). The state process still follows a multinomial distribution with cells that are a function of ϕ_α and ϕ_j for the state transition from post-birth to pre-reproduction sessions (Figure S 5), because we considered that the survival probability was the same for mothers and non-mothers. Cells considering the transition from Adults to Mothers or Non-mothers are a function of fecundity (F). We directly included the parentage assignment results in the CMR data by adding the observations "assigned as mother" and "assigned as juvenile" in the observation process (Figure S 4). The parentage assignment protocol implies that an individual can only be assigned as a mother if it was previously sampled, and assigned as a juvenile if it is its first detection [22]. A previous study on *R. hipposideros* demonstrated that roost fidelity, and thus detection probability is higher in mothers than in non-mothers [22]. The multinomial distribution of the observation process is thus a function of the Adult, Mother, and Non-mother detection probabilities, respectively (p_A , p_M , and p_N , with p_M set to be higher than p_N) and parameters considering assignment error. Juveniles can only be sampled during their first detection, hence their detection probability cannot be quantified and is not considered in the model. The proportions of Mothers and Juveniles that were correctly assigned ($Mass$ and $Jass$, respectively,) were

set in the model without constraints: We expected a good parentage assignment between the potential mothers and potential juveniles from the Colony software, but accurate assignments require both the detection of the Mother before birth and the detection of the Juvenile, which will probably lower *Mass* and *Jass* [22]. The proportion of individuals wrongly assigned as Mother or Juvenile, termed *NasM*, *MasJ* and *NasJ* depending on their states and observation (see Figure S 5) were assumed to be low, and set to less than 5%. The initial state matrix, the transition matrix and the detection matrix containing the parameters of the multinomial distributions are displayed in Figure S4. The likelihood of this model (Figure S 6) is $L_{CMRPA} = (m | \phi_a, \phi_j, F, p_A, p_M, p_N, Mass, Jass, NasM, MasJ, NasJ)$. The JAGS script of this model is provided as a Supplementary File.

File S5: JAGS script of the Integrated Population Model, IPM

```
##### Values supplied to the model #####
# X.phi : vector used to distinguish from one transition to another,
# X.phi=c(1,2,1,2,1,2,1)
# CountA : Number of adult females estimated at each session
# CountJ : Number of juvenile females estimated at each post-
# reproduction session
# Adinit : Starting value for the number of adult females (estimation from
# the first session)
# y : CMR data
# f : Session of first detection for each individual
# n.occasions : number of sessions
# n.ind : number of individuals in the CMR data
#####

model {

# Between pre-birth and post-birth sessions: adult
# survival = 1, and juvenile survival = 0.
# Between post-birth and pre-birth sessions:
# fecundity = 0.
# For every other transitions: Vital rates are supposed constant.

    for (t in 1:(n.occasions-1)){
      phiAd[t] <- survAd[X.phi[t]]
    }

    for (t in 1:(n.occasions-1)){
      phiJu[t] <- survJu[X.phi[t]]
    }

    for (t in 1:(n.occasions-1)){
      Fec[t] <- Fecund[X.phi[t]]
    }

    survAd[1]~ dunif(0.999, 1)
    survAd[2]~ dunif(0, 1)

    survJu[1]~ dunif(0, 0.001)
    survJu[2]~ dunif(0, 1)

    Fecund[1]~ dunif(0, 1)
    Fecund[2]~ dunif(0, 0.001)

#####
#
# State-Space Model
#
#####
```

```

# Initial colony size (NJU: juvenile colony size, NAd: adult
# colony size).
# At the first session (pre-reproduction), there is not any juvenile

      n1 ~ dnorm(0, 1000000)T(0,0)
      nad ~ dnorm(Adinit, 0.1)T(0,)
      NJu[1] <- round(n1)
      NAd[1] <- round(nad)

# Juvenile colony size: 0 at pre-reproduction session,
# Fecundity * Adult colony size at post-reproduction session.
# index 7 and 8 are only used for the non-expanding population
# (only six sessions in the expanding one)

      mean1[2] <- Fecund[1] * NAd [1]
      mean1[4] <- Fecund[1] * NAd [3]
      mean1[6] <- Fecund[1] * NAd [5]
      mean1[8] <- Fecund[1] * NAd [7]
      mean1[1] <- 0
      mean1[3] <- 0
      mean1[5] <- 0
      mean1[7] <- 0

      NJu[2] ~ dpois(mean1[2] )
      NJu[4] ~ dpois(mean1[4] )
      NJu[6] ~ dpois(mean1[6] )
      NJu[8] ~ dpois(mean1[8] )
      NJu[3] <- 0
      NJu[5] <- 0
      NJu[7] <- 0

# Adult colony size: depend of the survival of individuals from
# one year to another

      for (t in 2:n.occasions){
        meanAd[t] <- survAd[X.phi[t-1]] * NAd [t-1] +
survJu[X.phi[t-1]] * NJu [t-1]
        NAd[t] ~ dpois(meanAd[t])
      }

# Count of colony size: include observation
# error with a Poisson distribution

      for (t in 1:n.occasions){
        CountA[t] ~ dpois(NAd[t])
      }

      CountJ[2] ~ dpois(NJu[2])
      CountJ[4] ~ dpois(NJu[4])
      CountJ[6] ~ dpois(NJu[6])
      CountJ[8] ~ dpois(NJu[8])

```

```

#####
#
# CMR
#
#####

# Probability of detection: Adults are only seen during pre-birth
# session.
# Other states are seen during post-birth session. pN are
# always inferior to pM.

pAd[1] ~ dunif(0, 1)
pAd[3] ~ dunif(0, 1)
pAd[5] ~ dunif(0, 1)
pAd[7] ~ dunif(0, 1)
pAd[2] <- 0
pAd[4] <- 0
pAd[6] <- 0
pAd[8] <- 0
pN[2] ~ dunif(0, pMo[2])
pMo[2] ~ dunif(0, 1)
pN[4] ~ dunif(0, pMo[4])
pMo[4] ~ dunif(0, 1)
pN[6] ~ dunif(0, pMo[6])
pMo[6] ~ dunif(0, 1)
pN[8] ~ dunif(0, pMo[8])
pMo[8] ~ dunif(0, 1)
pN[1] <- 0
pMo[1] <- 0
pN[3] <- 0
pMo[3] <- 0
pN[5] <- 0
pMo[5] <- 0
pN[7] <- 0
pMo[7] <- 0
JuvAssign ~ dunif(0, 1)
MAssignasJuv ~ dunif(0, 0.05)
MAssign ~ dunif(0, 1)
NAssignasJuv ~ dunif(0, 0.05)
NAssignasM ~ dunif(0, 0.05)

# Diritchlet distribution for gamma distribution

for (i in 1:4) {
a[i] ~ dgamma(1,1)
pi[i] <- a[i]/sum(a[])
}

##### Define state-transition and observation matrices #####

# Define state probability when an individual is sampled
for (i in 1:nind){

```

```

    for (t in f[i]:f[i]) {

        pj[i,t,1] <- pi[1]
        pj[i,t,2] <- pi[2]
        pj[i,t,3] <- pi[3]
        pj[i,t,4] <- pi[4]

# Define probabilities of observation(t) given the state(t) at the session
# of first marking. See initial state matrix of the CMRpa model

        plo[1,i,t,1] <- 1
        plo[1,i,t,2] <- 0
        plo[1,i,t,3] <- 0
        plo[1,i,t,4] <- 0
        plo[1,i,t,5] <- 0

        plo[2,i,t,1] <- 0
        plo[2,i,t,2] <- JuvAssign
        plo[2,i,t,3] <- 1-JuvAssign
        plo[2,i,t,4] <- 0
        plo[2,i,t,5] <- 0

        plo[3,i,t,1] <- 0
        plo[3,i,t,2] <- MAssignasJuv
        plo[3,i,t,3] <- (1-MAssignasJuv)
        plo[3,i,t,4] <- 0
        plo[3,i,t,5] <- 0

        plo[4,i,t,1] <- 0
        plo[4,i,t,2] <- NAssignasJuv
        plo[4,i,t,3] <- (1-NAssignasJuv)
        plo[4,i,t,4] <- 0
        plo[4,i,t,5] <- 0

    }

# Define probabilities of state(t+1) given state(t)
# See Transition matrix of the CMRpa model

    for (t in f[i):(n.occasions-1)) {

        ps[1,i,t,1] <- 0
        ps[1,i,t,2] <- 0
        ps[1,i,t,3] <- Fec[t]
        ps[1,i,t,4] <- 1-Fec[t]
        ps[1,i,t,5] <- 1-phiAd[t]
        ps[2,i,t,1] <- phiJu[t]
        ps[2,i,t,2] <- 0
        ps[2,i,t,3] <- 0
        ps[2,i,t,4] <- 0
        ps[2,i,t,5] <- 1-phiJu[t]
        ps[3,i,t,1] <- phiAd[t]

```

```

ps[3,i,t,2] <- 0
ps[3,i,t,3] <- 0
ps[3,i,t,4] <- 0
ps[3,i,t,5] <- 1-phiAd[t]
ps[4,i,t,1] <- phiAd[t]
ps[4,i,t,2] <- 0
ps[4,i,t,3] <- 0
ps[4,i,t,4] <- 0
ps[4,i,t,5] <- 1-phiAd[t]
ps[5,i,t,1] <- 0
ps[5,i,t,2] <- 0
ps[5,i,t,3] <- 0
ps[5,i,t,4] <- 0
ps[5,i,t,5] <- 1
}

```

```

# Define probabilities of observation(t) given state(t) after first sampling
# See detection matrix of the CMRpa model

```

```

for (t in (f[i]+1):(n.occasions)){

po[1,i,t,1] <- pAd[t]
po[1,i,t,2] <- 0
po[1,i,t,3] <- 0
po[1,i,t,4] <- 0
po[1,i,t,5] <- 0
po[1,i,t,6] <- 1-pAd[t]
po[2,i,t,1] <- 0
po[2,i,t,2] <- 0
po[2,i,t,3] <- 0
po[2,i,t,4] <- 0
po[2,i,t,5] <- 0
po[2,i,t,6] <- 0
po[3,i,t,1] <- 0
po[3,i,t,2] <- 0
po[3,i,t,3] <- 0
po[3,i,t,4] <- pMo[t] * MAssign
po[3,i,t,5] <- pMo[t] * (1-MAssign)
po[3,i,t,6] <- 1-pMo[t]
po[4,i,t,1] <- 0
po[4,i,t,2] <- 0
po[4,i,t,3] <- 0
po[4,i,t,4] <- pN[t] * (NAssignasM)
po[4,i,t,5] <- pN[t] * (1 - NAssignasM)
po[4,i,t,6] <- 1-pN[t]
po[5,i,t,1] <- 0
po[5,i,t,2] <- 0
po[5,i,t,3] <- 0
po[5,i,t,4] <- 0
po[5,i,t,5] <- 0
po[5,i,t,6] <- 1
}

```

```

    } }

##### Likelihood #####

    for (i in 1:nind){

# Define latent state at first capture

        z[i,f[i]] ~ dcat(pj[i,f[i],])
        y[i,f[i]] ~ dcat(plo[z[i,f[i]],i, f[i],])

        for (t in (f[i]+1):n.occasions){

# State process: draw state(t) given state(t-1)

            z[i,t] ~ dcat(ps[z[i,t-1],i,t-1,])

# Observation process: draw observation(t) given state(t)

            y[i,t] ~ dcat(po[z[i,t],i,t,])

        } #t

    } #i

} #model

```

Table S1: Relative bias, standard error, and mean squared error (MSE) of the three developed models for the estimation of adult survival, juvenile survival, and fecundity (results based on simulations).

Parameter	Model	expanding			non-expanding		
		Relative bias	Standard error	MSE	Relative bias	Standard error	MSE
Adult survival	CMRo	0.01	0.02	0.001	0.01	0.03	0.001
	CMRpa	0.01	0.03	0.001	0.01	0.03	0.001
	IPM	0.01	0.03	0.001	0.01	0.03	0.001
Juvenile survival	CMRo	0.20	0.06	0.010	0.24	0.07	0.014
	CMRpa	0.07	0.09	0.009	0.10	0.13	0.019
	IPM	0.07	0.07	0.006	0.11	0.12	0.017
Fecundity	CMRo	NA	NA	NA	NA	NA	NA
	CMRpa	0.86	0.06	0.122	1.05	0.03	0.176
	IPM	0.02	0.02	0.001	0.02	0.03	0.001

Table S2: Demographic parameters estimated for *Rhinolophus hipposideros* colonies

Colony	Population	Adult Survival	Juvenile Survival	Fecundity	Reproduction Rate	Growth Rate
Thu20	expanding	0.65 ± 0.04	0.45 ± 0.07	0.33 ± 0.05	0.15 ± 0.05	0.80 ± 0.09
Thu21	expanding	0.86 ± 0.06	0.66 ± 0.09	0.24 ± 0.04	0.16 ± 0.05	1.02 ± 0.11
Thu22	expanding	0.81 ± 0.05	0.49 ± 0.09	0.40 ± 0.06	0.20 ± 0.07	1.01 ± 0.11
Thu23	expanding	0.81 ± 0.07	0.47 ± 0.13	0.53 ± 0.18	0.25 ± 0.15	1.06 ± 0.23
Thu24	expanding	0.90 ± 0.09	0.52 ± 0.24	0.48 ± 0.20	0.25 ± 0.22	1.15 ± 0.31
Thu25	expanding	0.78 ± 0.11	0.59 ± 0.13	0.43 ± 0.12	0.25 ± 0.13	1.03 ± 0.24
Thu26	expanding	0.85 ± 0.06	0.67 ± 0.08	0.47 ± 0.09	0.32 ± 0.10	1.17 ± 0.16
Thu27	expanding	0.71 ± 0.07	0.47 ± 0.10	0.44 ± 0.12	0.21 ± 0.10	0.91 ± 0.17
Thu28	expanding	0.74 ± 0.05	0.53 ± 0.09	0.72 ± 0.12	0.38 ± 0.13	1.12 ± 0.18
Thu29	expanding	0.73 ± 0.06	0.54 ± 0.09	0.33 ± 0.06	0.18 ± 0.06	0.90 ± 0.12
Thu30	expanding	0.83 ± 0.07	0.60 ± 0.12	0.59 ± 0.09	0.35 ± 0.13	1.19 ± 0.19
Thu31	expanding	0.78 ± 0.08	0.58 ± 0.10	0.48 ± 0.13	0.27 ± 0.12	1.05 ± 0.20
Thu32	expanding	0.90 ± 0.07	0.67 ± 0.13	0.36 ± 0.07	0.24 ± 0.10	1.14 ± 0.16
Thu33	expanding	0.90 ± 0.05	0.68 ± 0.09	0.39 ± 0.08	0.27 ± 0.09	1.17 ± 0.14
Thu34	expanding	0.59 ± 0.12	0.34 ± 0.15	0.30 ± 0.10	0.10 ± 0.08	0.69 ± 0.19
Thu35	expanding	0.92 ± 0.06	0.65 ± 0.12	0.39 ± 0.09	0.25 ± 0.11	1.17 ± 0.16
Thu36	expanding	0.78 ± 0.07	0.49 ± 0.12	0.34 ± 0.06	0.16 ± 0.07	0.94 ± 0.14
Thu37	expanding	0.93 ± 0.05	0.66 ± 0.11	0.32 ± 0.09	0.22 ± 0.09	1.14 ± 0.14
Thu39	expanding	0.77 ± 0.06	0.61 ± 0.07	0.38 ± 0.07	0.23 ± 0.07	1.00 ± 0.12
Pic1	non-expanding	0.65 ± 0.07	0.38 ± 0.11	0.73 ± 0.14	0.28 ± 0.14	0.93 ± 0.21
Pic2	non-expanding	0.73 ± 0.05	0.26 ± 0.12	0.38 ± 0.11	0.10 ± 0.08	0.83 ± 0.13
Pic3	non-expanding	0.63 ± 0.05	0.33 ± 0.10	0.61 ± 0.09	0.20 ± 0.09	0.83 ± 0.14
Pic4	non-expanding	0.80 ± 0.05	0.39 ± 0.17	0.1 ± 0.03	0.04 ± 0.03	0.84 ± 0.08
Pic5	non-expanding	0.76 ± 0.04	0.55 ± 0.09	0.12 ± 0.03	0.06 ± 0.02	0.82 ± 0.06
Pic6	non-expanding	0.69 ± 0.03	0.35 ± 0.07	0.28 ± 0.05	0.10 ± 0.04	0.79 ± 0.07
Pic7	non-expanding	0.82 ± 0.05	0.31 ± 0.10	0.46 ± 0.11	0.14 ± 0.08	0.96 ± 0.12
Pic8	non-expanding	0.80 ± 0.04	0.19 ± 0.09	0.41 ± 0.11	0.08 ± 0.06	0.88 ± 0.10
Pic10	non-expanding	0.79 ± 0.06	0.28 ± 0.09	0.21 ± 0.06	0.06 ± 0.04	0.85 ± 0.09
Pic11	non-expanding	0.72 ± 0.05	0.19 ± 0.11	0.21 ± 0.05	0.04 ± 0.03	0.76 ± 0.08
Pic14	non-expanding	0.77 ± 0.04	0.30 ± 0.13	0.23 ± 0.04	0.07 ± 0.04	0.84 ± 0.08
Pic15	non-expanding	0.93 ± 0.05	0.65 ± 0.15	0.24 ± 0.07	0.16 ± 0.08	1.09 ± 0.13
Pic16	non-expanding	0.72 ± 0.03	0.30 ± 0.06	0.37 ± 0.04	0.11 ± 0.03	0.83 ± 0.06
Pic17	non-expanding	0.72 ± 0.07	0.43 ± 0.15	0.17 ± 0.05	0.07 ± 0.05	0.79 ± 0.12
Pic18	non-expanding	0.68 ± 0.04	0.27 ± 0.13	0.2 ± 0.06	0.06 ± 0.04	0.74 ± 0.08
Pic19	non-expanding	0.70 ± 0.07	0.39 ± 0.14	0.58 ± 0.2	0.22 ± 0.16	0.93 ± 0.23

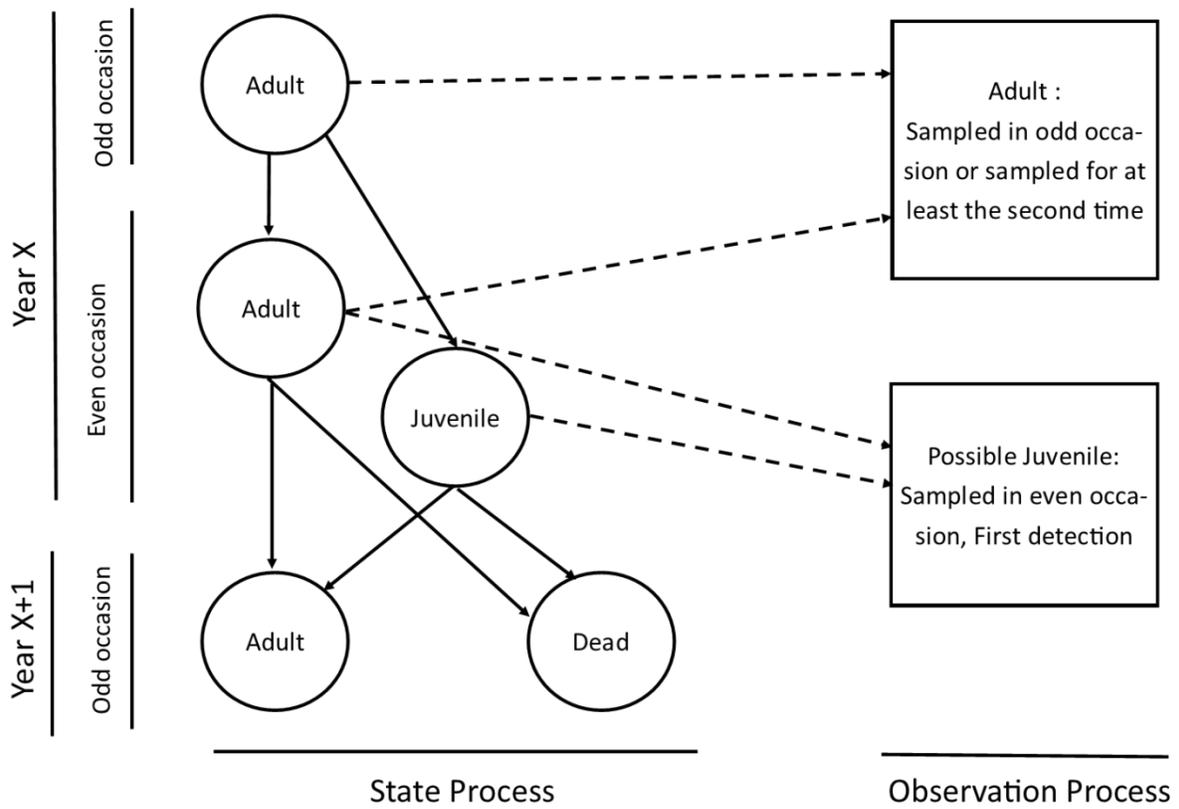


Figure S1: State and observation process of the CMRo model (model using CMR data only). More details are given in the section File S2: CMRo model in Supplementary Materials and in 'Integrated Population Model' section of the main manuscript.

Initial State Matrix

$$I = \begin{bmatrix} 1 - lA & lA \\ 0 & 1 \end{bmatrix}$$

Transition Matrix

$$T = \begin{bmatrix} \phi_a & 0 & 1 - \phi_a \\ 0 & \phi_j & 1 - \phi_j \\ 0 & 0 & 1 \end{bmatrix}$$

Detection matrix

$$D = \begin{bmatrix} p & 0 & 1 - p \\ 0 & 0 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Figure S2: Matrices containing the parameters of the multinomial distributions of the CMRo model. See methods or figure S3 for the definition of parameters. Initial state matrix shows the probability of detection (column – Adult and Possible juvenile) for any state (row – Adult and Juvenile) at first encounter. Transition matrix shows the probability of transition from a state at time t (rows – Adult, Juvenile and Dead) to t+1 (columns – same order). Detection matrix shows the probability of detection (column – Adult, Possible juvenile, Not sampled) for any state (row – Adult, Juvenile and Dead) after first encounter.

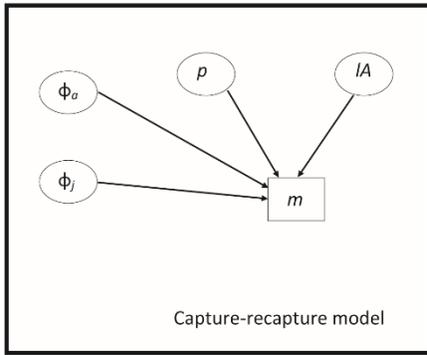


Figure S3: Acyclic graph illustrating the components of model likelihood in the CMRo model. ϕ_j =apparent juvenile survival, ϕ_a =adult survival, p =adult detection probability, IA =proportion of adults detected at post-reproduction sampling.

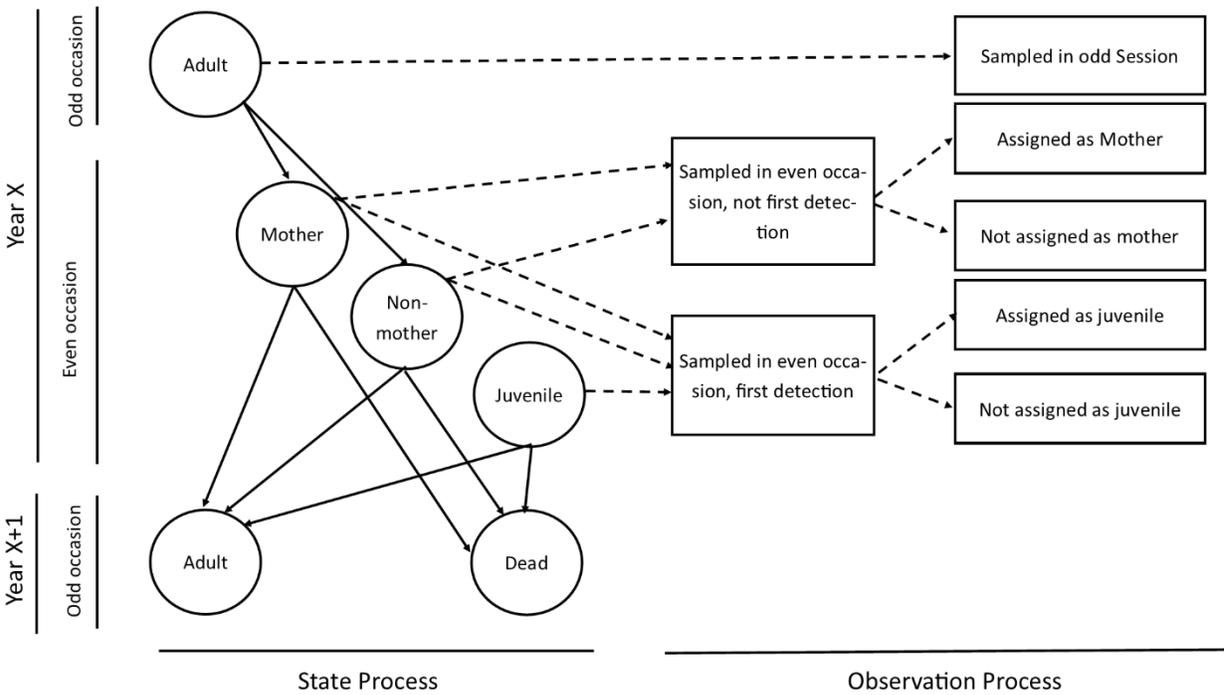


Figure S4: State and observation process of the CMRpa model (model using CMR data and parentage assignment). More details are given in the CMRpa model section in Supplementary Materials and in the section 'Integrated Population Model' of the main manuscript.

Initial State Matrix

$$I = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & J_{ass} & 1 - J_{ass} & 0 & 0 \\ 0 & M_{asj} & (1 - M_{asj}) & 0 & 0 \\ 0 & N_{asj} & (1 - N_{asj}) & 0 & 0 \end{bmatrix}$$

Transition Matrix

$$T = \begin{bmatrix} 0 & 0 & Fec & 1 - Fec & 0 \\ \phi_j & 0 & 0 & 0 & 1 - \phi_j \\ \phi_a & 0 & 0 & 0 & 1 - \phi_a \\ \phi_a & 0 & 0 & 0 & 1 - \phi_a \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

Detection matrix

$$D = \begin{bmatrix} p_A & 0 & 0 & 0 & 0 & 1 - p_A \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & p_M * Mass & p_M * (1 - Mass) & 1 - p_M \\ 0 & 0 & 0 & p_N * NasM & p_N * (1 - NasM) & 1 - p_N \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

Figure S5: Matrices containing the parameters of the multinomial distributions of the CMRpa model. See methods or Figure S6 for the definition of parameters. Initial state matrix shows the probability of detection (column – Adults, Assigned juvenile, Not assigned as juvenile, Assigned as mother and Not assigned as mother) for any state (row – Adult, Juvenile, Mother, Non-mother) at first encounter. Transition matrix shows the probability of transition from a state at time t (rows – Adult, Juvenile, Mother, Non-mother and Dead) to t+1 (columns – same order). Detection matrix shows the probability of detection (column – Adults, Assigned juvenile, Not assigned as juvenile, Assigned as mother, Not assigned as mother and Not detected) for any state (row – Adult, Juvenile, Mother, Non-mother, and Dead) after first encounter.

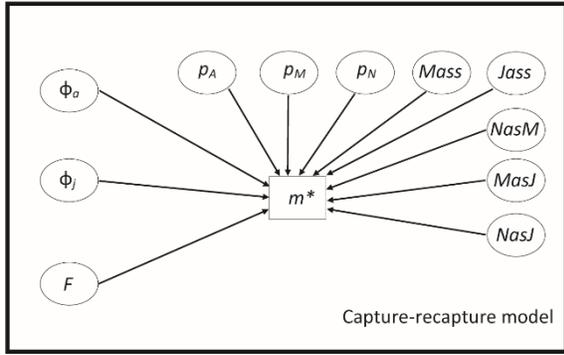


Figure S6: Acyclic graph illustrating the components of model likelihood in the CMRpa model. ϕ_j =apparent juvenile survival, ϕ_a =adult survival, F = fecundity, p_A = adult detection probability, p_M = mother detection probability, p_N = non-mother detection probability, $Mass$ = proportion of Mothers correctly assigned, $Jass$ = proportion of Juveniles correctly assigned, $NasM$ = proportion of Non-mothers wrongly assigned as a Mothers, $MasJ$ = proportion of Mothers wrongly assigned as Juvenile, $NasJ$ = proportion of Non-mothers wrongly assigned as a Juvenile.

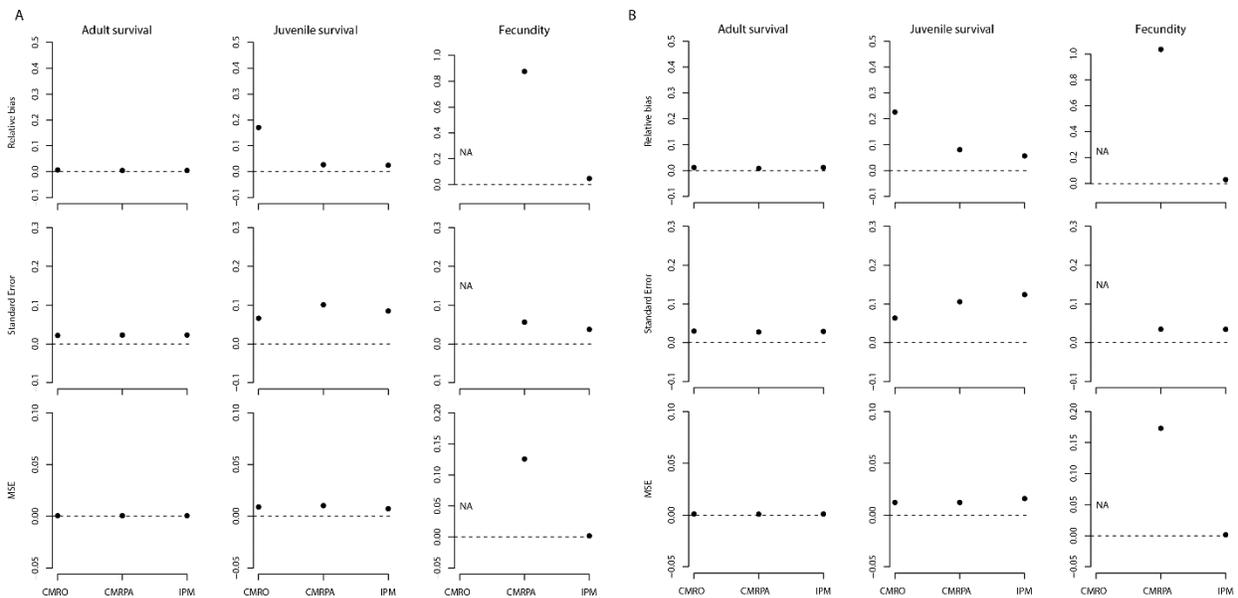


Figure S7: Results from simulations illustrating the relative bias, standard error, and mean squared error (MSE) of the three developed models for the estimation of adult survival, juvenile survival, and fecundity in the expanding (A) and the non-expanding population (B).