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2021. Chick survival and hunting are important drivers for the dynamics of two Alpine black grouse *Lyrurus tetrix* populations. – Wildlife Biology 2021: wlb.00874

Appendix 1

Appendix

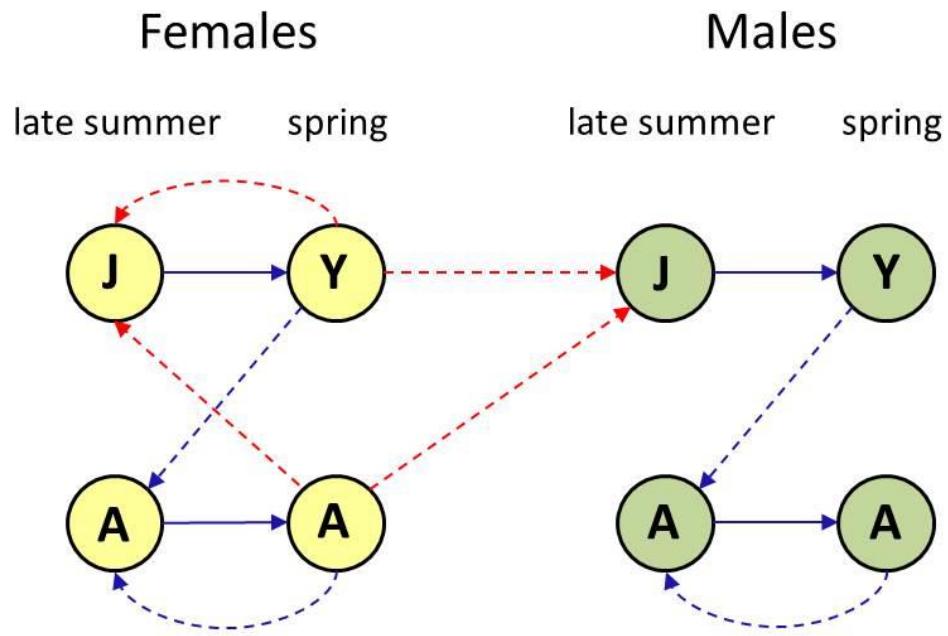


Figure A1. Life-cycle graph used for the two-sexes, seasonal black grouse population model with survey periods in spring and late summer. The nodes are J (juveniles), Y (yearlings) and A (adults). The demographic processes are shown by arrows (red: recruitment; blue: survival), broken arrows show the transition between spring and late summer (3.5 months period), full arrows the transitions between late summer and spring (8.5 months period). The demographic rates that govern the demographic processes are not shown on the graph. Only the model from one population is shown, but since the model does not consider any exchange of individuals between the populations the graphs are identical.

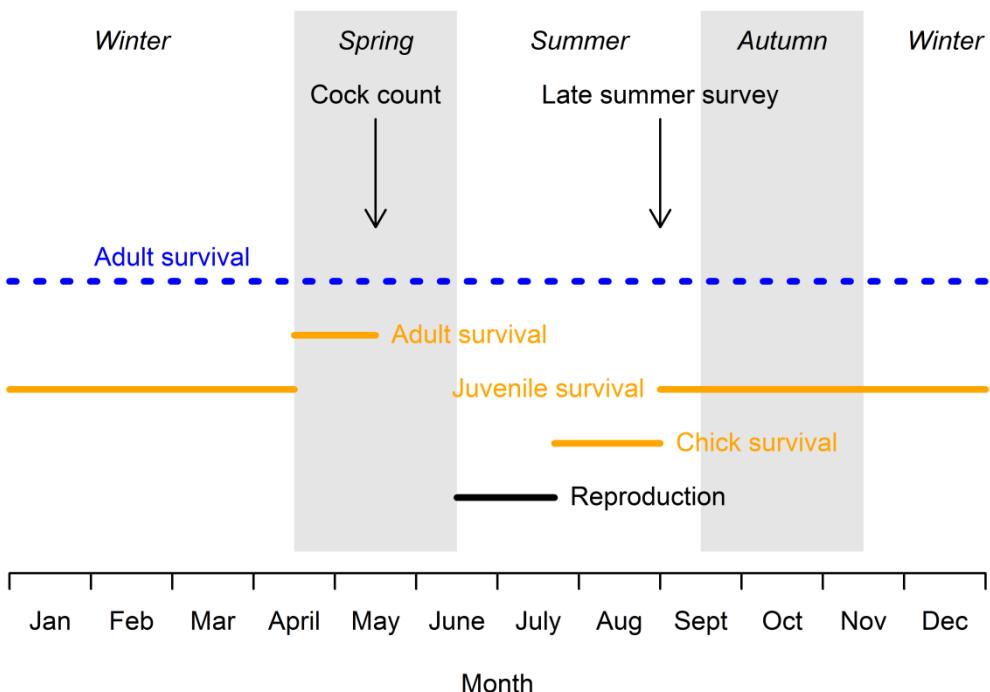


Figure A2. Presentation of the demographic events and the population surveys in the course of a year as used in this study. An individual is born during the reproduction period (black), it then survives with chick survival, followed by juvenile survival and finally with adult survival (orange). By 15 May it is nearly one year old ('yearling'). Individuals that are yearlings or older ('adults'), survive the year with adult survival (blue, dotted line). All survival probabilities have a seasonal resolution and the duration of the seasons are shown by the succession of white and grey bars. The two population surveys occurred in spring ('Cock count', includes all cocks) and in summer ('Late summer count', performed by means of pointing dogs and includes potentially all individuals).

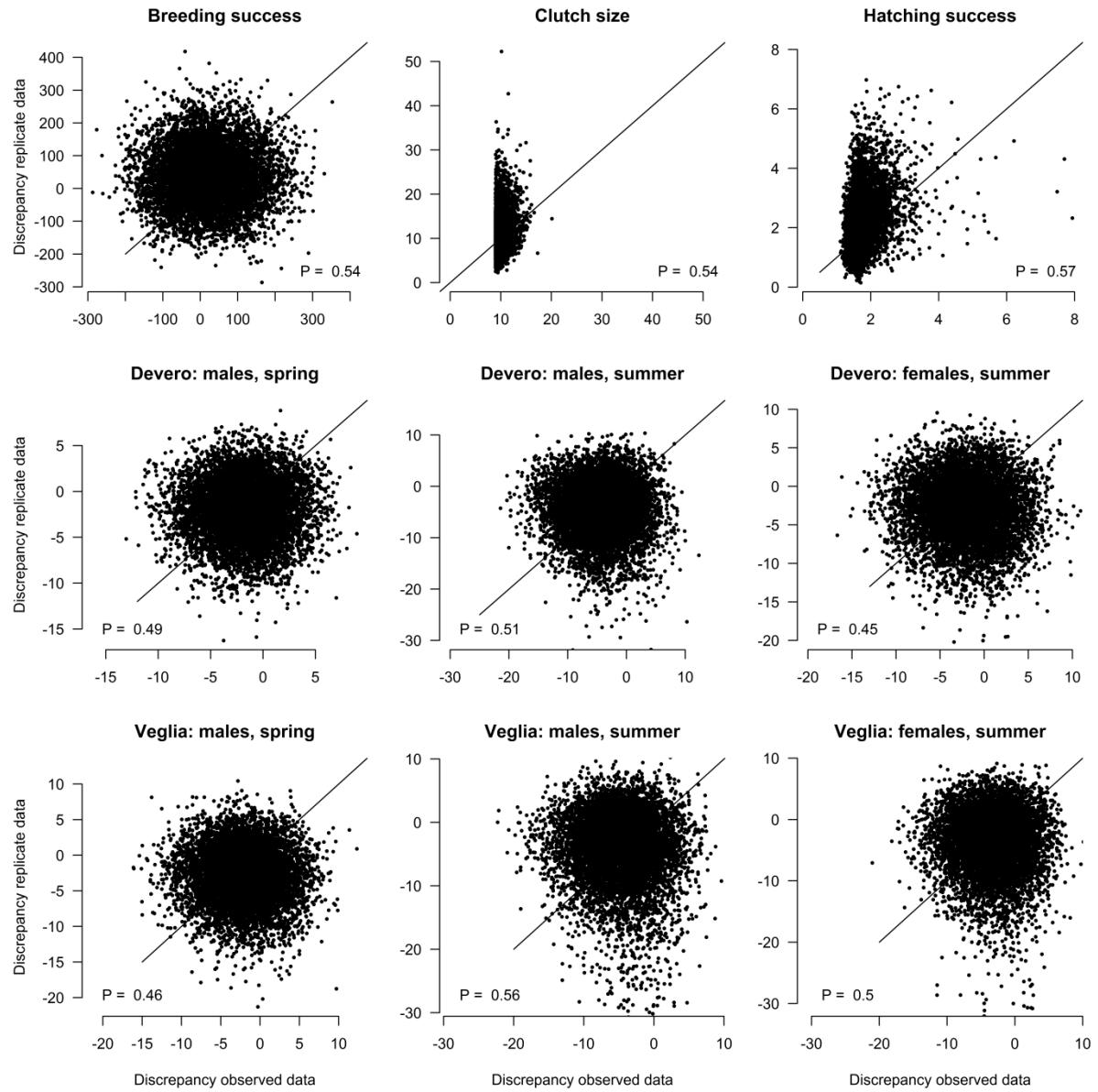


Figure A3. Scatter plots of replicate versus observed discrepancy measures of different IPM components for the black grouse data sets (posterior predictive checks). The applied discrepancy measures were the deviance for breeding success data, the Pearson chi-square for clutch size and hatching success, and absolute percentage error for the count data in spring and summer. Given are also the Bayesian P-values (P). None of the test components show lack of fit. No posterior predictive check could be performed for the binary data.

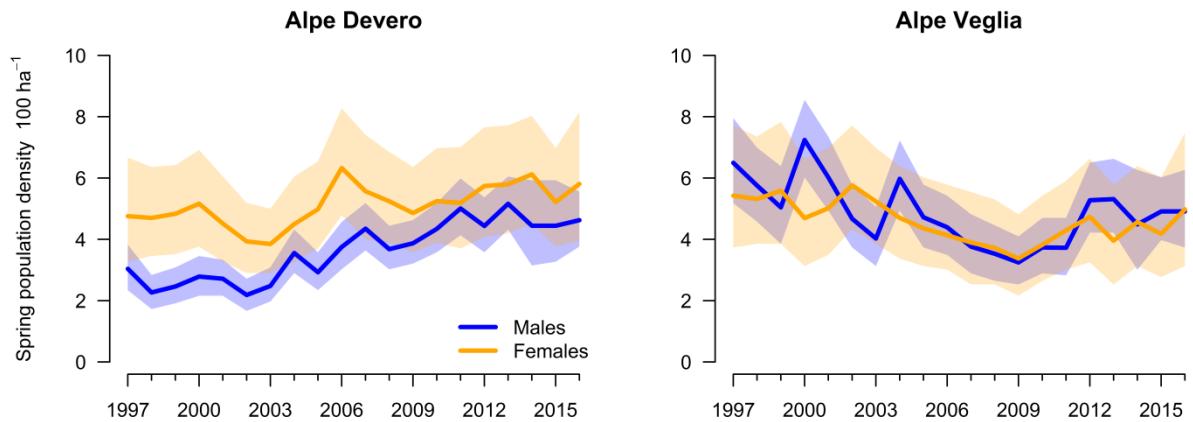


Figure A4. Estimated black grouse population density (number of individuals per 100 ha) in spring in the two study areas by sex. Shown are posterior means (lines) and the limits of the 95% credible intervals (areas).

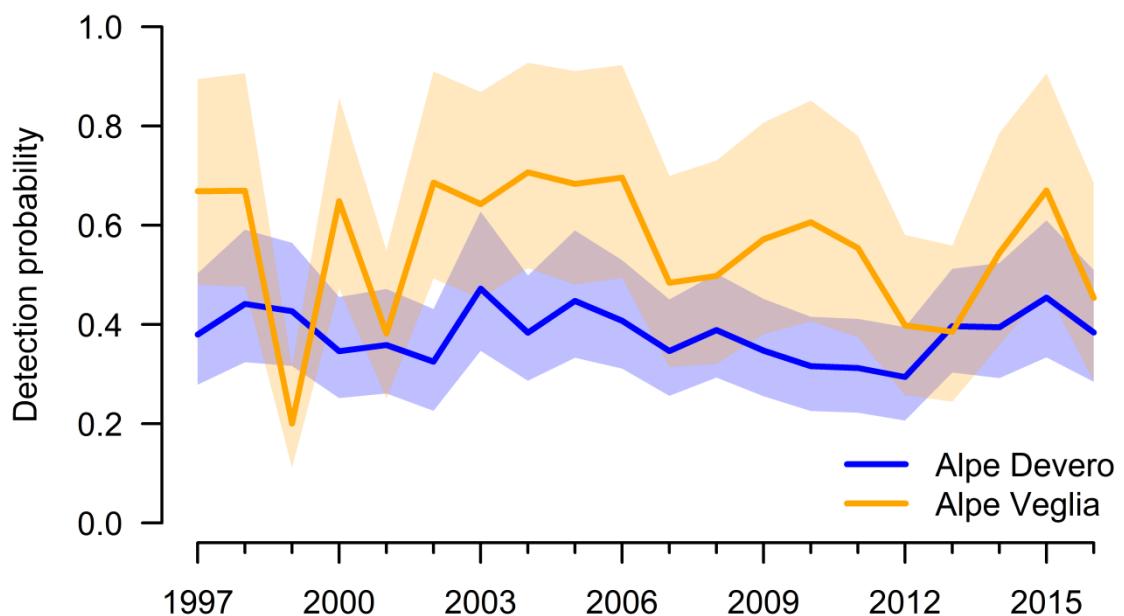


Figure A5. Estimated detection probabilities of adult black grouse during the summer surveys carried out by means of pointing dogs in the two study populations. The lines show the posterior means across time and the area indicate the limits of the 95% credible intervals. The detection probability tended to be higher at the Alpe Veglia compared to the Alpe Devero, which is likely due to larger sampling coverage in the former study area.

Table A1. Number of black grouse captured and radio-collared at the Alpe Devero and Veglia in the period 1998-2006, divided by age and sex. The age refers to the time when the individuals were marked. ‘Juveniles’ are individuals that are about 5 weeks old (captured in August and September), ‘Yearlings’ are individuals that are one year old (captured in May and June) and ‘Adults’ are individuals that are at least two years old (captured in May and June). The numbers in parentheses refer to the 16 tagged individuals that died or disappeared within two weeks after tagging and that were excluded from the analyses.

Age	Alpe Devero		Alpe Veglia	
	Males	Females	Males	Females
Juveniles	12 (6)	11 (2)	6 (2)	3 (1)
Yearlings	28 (1)	12 (1)	14 (0)	3 (0)
Adults	25 (1)	6 (0)	19 (2)	4 (0)
Total	65 (8)	29 (3)	39 (4)	10 (1)

Table A2. List of all parameters of the integrated population model including the symbol and the used prior distribution (if appropriate). We also added the derived annual survival probabilities and how they were calculated from the monthly survival probabilities. Note that the normal distribution is parameterised with the mean and the variance. dU = discrete uniform distribution; U = uniform distribution.

Parameter	Prior distribution
$S_{y,t}^{m,p}$: Number of yearling males in spring in year t in population p	$S_{y,1}^{m,p} \sim dU(1,100)$
$S_{a,t}^{m,p}$: Number of adult males in spring in year t in population p	$S_{a,1}^{m,p} \sim dU(1,100)$
$S_{y,t}^{f,p}$: Number of yearling females in spring in year t in population p	$S_{y,1}^{f,p} \sim dU(1,100)$
$S_{a,t}^{f,p}$: Number of adult females in spring in year t in population p	$S_{a,1}^{f,p} \sim dU(1,100)$
$A_{j,t}^{m,p}$: Number of juvenile males in late summer in year t in population p	-
$A_{a,t}^{m,p}$: Number of adult males in late summer in year t in population p	-
$A_{j,t}^{f,p}$: Number of juvenile females in late summer in year t in population p	-
$A_{a,t}^{f,p}$: Number of adult females in late summer in year t in population p	-
$\phi_{j,s,t}^{m,p}$: Monthly juvenile male survival in season s , year t and population p	-
$\bar{\phi}_{j,s}^{m,p}$: Mean monthly juvenile male survival in season s and population p	$\bar{\phi}_{j,s}^{m,p} \sim U(0,1)$
$\phi_{a,s,t}^{m,p}$: Monthly adult male survival in season s , year t and population p	-
$\bar{\phi}_{a,s}^{m,p}$: Mean monthly adult male survival in season s and population p	$\bar{\phi}_{a,s}^{m,p} \sim U(0,1)$
$\phi_{j,s,t}^{f,p}$: Monthly juvenile female survival in season s , year t and population p	-
$\bar{\phi}_{j,s}^{f,p}$: Mean monthly juvenile female survival in season s and population p	$\bar{\phi}_{j,s}^{f,p} \sim U(0,1)$
$\phi_{a,s,t}^{f,p}$: Monthly adult female survival in season s , year t and population p	-
$\bar{\phi}_{a,s}^{f,p}$: Mean monthly adult female survival in season s and population p	$\bar{\phi}_{a,s}^{f,p} \sim U(0,1)$
$\sigma_{\phi(j)}^2$: Temporal variability of monthly juvenile survival	$\sigma_{\phi(j)} \sim U(0,3)$
$\sigma_{\phi(a)}^2$: Temporal variability of monthly adult survival	$\sigma_{\phi(a)} \sim U(0,3)$
τ_t^p : Probability that an adult female reproduces in year t in population p (breeding propensity)	-
$\bar{\tau}^p$: Mean breeding propensity in population p	$\bar{\tau}^p \sim U(0,1)$
σ_τ^2 : Temporal variability of breeding propensity	$\sigma_\tau \sim U(0,3)$
ξ^p : Mean clutch size in population p	$\xi^p \sim U(2,10)$

σ_ξ^2 : Residual variance of clutch size	$\sigma_\xi \sim U(0,3)$
ψ^p : Mean probability that the nest was successful (i.e., produced at least one hatchling) in population p (nest success)	$\psi^p \sim U(0,1)$
κ_t^p : Probability that an egg of a successful nest in year t and population p hatches (hatching success)	-
$\bar{\kappa}^p$: Mean hatching success in population p	$\bar{\kappa}^p \sim U(0,1)$
σ_κ^2 : Temporal variability of hatching success	$\sigma_\kappa \sim U(0,3)$
ω_t^p : Probability that a hatchling from population p in year t survives the first 5 weeks (chick survival)	-
$\bar{\omega}^p$: Mean chick survival in population p	$\bar{\omega}^p \sim U(0,1)$
η : Regression parameter of temperature on chick survival	$\eta \sim Normal(0,100)$
σ_ω^2 : Residual temporal variability of chick survival	$\sigma_\omega \sim U(0,5)$
ρ_t^p : Number of 5-weeks old chicks per adult female on 31 August in population p and year t (breeding success). $\rho_t^p = \tau_t^p \xi^p \psi^p \kappa_t^p \omega_t^p$	-
p_t^p : Detection probability of grouse on the summer survey in year t and population p	-
\bar{p}^p : Mean detection probability of grouse on the summer survey in population p	$\bar{p}^p \sim U(0,1)$
$\sigma_{p(p)}^2$: Temporal variability of detection probability of grouse on the summer survey in population p	$\sigma_{p(p)} \sim U(0,5)$
<i>Derived parameters</i>	
$s_{j,p}^m$: mean annual juvenile survival of males	-
$s_{j,p}^m = \sqrt{\bar{\phi}_{j,summer}^{m,p}} \left(\bar{\phi}_{j,autumn}^{m,p} \right)^2 \left(\bar{\phi}_{j,winter}^{m,p} \right)^5 \bar{\phi}_{a,spring}^{m,p}$	-
$s_{a,p}^m$: mean annual adult survival of males	-
$s_{a,p}^m = \left(\bar{\phi}_{a,spring}^{m,p} \right)^2 \left(\bar{\phi}_{a,summer}^{m,p} \right)^3 \left(\bar{\phi}_{a,autumn}^{m,p} \right)^2 \left(\bar{\phi}_{a,winter}^{m,p} \right)^5$	-
$s_{j,p}^f$: mean annual juvenile survival of females	-
$s_{j,p}^f = \sqrt{\bar{\phi}_{j,summer}^{f,p}} \left(\bar{\phi}_{j,autumn}^{f,p} \right)^2 \left(\bar{\phi}_{j,winter}^{f,p} \right)^5 \bar{\phi}_{a,spring}^{f,p}$	-
$s_{a,p}^f$: mean annual adult survival of females	-
$s_{a,p}^f = \left(\bar{\phi}_{a,spring}^{f,p} \right)^2 \left(\bar{\phi}_{a,summer}^{f,p} \right)^3 \left(\bar{\phi}_{a,autumn}^{f,p} \right)^2 \left(\bar{\phi}_{a,winter}^{f,p} \right)^5$	-

Table A3. Posterior means, posterior modes and 95% credible intervals (CRI) of the temporal variabilities (i.e. the degree by which the rates varied over years) of some demographic parameters. The temporal variability is expressed as standard deviations on the logit scale, since all parameters are probabilities. These measures of temporal variability are shared among the two populations (but not the annual deviations).

Temporal variability of	Mean	Mode	CRI
Juvenile survival ($\sigma_{\phi(j)}^2$)	0.341	0.343	0.031; 0.677
Adult survival ($\sigma_{\phi(a)}^2$)	0.115	0.036	0.005; 0.311
Breeding propensity (σ_τ^2)	0.524	0.369	0.027; 1.391
Hatching success (σ_κ^2)	0.522	0.025	0.021; 1.502
Chick survival (σ_ω^2)	0.518	0.467	0.298; 0.834
Detection probability (σ_p^2 , Devero)	0.311	0.278	0.105; 0.548
Detection probability (σ_p^2 , Veglia)	0.778	0.653	0.448; 1.380

JAGS code of the black grouse IPM

```

# 1. Priors and constraints
# 1.1. Survival parameters
for (i in 1:nind){
  for (t in f[i]:(nocc-1)){
    sur[i,t] <- phi[age[i,t], sex[i], location[i], season[t], sur.year[t]]
  } #t
} #i
for (i in 1:2){                                # age
  for (j in 1:2){                            # sex (1: male, 2: female)
    for (l in 1:2){                          # location (1: Devero, 2: Veglia)
      for (m in 1:4){                      # season
        mean.phi[i,j,l,m] ~ dunif(0, 1)
        logit.mean.phi[i,j,l,m] <- logit(mean.phi[i,j,l,m])
        for (t in 1:ny){
          phi[i,j,l,m,t] <- ilogit(logit.mean.phi[i,j,l,m] + eps[i,j,l,t])
        } #t
      } #m
      for (g in 1:ny){
        eps[i,j,l,g] ~ dnorm(0, tau.phi[i])
      } #g
    } #l
  } #j
} #i

# Just use different temporal variance for the age classes
for (i in 1:2){
  sigma.phi[i] ~ dunif(0, 3)
  tau.phi[i] <- pow(sigma.phi[i], -2)
}

ann.s[1,1,1] <- mean.phi[1,1,1,2]^0.5 * mean.phi[1,1,1,3]^2 *
mean.phi[1,1,1,4]^5 * mean.phi[2,1,1,1]  # it's survival from autumn count
until reproduction
ann.s[2,1,1] <- mean.phi[2,1,1,1]^2 * mean.phi[2,1,1,2]^3 *
mean.phi[2,1,1,3]^2 * mean.phi[2,1,1,4]^5
ann.s[1,2,1] <- mean.phi[1,2,1,2]^0.5 * mean.phi[1,2,1,3]^2 *
mean.phi[1,2,1,4]^5 * mean.phi[2,2,1,1]
ann.s[2,2,1] <- mean.phi[2,2,1,1]^2 * mean.phi[2,2,1,2]^3 *
mean.phi[2,2,1,3]^2 * mean.phi[2,2,1,4]^5

ann.s[1,1,2] <- mean.phi[1,1,2,2]^0.5 * mean.phi[1,1,2,3]^2 *
mean.phi[1,1,2,4]^5 * mean.phi[2,1,2,1]
ann.s[2,1,2] <- mean.phi[2,1,2,1]^2 * mean.phi[2,1,2,2]^3 *
mean.phi[2,1,2,3]^2 * mean.phi[2,1,2,4]^5
ann.s[1,2,2] <- mean.phi[1,2,2,2]^0.5 * mean.phi[1,2,2,3]^2 *
mean.phi[1,2,2,4]^5 * mean.phi[2,2,2,1]
ann.s[2,2,2] <- mean.phi[2,2,2,1]^2 * mean.phi[2,2,2,2]^3 *
mean.phi[2,2,2,3]^2 * mean.phi[2,2,2,4]^5

# 1.2. Chick survival (omega)
for (t in 1:ny){
  for (j in 1:2){
    logit.omega[j,t] ~ dnorm(logit.mean.omega[j] + eta * p40[t], tau.omega)
    omega[j,t] <- ilogit(logit.omega[j,t])
  } #j
} #t
eta ~ dnorm(0, 0.01)
for (j in 1:2){
  mean.omega[j] ~ dunif(0, 1)
}

```

```

logit.mean.omega[j] <- logit(mean.omega[j])
}
sigma.omega ~ dunif(0, 5)
tau.omega <- pow(sigma.omega, -2)

# 1.3. Clutch size (xi)
for (j in 1:2){
  xi[j] ~ dunif(2, 10)
}
tau.res.xi <- pow(sigma.res.xi, -2)
sigma.res.xi ~ dunif(0, 3)

# 1.4. Hatching success (kappa)
for (j in 1:2){
  for (t in 1:ny){
    logit.kappa[j,t] ~ dnorm(logit.mean.kappa[j], tau.kappa)
    kappa[j,t] <- ilogit(logit.kappa[j,t])
    psi[j,t] <- mean.psi[j]
  } #t
  mean.kappa[j] ~ dunif(0, 1)
  logit.mean.kappa[j] <- logit(mean.kappa[j])
  mean.psi[j] ~ dunif(0, 1)
} #j
tau.kappa <- pow(sigma.kappa, -2)
sigma.kappa ~ dunif(0, 3)

# 1.5. Breeding propensity (tau)
for (j in 1:2){
  for (t in 1:ny){
    logit.tau[j,t] ~ dnorm(logit.mean.tau[j], tau.tau)
    tau[j,t] <- ilogit(logit.tau[j,t])
  } #t
  mean.tau[j] ~ dunif(0, 1)
  logit.mean.tau[j] <- logit(mean.tau[j])
} #j
tau.tau <- pow(sigma.tau, -2)
sigma.tau ~ dunif(0, 3)

# 1.6. Initial population size
for (j in 1:2){
  S[1,1,j,1] ~ dcat(pinit[])
  S[2,1,j,1] ~ dcat(pinit[])
  S[1,2,j,1] ~ dcat(pinit[])
  S[2,2,j,1] ~ dcat(pinit[])
}

# 1.7. Resighting probability in the counts (p)
for (j in 1:2){
  for (t in 1:ny){
    logit.p[j,1,t] ~ dnorm(lmean.p[j], tau.p[j])
    p[j,1,t] <- ilogit(logit.p[j,1,t])
    p[j,2,t] <- p[j,1,t] # males and females have the same sighting
probabilities
  } #t
  mean.p[j] ~ dbeta(1, 1)
  lmean.p[j] <- logit(mean.p[j])
  sigma.p[j] ~ dunif(0, 5)
  tau.p[j] <- pow(sigma.p[j], -2)
} #j

# 2. Likelihood

```

```

# 2.1. State-space model
# 2.1.1. State process models
# Population sizes in spring
for (t in 1:(ny-1)){
  for (j in 1:2){
    S[1,1,j,t+1] ~ dbin(phi[1,1,j,2,t]^0.5 * phi[1,1,j,3,t]^2 *
phi[1,1,j,4,t]^5 * phi[2,1,j,1,t+1], A[1,1,j,t])      # Number of 1y males
in spring
    S[2,1,j,t+1] ~ dbin(phi[2,1,j,2,t]^0.5 * phi[2,1,j,3,t]^2 *
phi[2,1,j,4,t]^5 * phi[2,1,j,1,t+1], A[2,1,j,t])      # Number of +1y males
in spring

    # Females
    S[1,2,j,t+1] ~ dbin(phi[1,2,j,2,t]^0.5 * phi[1,2,j,3,t]^2 *
phi[1,2,j,4,t]^5 * phi[2,2,j,1,t+1], A[1,2,j,t])      # Number of 1y
females in spring
    S[2,2,j,t+1] ~ dbin(phi[2,2,j,2,t]^0.5 * phi[2,2,j,3,t]^2 *
phi[2,2,j,4,t]^5 * phi[2,2,j,1,t+1], A[2,2,j,t])      # Number of +1y
females in spring
  } #j
} #t
# Population sizes in later summer
for (t in 1:ny){
  for (j in 1:2){
    F[j,t] ~ dpois((S[1,2,j,t] + S[2,2,j,t]) * phi[2,2,j,1,t] * tau[j,t] *
xi[j] * psi[j,t] * kappa[j,t] * omega[j,t])      # Number of juveniles
in autumn
    A[1,1,j,t] ~ dbin(0.5, F[j,t])      # Number of juvenile males in
autumn
    A[1,2,j,t] <- F[j,t] - A[1,1,j,t]      # Number of juvenile females
chicks
    A[2,1,j,t] ~ dbin(phi[2,1,j,1,t] * phi[2,1,j,2,t]^2.5, (S[1,1,j,t] +
S[2,1,j,t]))      # Number of ad males in autumn
    A[2,2,j,t] ~ dbin(phi[2,2,j,1,t] * phi[2,2,j,2,t]^2.5, (S[1,2,j,t] +
S[2,2,j,t]))      # Number of ad females in autumn
  } #j
} #t

# 2.1.2. Observation models
for (t in 1:ny){
  for (j in 1:2){
    Csp[j,t] ~ dpois((S[1,1,j,t] + S[2,1,j,t]))      # Spring counts of males
    Cau[j,1,t] ~ dbin(p[j,1,t], A[2,1,j,t])      # Summer counts of males
    Cau[j,2,t] ~ dbin(p[j,2,t], A[2,2,j,t])      # Summer counts of females

    # Elements for GOF
    Csp.pred[j,t] ~ dpois((S[1,1,j,t] + S[2,1,j,t]))      # Spring counts of
males
    Cau.pred[j,1,t] ~ dbin(p[j,1,t], A[2,1,j,t])      # Summer counts of
males
    Cau.pred[j,2,t] ~ dbin(p[j,2,t], A[2,2,j,t])      # Summer counts of
females

    # Discrepancy measure: absolute percentage error
    d.Csp.org[j,t] <- (Csp[j,t] - (S[1,1,j,t] + S[2,1,j,t])) / (Csp[j,t] +
0.001)
    d.Cau.org[j,1,t] <- (Cau[j,1,t] - p[j,1,t] * A[2,1,j,t]) / (Cau[j,1,t] +
0.001)
    d.Cau.org[j,2,t] <- (Cau[j,2,t] - p[j,2,t] * A[2,2,j,t]) / (Cau[j,2,t] +
0.001)
  }
}

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d.Csp.new[j,t] <- (Csp.pred[j,t] - (S[1,1,j,t] + S[2,1,j,t])) /
(Csp.pred[j,t] + 0.001)
d.Cau.new[j,1,t] <- (Cau.pred[j,1,t] - p[j,1,t] * A[2,1,j,t]) /
(Cau.pred[j,1,t] + 0.001)
d.Cau.new[j,2,t] <- (Cau.pred[j,2,t] - p[j,2,t] * A[2,2,j,t]) /
(Cau.pred[j,2,t] + 0.001)
} #j
} #t

fit6[1] <- 100 / ny * sum(d.Csp.org[1,])
fit6[2] <- 100 / ny * sum(d.Csp.new[1,])
fit7[1] <- 100 / ny * sum(d.Cau.org[1,1,])
fit7[2] <- 100 / ny * sum(d.Cau.new[1,1,])
fit8[1] <- 100 / ny * sum(d.Cau.org[1,2,])
fit8[2] <- 100 / ny * sum(d.Cau.new[1,2,])
fit9[1] <- 100 / ny * sum(d.Csp.org[2,])
fit9[2] <- 100 / ny * sum(d.Csp.new[2,])
fit10[1] <- 100 / ny * sum(d.Cau.org[2,1,])
fit10[2] <- 100 / ny * sum(d.Cau.new[2,1,])
fit11[1] <- 100 / ny * sum(d.Cau.org[2,2,])
fit11[2] <- 100 / ny * sum(d.Cau.new[2,2,])

# 2.2. Telemetry data (survival)
for (i in 1:nind){
  for (t in (f[i]+1):k[i]){
    y[i,t] ~ dbern(sur[i,t-1] * y[i,t-1])
  } #t
} #i

# 2.3. Productivity data (Autumn)
for (i in 1:n){
  J[i] ~ dpois(R[i] * tau[location.su[i], year[i]] * xi[location.su[i]] *
psi[location.su[i], year[i]] * kappa[location.su[i], year[i]] *
omega[location.su[i], year[i]])

  J.pred[i] ~ dpois(R[i] * omega[location.su[i], year[i]] *
xi[location.su[i]] * psi[location.su[i], year[i]] * kappa[location.su[i],
year[i]] * tau[location.su[i], year[i]])
  J.exp[i] <- R[i] * omega[location.su[i], year[i]] * xi[location.su[i]] *
psi[location.su[i], year[i]] * kappa[location.su[i], year[i]] *
tau[location.su[i], year[i]]
  # Discrepancy measure (deviance)
  dev.org[i] <- J[i] * log(J[i] / J.exp[i])
  dev.new[i] <- J.pred[i] * log(J.pred[i] / J.exp[i])
}

fit1[1] <- 2*sum(dev.org)
fit1[2] <- 2*sum(dev.new)

# 2.4. Clutch size
for (i in 1:n.E){
  E[i] ~ dnorm(xi[site.E[i]], tau.res.xi)
  E.pred[i] ~ dnorm(xi[site.E[i]], tau.res.xi)
  # Discrepancy measure: Pearson chi2
  Chi.org4[i] <- pow((E[i] - xi[site.E[i]]), 2) / xi[site.E[i]]
  Chi.new4[i] <- pow((E.pred[i] - xi[site.E[i]]), 2) / xi[site.E[i]]
}

fit4[1] <- sum(Chi.org4)
fit4[2] <- sum(Chi.new4)

# 2.5. Hatching success (zero-inflated Binomial)

```

```

for (i in 1:n.E){
  z[i] ~ dbern(psi[site.E[i], year.E[i]])
  H[i] ~ dbin(kappa[site.E[i], year.E[i]] * z[i], EH[i])
  H.pred[i] ~ dbin(kappa[site.E[i], year.E[i]] * z[i], EH[i])
  H.exp[i] <- kappa[site.E[i], year.E[i]] * EH[i] * z[i]
  # Discrepancy measure: Pearson chi-square
  Chi.org5[i] <- pow(H[i] - H.exp[i], 2) / (H.exp[i] + 0.001)
  Chi.new5[i] <- pow(H.pred[i] - H.exp[i], 2) / (H.exp[i] + 0.001)
}

fit5[1] <- sum(Chi.org5)
fit5[2] <- sum(Chi.new5)

# 2.6. Breeding propensity
for (i in 1:n.D){
  D[i] ~ dbern(tau[site.D[i], year.D[i]])
}
}
")

```

R code to perform prospective and retrospective population analyses based on the output from the IPM

```

# Load the IPM result file
load("BlackGrouseFinal.Rdata")

draws <- mod$sims.list    # store MCMC draws in an object to simplify
n.draws <- mod$mcmc.info$n.samples

# Spring population growth rate (symbolic)
lambda <- expression(((n1 + n2) * 0.5 * tau * xi * psi * kappa *
omega * (phijf + phijm) + (n1 + n2) * phiaf + (n3 + n4) * phiam) /
(n1 + n2 + n3 + n4))

# Define population for which calculation is done
loc <- 1  # Devero (2: Veglia)

# Calculate the annual survival
phijf <- draws$phi[,2,2,loc,1,1:19] * draws$phi[,1,2,loc,2,1:19]^0.5
* draws$phi[,1,2,loc,3,1:19]^2 * draws$phi[,1,2,loc,4,1:19]^5 *
draws$phi[,2,2,loc,1,2:20]
phijm <- draws$phi[,2,2,loc,1,1:19] * draws$phi[,1,1,loc,2,1:19]^0.5
* draws$phi[,1,1,loc,3,1:19]^2 * draws$phi[,1,1,loc,4,1:19]^5 *
draws$phi[,2,1,loc,1,2:20]
phiaf <- draws$phi[,2,2,loc,1,1:19] * draws$phi[,2,2,loc,2,1:19]^3 *
draws$phi[,2,2,loc,3,1:19]^2 * draws$phi[,2,2,loc,4,1:19]^5 *
draws$phi[,2,2,loc,1,2:20]
phiam <- draws$phi[,2,1,loc,1,1:19] * draws$phi[,2,1,loc,2,1:19]^3 *
draws$phi[,2,1,loc,3,1:19]^2 * draws$phi[,2,1,loc,4,1:19]^5 *
draws$phi[,2,1,loc,1,2:20]

# Calculate proportional population sizes
n.years <- 20
Ntot <- apply(draws$S[,,,loc,,], c(1,4), sum)
n1 <- draws$S[, 1, 2, loc, 1:n.years] / Ntot[, 1:n.years]    # 1y
females

```

```

n2 <- draws$S[, 2, 2, loc, 1:n.years] / Ntot[, 1:n.years]      # 1y+
females
n3 <- draws$S[, 1, 1, loc, 1:n.years] / Ntot[, 1:n.years]      # 1y
males
n4 <- draws$S[, 2, 1, loc, 1:n.years] / Ntot[, 1:n.years]      # 1y+
males

# Calculate realized population growth rates (log scale)
log_lam <- log(Ntot[,2:20]) - log(Ntot[,1:19])
# Mean growth
mlog_lam <- apply(log_lam, 1, mean)
m_lam <- exp(mlog_lam)                                     # on natural scale

# Extract the mean demographic rates and population sizes and store
# them in a list
mu <- list(phijf=apply(phijf, 1, mean), phiaf=apply(phiaf, 1, mean),
            phijm=apply(phijm, 1, mean), phiam=apply(phiam, 1, mean),
            tau=apply(draws$tau[,loc,], 1, mean), xi=draws$xi[,loc],
            psi=apply(draws$psi[,loc,], 1, mean),
            kappa=apply(draws$kappa[,loc,], 1, mean),
            omega=apply(draws$omega[,loc,], 1, mean), n1=apply(n1, 1, mean),
            n2=apply(n2, 1, mean), n3=apply(n3, 1, mean), n4=apply(n4, 1, mean))

# Calculate growth rate sensitivities
sens <- matrix(NA, n.draws, 13)
colnames(sens) <- c("phiif", "phiaf", "phijm", "phiam", "tau", "xi",
                    "psi", "kappa", "omega", "n1", "n2", "n3", "n4")
sens[, "phiif"] <- eval(D(lambda, "phiif"), envir=mu)
sens[, "phiaf"] <- eval(D(lambda, "phiaf"), envir=mu)
sens[, "phijm"] <- eval(D(lambda, "phijm"), envir=mu)
sens[, "phiam"] <- eval(D(lambda, "phiam"), envir=mu)
sens[, "tau"] <- eval(D(lambda, "tau"), envir=mu)
sens[, "xi"] <- eval(D(lambda, "xi"), envir=mu)
sens[, "psi"] <- eval(D(lambda, "psi"), envir=mu)
sens[, "kappa"] <- eval(D(lambda, "kappa"), envir=mu)
sens[, "omega"] <- eval(D(lambda, "omega"), envir=mu)
sens[, "n1"] <- eval(D(lambda, "n1"), envir=mu)
sens[, "n2"] <- eval(D(lambda, "n2"), envir=mu)
sens[, "n3"] <- eval(D(lambda, "n3"), envir=mu)
sens[, "n4"] <- eval(D(lambda, "n4"), envir=mu)

# Define matrix to store results for contributions
cont <- matrix(NA, nrow=n.draws, ncol=13)
colnames(cont) <- c("phiif", "phiaf", "phijm", "phiam", "tau", "xi",
                    "psi", "kappa", "omega", "n1", "n2", "n3", "n4")

# Calculate contributions for each demographic rate and stage-
# structured population size at each MCMC draw
for (s in 1:n.draws){
  dp_stoch <- cbind(phiif[s,], phiaf[s,], phijm[s,], phiam[s,],
                     draws$tau[s,loc,1:19], rep(draws$xi[s,loc],19),
                     draws$psi[s,loc,1:19], draws$kappa[s,loc,1:19],
                     draws$omega[s,loc,1:19], n1[s,1:19], n2[s,1:19], n3[s,1:19],
                     n4[s,1:19])
}

```

```

# Derive process variance and covariance among demographic
parameters using shrunken estimates of demographic rates and
proportional pop. sizes
dp_varcov <- var(dp_stoch)
sensvec <- sens[s, ]
# Calculate demographic contributions
contmatrix <- dp_varcov * outer(sensvec, sensvec)
cont[s, ] <- rowSums(contmatrix)
}

# Calculate growth rate elasticities
elas <- matrix(NA, n.draws, 13)
colnames(elas) <- c("phijf", "phiaf", "phijm", "phiam", "tau", "xi",
"psi", "kappa", "omega", "n1", "n2", "n3", "n4")
elas[, "phijf"] <- sens[, "phijf"] * mu$phijf / m_lam
elas[, "phiaf"] <- sens[, "phiaf"] * mu$phiaf / m_lam
elas[, "phijm"] <- sens[, "phijm"] * mu$phijm / m_lam
elas[, "phiam"] <- sens[, "phiam"] * mu$phiam / m_lam
elas[, "tau"] <- sens[, "tau"] * mu$tau / m_lam
elas[, "xi"] <- sens[, "xi"] * mu$xi / m_lam
elas[, "psi"] <- sens[, "psi"] * mu$psi / m_lam
elas[, "kappa"] <- sens[, "kappa"] * mu$kappa / m_lam
elas[, "omega"] <- sens[, "omega"] * mu$omega / m_lam
elas[, "n1"] <- sens[, "n1"] * mu$n1 / m_lam
elas[, "n2"] <- sens[, "n2"] * mu$n2 / m_lam
elas[, "n3"] <- sens[, "n3"] * mu$n3 / m_lam
elas[, "n4"] <- sens[, "n4"] * mu$n4 / m_lam

```