

SUPPORTING INFORMATION FOR CAILLAT ET al.

S1: Covariate data and sampling methodology:

1-Prey Data

Table S1.1: Normalised prey data. For herring, cod and sprat the normalized value was calculated from the annual standing stock biomass (SSB) estimated by the International Council for the Exploration of the Sea (ICES) and available at <http://standardgraphs.ices.dk/stockList.aspx> . The sandeel proxy is the normalized breeding success (number of clicks fledged) of a population of black-legged kittiwake present at North Sutor.

| Year | Herring | Cod | Sprat | Sandeel proxy |
|------|---------|---------|---------|---------------|
| 1988 | -0.0922 | 0.4853 | -1.4579 | |
| 1989 | 0.0305 | 1.7752 | -0.5255 | |
| 1990 | 0.1090 | -0.0653 | -1.0321 | |
| 1991 | -0.3604 | 0.0568 | -1.3803 | 1.0607 |
| 1992 | -1.0669 | 1.6702 | -0.0079 | 0.2384 |
| 1993 | -1.7320 | 0.2500 | 0.3970 | 1.0607 |
| 1994 | -1.6045 | 2.1620 | 0.8361 | 1.3348 |
| 1995 | -1.5079 | 0.6471 | -0.7718 | 1.8830 |
| 1996 | -1.2358 | 0.0629 | -1.0495 | -0.0358 |
| 1997 | -0.9260 | 2.5468 | 1.2493 | -0.8581 |
| 1998 | -0.4224 | -0.8140 | 1.0585 | 1.0607 |
| 1999 | -0.2756 | -0.3075 | -0.0316 | -0.0358 |
| 2000 | -0.2939 | 0.6220 | 0.8222 | -0.0358 |
| 2001 | 0.7988 | -0.6682 | -0.3031 | 0.7866 |
| 2002 | 1.4265 | -0.4816 | -1.4606 | -0.0358 |
| 2003 | 1.5375 | -0.9796 | -0.3007 | -0.5840 |
| 2004 | 1.4744 | -0.7112 | -1.3528 | -1.4063 |
| 2005 | 1.2302 | -0.9596 | 1.7375 | -1.4063 |
| 2006 | 0.2321 | -0.1724 | -0.0500 | -0.8581 |
| 2007 | -0.4659 | -0.9202 | -0.7659 | -1.4063 |
| 2008 | -0.3454 | -0.8172 | 0.0983 | -1.4063 |
| 2009 | 0.3337 | -0.7762 | 1.7780 | -0.1728 |
| 2010 | 0.4420 | -0.4356 | 1.0925 | 1.0607 |
| 2011 | 1.2302 | -0.9131 | 1.2529 | -1.4063 |
| 2012 | 1.4841 | -0.6595 | 0.1674 | 0.3754 |

2-Environmental data:

The normalized NAO winter Index was directly available from the NCAR website.

Daily mean NOAA High Resolution SST data for each of the spatial grids covering the North Sea (1.5W_57.5N, 1.5W_58.5N, 2.5W_57.5N, 2.5W_58.5N, 3.5W_57.5N, 3.5W_58.5N, 4.5W_57.5N, 4.5W_58.5N) were provided the NOAA/OAR/ESRL PSD, Boulder, Colorado, USA, from their Web site at <https://www.esrl.noaa.gov/psd/> . Then, the monthly average across the spatial grid cells was calculated

Table S1.2: Normalized NAO index and SST from April to September of the breeding year and from March in year (t-1) to May of the breeding year.

| | NAO Index | Apr-Sept | Mar _(t-1) -May _(t) |
|------|-----------|----------|--|
| 1988 | 0.7200 | -0.1638 | 1.8441 |
| 1989 | 5.0800 | -0.0931 | 0.4295 |
| 1990 | 3.9600 | -0.3375 | -0.0148 |
| 1991 | 1.0300 | 0.1029 | -0.3324 |
| 1992 | 3.2800 | -0.1648 | -0.0416 |
| 1993 | 2.6700 | -2.3160 | -1.2764 |
| 1994 | 3.0300 | -1.8868 | -2.9055 |
| 1995 | 3.9600 | -0.5556 | -0.8561 |
| 1996 | -3.7800 | -1.3697 | -0.5037 |
| 1997 | -0.1700 | 0.6462 | -0.4966 |
| 1998 | 0.7200 | -0.6162 | 1.6474 |
| 1999 | 1.7000 | -0.1890 | -0.9686 |
| 2000 | 2.8000 | -0.4577 | -0.1459 |
| 2001 | -1.9000 | -0.8132 | -0.2352 |
| 2002 | 0.7600 | 1.4017 | 0.3510 |
| 2003 | 0.2000 | 2.1925 | 0.9211 |
| 2004 | -0.0700 | 0.9664 | 0.9827 |
| 2005 | 0.1200 | 0.0827 | 0.4572 |
| 2006 | -1.0900 | 0.4372 | 0.5303 |
| 2007 | 2.7900 | 0.3291 | 1.3485 |
| 2008 | 2.1000 | 0.6119 | -0.2539 |
| 2009 | -0.4100 | 1.7926 | -0.4868 |
| 2010 | -4.6400 | -0.0719 | 0.4822 |
| 2011 | -1.5700 | 0.6129 | -1.0676 |
| 2012 | 3.1700 | -0.1405 | 0.5910 |

3-Biotoxin data origin:

The biotoxin data were collected as part of the Food Standards Scotland shellfish monitoring program (<http://marine.gov.scot/themes/biotoxin-monitoring>). Measurements of toxin in mussels were made several times per months. We then averaged these concentrations per month, per year and then we normalized them.

Table S1.3: Normalized concentration of saxitoxin (SXT) and domoic acid (DA) present in mussels.

| | SXT | D.A. |
|------|---------|------|
| 1990 | -0.4757 | |
| 1991 | -0.2334 | |
| 1992 | -0.2752 | |
| 1993 | 0.7641 | |
| 1994 | -0.1430 | |
| 1995 | -0.2219 | |
| 1996 | 4.1403 | |

| | | |
|------|---------|---------|
| 1997 | -0.4757 | |
| 1998 | 0.1487 | |
| 1999 | -0.4757 | 0.0890 |
| 2000 | -0.4757 | -2.0864 |
| 2001 | -0.4757 | 1.3041 |
| 2002 | -0.4757 | -0.9591 |
| 2003 | -0.4757 | -0.9244 |
| 2004 | | |
| 2005 | | |
| 2006 | | |
| 2007 | -0.3843 | 1.6429 |
| 2008 | -0.1453 | 1.5186 |
| 2009 | -0.2278 | -0.1751 |
| 2010 | -0.4757 | 0.1512 |
| 2011 | -0.3909 | -0.0664 |
| 2012 | 0.4338 | -0.0508 |

4-Grey seal counts

Table S1.4: Annual average number of grey seals counted by aerial survey during the moult in the northern Moray Firth.

| | Average number of grey seals |
|------|------------------------------|
| 2006 | 871 |
| 2007 | 1005 |
| 2008 | 1064 |
| 2009 | 665 |
| 2010 | 355 |
| 2011 | 799 |
| 2012 | 724 |
| 2012 | 860 |
| 2013 | 757 |

S2: Model description:

1-Demographic model parameters:

Male and female harbour seals were separated because they have different haul-out patterns (Lonergan et al. 2013) both during the pupping and the moulting season.

Priors of the baseline parameters for adult female survival and the reproductive rate were based on estimates measured from two mark-recapture studies carried out in the Moray Firth between 1999-2002 (Mackey et al. 2007) and 2006-2011 (Cordes 2014). For the other

age and sex classes the priors of baseline parameters were based on values estimated in Thompson et al. (2007) and Härkönen and Heide-Jørgensen (1990) (Table 2). Juvenile survival rate was adjusted to increase at a constant rate between the pup and adult baseline values.

The shooting parameter was the same as the one used by Matthiopoulos et al (2013), using estimates of seals shot in the Moray Firth during the period 1994-2004. During this period the shooting effort underwent two regimes change. Prior to 1999 shooting effort was low. It increased dramatically after 1999 until the Moray Firth Seal Management Plan was implemented in 2003, which initiated a decrease by a tenth within a year. See Matthiopoulos et al. (2013) for details of, the assumptions associated with these data, the selection of the parameter μ and m and the prior analysis.

2-Additional haul-out site at Brora/Helmsdale:

In the model, the total abundance including all the sites (Dornoch Firth, Loch Fleet, Brora and Helmsdale) was estimated during the entire time series. Consequently, for the data prior to 2006 when no Brora and Helmsdale data were available in the survey data, it was necessary to estimate the number of seals at these sites and then subtract it from the estimated total abundance in order to match the observed survey data. To do so, the number of seals present at Brora and Helmsdale between 1988 and 2005 were estimated using a generalized linear model (GLM) representing the relationship between ρ and time where ρ (Eq.S1) is the ratio of seals counted at Brora and Helmsdale (n_{BH}) and seals counted on the two other main sites (n_{MS}). For different age and sex classes (k), we estimated the ratio

$$\rho_k = \frac{n_{kBH}}{n_{kMS}} \quad \text{Eq.S1}$$

ρ was treated as a function of year t and represented using a logistic equation

$$\rho_{ks} = \frac{\exp(\rho_{0ks} + \rho_{1s}t)}{(1 + \exp(\rho_{0ks} + \rho_{1s}t))} \quad \text{Eq.S2}$$

Where k refers to age and sex category, (pups, juveniles, adult males or females) and s stands for the survey season (breeding or moult).

The fitted GLMs showed a significant positive linear trend between ρ and t for both pups and adults during the breeding season (TableS2.1).

Table S2.1: R GLM results of the relationship between the ratio of the seals counted in Brora and Helmsdale (n_{BH}) and the seals counted on the two other main sites and time for the pups, the non-pups during breeding and the non-pups during moult. *** indicate a significant value.

| GLM output for pups | | | | |
|---|---|-----------|----------|--------------|
| Model | glm(formula = cbind(BroPaverage, noBroPaverage) ~ yearbaverage, family = binomial(logit)) | | | |
| | Estimate | Std.Error | Z value | Pr(> z) |
| Intercept (ρ_{0pb}) | -7.19340 | 1.47878 | -4.864 | 1.15e-06 *** |
| Yearbaverage (ρ_{1pb}) | 0.21810 | 0.06478 | 3.367 | 0.000761 *** |
| Null deviance: | 24.3422 on 8 degrees of freedom | | | |
| Residual deviance: | 5.7117 on 7 degrees of freedom | | | |
| AIC: | 37.444 | | | |
| GLM of non-pups during breeding season | | | | |
| Model | glm(formula = cbind(BroAbaverage, noBroAbaverage) ~ yearbaverage, family = binomial(logit)) | | | |
| | Estimate | Std.Error | Z value | Pr(> z) |
| Intercept (ρ_{0npb}) | -3.35128 | 0.28119 | - 11.918 | < 2e-16 *** |
| Yearbaverage (ρ_{1npb}) | 0.07658 | 0.01322 | 5.793 | 6.93e-09 *** |
| Null deviance: | 47.0386 on 8 degrees of freedom | | | |
| Residual deviance: | 6.7799 on 7 degrees of freedom | | | |
| AIC: | 58.539 | | | |
| GLM of non-pups during moult season | | | | |
| Model | glm(cbind(BroAmaverage, nBroAmaverage)~yearmaverage,family=binomial(logit)) | | | |
| | Estimate | Std.Error | Z value | Pr(> z) |
| Intercept (ρ_{0npb}) | -1.1357964 | 0.0961257 | -11.816 | < 2e-16 *** |
| Yearbaverage (ρ_{1npb}) | -0.0001821 | 0.0054463 | -0.033 | 0.973 |

| | |
|--------------------|---------------------------------|
| Null deviance: | 142.51 on 11 degrees of freedom |
| Residual deviance: | 142.50 on 10 degrees of freedom |
| AIC: | 220.06 |

In our model, the priors for ρ_{0pb} , ρ_{1pb} , ρ_{0npb} and ρ_{1npb} were a normal distribution with a mean and a precision being the estimate and $1/(\text{std.error})^2$ of the GLMs model, respectively (TableS2.1). Given the absence of significant relationship between the ratio of counts during the moult and years, the priors for ρ_{npm} was a beta distribution with the mean and the variance being the ratio mean and variance observed with the non-pups breeding data.

3 Haul-out parameters and sensitivity analysis:

To conduct the sensitivity analysis on the haul-out probability, 9 different models were tested, with different baseline haul-out probabilities (mean of the beta prior distribution) and different daily variability (variance of the beta prior distribution). The baseline haul-out probabilities tested were the mean haul-out probabilities estimated by Hubert et al (2001), and their lower and the upper confidence interval values (TableS3.1).

Three levels of daily variability corresponding to the beta prior distribution variance of 0.0025, 0.01 and 0.05 were tested (Table S3.2). The lowest value of 0.0025 was calculated from Cunningham et al (2009) results. Then, several other variances were tested, for variance above 0.05 the models were not converging anymore probably due to too many sources of uncertainties in the model. We then choose one variance in between 0.0025 and 0.05.

Table S3.1: Baseline Haul-out probabilities tested for each age class and season.

| | | Low haul-out probabilities | | Average haul-out probabilities | | High haul-out probabilities | |
|---------|----------|----------------------------|----------|--------------------------------|----------|-----------------------------|----------|
| | | Pupping | Moulting | Pupping | Moulting | Pupping | Moulting |
| Females | Adult | 0.65 | 0.50 | 0.75 | 0.50 | 0.95 | 0.60 |
| | Juvenile | 0.40 | 0.40 | 0.50 | 0.50 | 0.60 | 0.60 |
| | Pup | 0.75 | 0.15 | 0.85 | 0.25 | 0.95 | 0.35 |

| | | | | | | | |
|-------|----------|------|------|------|------|------|------|
| Males | Adult | 0.40 | 0.50 | 0.50 | 0.60 | 0.60 | 0.70 |
| | Juvenile | 0.40 | 0.40 | 0.50 | 0.50 | 0.60 | 0.60 |
| | Pup | 0.75 | 0.15 | 0.85 | 0.25 | 0.95 | 0.35 |

Table S3.2: Name of the models tested with different baseline haul-out probability and different daily variability. The black cell indicates a non-convergent model.

| Variance | Low baseline haul-out probability | Mean baseline haul-out probability | High baseline haul-out probability |
|----------|-----------------------------------|------------------------------------|------------------------------------|
| 0.0025 | Low_0.0025 | Average_0.0025 | |
| 0.01 | Low_0.010 | Average_0.010 | High_0.010 |
| 0.05 | Low_0.050 | Average_0.050 | High_0.05 |

Figure S3.1 shows similar trends in population abundance regardless of the baseline haul-out probability and its daily variability. We therefore concluded that our model is robust to plausible change in haul-out probabilities.

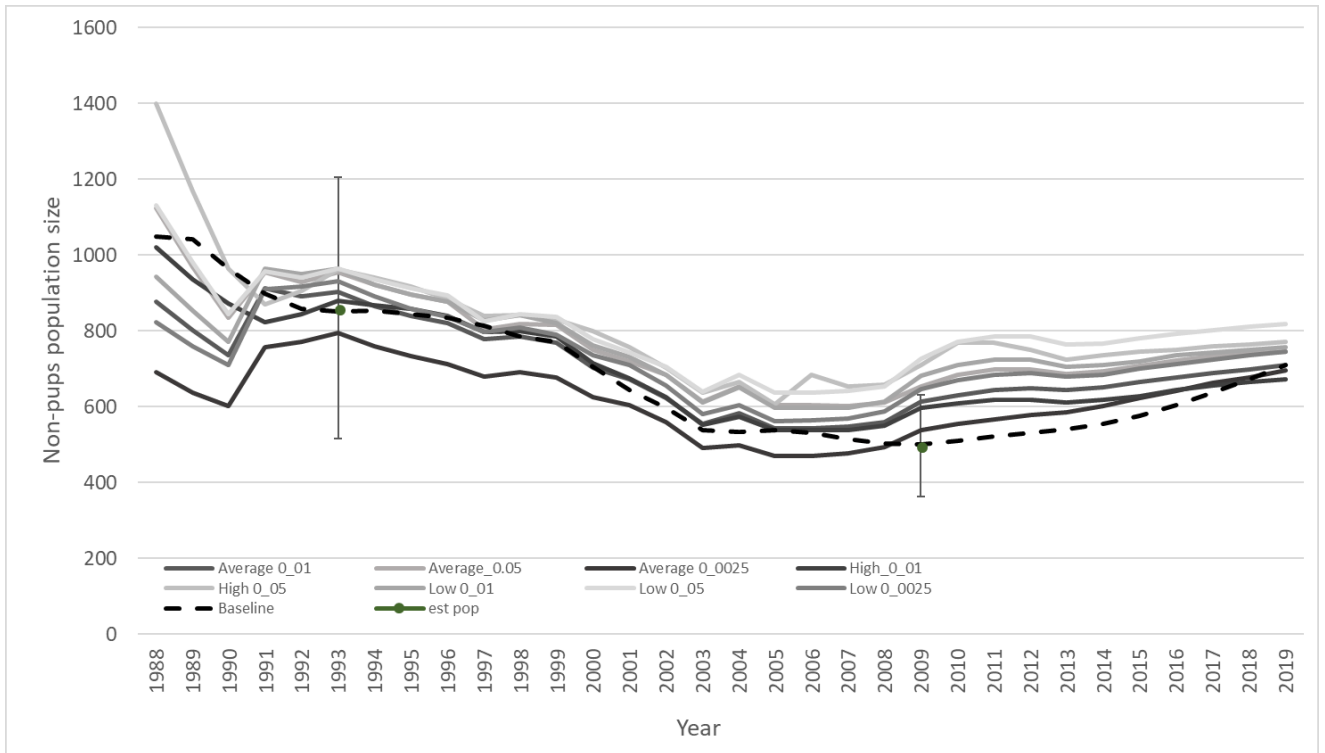


Figure S3.1: Non-pups population size estimate with different baseline haul-out probabilities and different daily variability. The name of each line is associated with the model described in the Table S3.3a

S3: Prior and posterior distributions:

Matthiopoulos et al. (2013) used re-scaled beta distributions for all informative priors to avoid problem of convergence and mixing that can occur when there are too many parameters in a model. Given, they carefully conducted prior sensitivity analysis and explored different model specifications using simulated data to select priors, we used the same prior as them for the coefficients associated with year and population density for all the demographic rates (Table S3.1). For the prior of the coefficients associated with environmental covariates, the same bounded beta distribution was used, and a prior sensitivity analysis was conducted.

Table S3.1: Prior and posterior information on the baseline model’s parameters. To facilitate visual inspection of parameter credible intervals that did not span around 0 are shown in bold.

| <i>Parameter</i> | | <i>Prior distribution</i> | | | <i>Posterior distribution</i> | |
|------------------|--|---------------------------|-------------|---------------------------|-------------------------------|-----------------------|
| <i>Symbol</i> | <i>Description</i> | <i>Type</i> | <i>Mean</i> | 95- <i>percentiles</i> | <i>Mean</i> | <i>95-percentiles</i> |
| b_0 | Fecundity in 2009 | Beta | 0.87 | (0.83,0.91) | 0.8411 | (0.80,0.88) |
| β_1 | Linear time coefficient for fecundity | Beta | 0 | (-0.03, 0.03) | -0.0008 | (-0.02,0.02) |
| β_N | Density dependent coefficient for fecundity | Beta | 0 | (-0.02, 0.02) | -0.007 | (-0.009,-0.006) |
| β_c | Covariate coefficient for fecundity in the sandeel model | Beta | 0 | (-0.2,0.2) | 0.1135 | (0.016-0.18) |

| | | | | | | |
|---------------------|--|------|------|--------------|--------|--------------------|
| β_C | Covariate coefficient for fecundity in the NAO model | Beta | 0 | (-0.2,0.2) | 0.05 | (0.01-0.11) |
| σ_{p22} | Pup survival in 2009 | Beta | 0.7 | (0.60,0.80) | 0.63 | (0.59,0.70) |
| $\sigma_{j_{1,22}}$ | Juvenile 1 survival in 2009 | Beta | 0.78 | (0.68,0.88) | 0.69 | (0.66,0.63) |
| $\sigma_{j_{2,22}}$ | Juvenile 2 survival in 2009 | Beta | 0.86 | (0.77,0.94) | 0.78 | (0.75,0.82) |
| $\sigma_{j_{3,22}}$ | Juvenile 3 survival in 2009 | Beta | 0.90 | (0.85,0.94) | 0.84 | (0.83,0.86) |
| σ_{f22} | Female survival in 2009 | Beta | 0.97 | (0.94,0.99) | 0.93 | (0.91,0.94) |
| σ_{m22} | Male survival in 2009 | Beta | 0.87 | (0.80,0.95) | 0.85 | (0.85,0.97) |
| σ_p | Linear time coefficient for survival of pup | Beta | 0 | (-0.03,0.03) | -0.003 | (-0.02,0.03) |
| σ_j | Linear time coefficient for survival of young | Beta | 0 | (-0.03,0.03) | 0.002 | (-0.02,0.03) |
| $\sigma_m \sigma_f$ | Linear time coefficient for survival of adults | Beta | 0 | (-0.03,0.03) | 0.003 | (-0.02,0.03) |

| | | | | | | |
|---------------------------|---|---------|-------|---------------|--------|------------------------|
| σ_{Np} | Density dependence in pup survival | Beta | 0 | (-0.02,0.02) | 0.00 | (-0.002,0.006) |
| σ_{Nj} | Density dependence in young survival | Beta | 0 | (-0.02,0.02) | 0.003 | (-0.0002,0.008) |
| $\sigma_{Nm} \sigma_{Nf}$ | Density dependence in adult survival | Beta | 0 | (-0.02,0.02) | 0.009 | (0.004,0.01) |
| σ_{pc} | Covariate coefficient for pup survival in the grey seal model | Beta | 0 | (-0.03,0.03) | -0.002 | (-0.003,-0.001) |
| m | Maximum per capita shooting mortality | Beta | 0.125 | (0.06,0.19) | 0.13 | (0.116,0.143) |
| u_{1999} | Relative shooting effort before 1999 | Uniform | 0.5 | (0.405,0.595) | 0.57 | (0.51,0.6) |
| u_{2004} | Relative shooting effort after 2004 | Uniform | 0.1 | (0.053,0.148) | 0.14 | (0.12,0.15) |
| ρ | Scalar for numbers shot across the entire Firth relative to northern part | Beta | 2 | (1.99,2.01) | 2 | (1.992,2.008) |

| | | | | | | |
|--------------|--|-----------------------------|-------|---------------|-------|---------------|
| c_f | Age decay parameter for initial female population structure | Beta | 0.17 | (0.10,0.24) | 0.16 | (0.11,0.22) |
| c_m | Age decay parameter for initial male population structure | A function of c_f | 0.19 | (0.14,0.26) | 0.15 | (0.13,0.19) |
| N_f | Initial number of females in population | Uniform | 500 | (200,1000) | 409 | (353,452) |
| N_m | Initial number of males in population | A function of $N_f c_m c_f$ | | | 294 | (265,319) |
| ρ_{0P} | Baseline count ratio between BH and MS sites for the pups | Normal | -7.19 | (-8.15,-6.13) | -6.46 | (-7.54,-5.31) |
| ρ_{0Ab} | Baseline count ratio between BH and MS sites for the non-pups during breeding. | Normal | -3.35 | (-3.53,-3.18) | -3.22 | (-3.38,-2.95) |

| | | | | | | |
|--------------|--|--------|------|-------------|------|-------------|
| ρ_{1P} | Linear time coefficient for the count ratio between BH and MS sites for the pups | Normal | 0.22 | (0.18,0.27) | 0.18 | (0.13,0.23) |
| ρ_{1Ab} | Linear time coefficient for the Count ratio between BH and MS sites for the non-pups during breeding | Normal | 0.08 | (0.06,0.09) | 0.07 | (0.06,0.08) |
| ρ_{Am} | Count ratio between BH and MS sites for non-pups during moulting | Beta | 0.54 | (0.01,0.98) | 0.24 | (0.23,0.26) |

S4: OpenBug code

Code for the baseline model:

```

model{
  # Time loop
  for (t in 1:tmax-1)
  {
    # PROCESS MODEL
    ##### Survival
    for (i in 1:10)
    {
      # Background survival probability

```

```

logit(s[i,t]) <- s0[i]+s1[i]*(t-dtsur[i])+s2[i]*ntotmu[t]
sur[i,t]<-s[i,t]*(1-mort*str[t])
# Check for zero number of trials
ni[i,t]<-equals(n[i,t],0)+n[i,t]-equals(n[i,t],0)*n[i,t]
sdum[i,t]<-sur[i,t]-equals(n[i,t],0)*sur[i,t]
# Number of survivors from each class
sS[i,t] ~ dbin(sdum[i,t],ni[i,t])
shotbyclass[i,t]<-mort*str[t]*n[i,t]
}
# Shooting mortality for outer Moray Firth
shotSeals[t]<-split*sum(shotbyclass[1:10,t])
shot[t]~ dpois(shotSeals[t])

### Fecundity
# Birth probability
logit(b[t]) <- b0+b1*(t-22)+b2*ntotmu[t]
# Check for zero number of trials
ni3[t]<-equals(sS[10,t],0)+sS[10,t]-equals(sS[10,t],0)*sS[10,t]
bdum[t]<-b[t]-equals(sS[10,t],0)*b[t]
# Total births
bBi[t] ~ dbin(bdum[t],ni3[t])
# Check for zero number of trials
sexdum[t]<-0.5-equals(bBi[t],0)*0.5
bBisex[t]<-equals(bBi[t],0)+bBi[t]-equals(bBi[t],0)*bBi[t]
# Number of male births
bBm[t] ~ dbin(sexdum[t], bBisex[t])
# Number of female births
bBf[t]<-bBi[t]-bBm[t]

##BroraProportion

logit(poBroPup[t])<- p0P+p1P*t
logit(poBroAdB[t])<-p0Ab+p1Ab*t
poBroAdM[t]<-poBroAdm
# Update rules for process model
n[1,t+1] <- bBm[t]
n[2,t+1] <- sS[1,t]
n[3,t+1] <- sS[2,t]
n[4,t+1] <- sS[3,t]
n[5,t+1] <- sS[4,t]+sS[5,t]
n[6,t+1] <- bBf[t]
n[7,t+1] <- sS[6,t]
n[8,t+1] <- sS[7,t]
n[9,t+1] <- sS[8,t]
n[10,t+1] <- sS[9,t]+sS[10,t]

# Tracks total population size
ntotmu[t]<-sum(n[2:5,t])+sum(n[7:10,t])
Allage[t]<-sum(n[1:10,t])
# Calculates precision for observed population sizes (applies to 1993&2009)
prec[t]<-1/pow((cvpops[t]*ntotmu[t]),2)
ntot[t]~dnorm(ntotmu[t],prec[t])

# OBSERVATION MODEL

for (j in 1:noSurv[t]) # Loops through surveys for year t
{
  for (i in 1:10) # Loops through age classes

```

```

{

# Prop animals hauled out

pd[i,t,j] <- pHo[seas[totsurv[t]+j],i]

p.bound[i,t,j] <- max(0, min(1, pd[i,t,j]))

#define the variance wanted for the daily variation of the prob.
haulout
varp[i,t,j]<-0.05
alp[i,t,j]<-p.bound[i,t,j]*p.bound[i,t,j]*((1-
p.bound[i,t,j])/varp[i,t,j]-1/p.bound[i,t,j])
bep[i,t,j]<-(1-p.bound[i,t,j])*(p.bound[i,t,j]*(1-
p.bound[i,t,j])/varp[i,t,j]-1)

p[i,t,j]~dbeta(alp[i,t,j],bep[i,t,j])

# Check for zero number of trials
pdum[i,t,j]<-p[i,t,j]-equals(n[i,t],0)*p[i,t,j]
# Numbers hauled-out on survey date d by class i
pP[i,totsurv[t]+j] ~ dbin(pdum[i,t,j],ni[i,t])
}

# Total number of pups on the beach
pups[t,j]<-(pP[1,totsurv[t]+j]+pP[6,totsurv[t]+j])*(2-
seas[totsurv[t]+j]) #total number of pups born and one the beach

TotPupsExp[totsurv[t]+j]<-pobsp[totsurv[t]+j]*pups[t,j]
#Estimate of the number of pups observed on the beach on 3 sites

PupBroExp[totsurv[t]+j]<-
poBroPup[t]*TotPupsExp[totsurv[t]+j]*equals(seas[totsurv[t]+j],1) #Expected
number of pups in Brora

PupsExp[totsurv[t]+j]<- TotPupsExp[totsurv[t]+j]-
PupBroExp[totsurv[t]+j]*(2-sType[totsurv[t]+j]) #Expected number of pup
outside Brora

Brora[totsurv[t]+j]~dpois(PupBroExp[totsurv[t]+j]) #Compare prediction
of the number of pup in Brora to Brora Observation

P_d[totsurv[t]+j]~dpois(PupsExp[totsurv[t]+j]) #Compare prediction of
the number of pup in total to all observations

# Total number of non-pups on the beach
#total number of non pups born and one the beach
adjuv[t,j] <- sum(pP[2:5,totsurv[t]+j])+sum(pP[7:10,totsurv[t]+j])
+ (pP[1,totsurv[t]+j]+pP[6,totsurv[t]+j])*(seas[totsurv[t]+j]-1)
TotAdjuvExp[totsurv[t]+j]<-pobsa[totsurv[t]+j]*adjuv[t,j] #Estimate of
the number of non pups observed on the beach on 3 sites

AdBroExp[totsurv[t]+j]<-
poBroAdB[t]*TotAdjuvExp[totsurv[t]+j]*equals(seas[totsurv[t]+j],1)+
poBroAdM[t]*TotAdjuvExp[totsurv[t]+j]*equals(seas[totsurv[t]+j],2)

AdjuvExp[totsurv[t]+j]<- TotAdjuvExp[totsurv[t]+j]-
AdBroExp[totsurv[t]+j]*(2-sType[totsurv[t]+j])

```

```

AdBrora[totsurv[t]+j]~dpois(AdBroExp[totsurv[t]+j])
A_d[totsurv[t]+j]~dpois(AdjuvExp[totsurv[t]+j])
}

```

PRIOR DISTRIBUTIONS

Constructs a standard Beta template for all the priors

```

var<-0.05
mu<-0.5
al<-mu*(mu*(1-mu)/var-1)
be<-(1-mu)*(mu*(1-mu)/var-1)

```

Breeding Ho prob

```

pHo[1,1]<- 0.85;pHo[1,2]<-0.50;pHo[1,3]<-0.50;pHo[1,4]<-0.50;pHo[1,5]<-
0.50
pHo[1,6]<-0.85;pHo[1,7]<-0.50;pHo[1,8]<-0.50;pHo[1,9]<-0.50;pHo[1,10]<-
0.75

```

Moulting Ho prob

```

pHo[2,1]<- 0.10;pHo[2,2]<-0.5;pHo[2,3]<-0.5;pHo[2,4]<-0.5;pHo[2,5]<-
0.61
pHo[2,6]<- 0.10;pHo[2,7]<-0.5;pHo[2,8]<-0.5;pHo[2,9]<-0.5;pHo[2,10]<-0.50

```

Baseline vital rates

```

dbfec0~dbeta(al,be)
dsurvp~dbeta(al,be)
dsurvf~dbeta(al,be)
dsurvm~dbeta(al,be)
dsurvj~dbeta(al,be)
bfec0<-0.83+dbfec0*0.08
survp<-0.60+dsurvp*0.2
survj2<-0.68+dsurvj*0.2
survj3<-0.77+dsurvj*0.2
survj4<-0.85+dsurvj*0.06
survj7<-0.68+dsurvj*0.2
survj8<-0.77+dsurvj*0.2
survj9<-0.85+dsurvj*0.06
survf<-0.94+dsurvf*0.06
survm<-survf*(0.85+dsurvm*0.1)

```

Baseline rate-to-intercept conversions

```

b0 <- log(bfec0/(1-bfec0)) - b2*ntot[22]
sp <- log(survp/(1-survp)) - s2p*ntot[22]
sj2 <- log(survj2/(1-survj2)) - s2j*ntot[22]
sj3 <- log(survj3/(1-survj3)) - s2j*ntot[22]
sj4 <- log(survj4/(1-survj4)) - s2j*ntot[22]
sj7 <- log(survj7/(1-survj7)) - s2j*ntot[22]
sj8 <- log(survj8/(1-survj8)) - s2j*ntot[22]
sj9 <- log(survj9/(1-survj9)) - s2j*ntot[22]
sm <- log(survm/(1-survm)) - s2a*ntot[22]
sf <- log(survf/(1-survf)) - s2a*ntot[22]
s0[1]<-sp;s0[2]<-sj2;s0[3]<-sj3;s0[4]<-sj4;s0[5]<-sm;s0[6]<-sp;s0[7]<-
sj7;s0[8]<-sj8;s0[9]<-sj9;s0[10]<-sf

```

#Class-specific trend parameters for vital rates with time - Non-informative

```

db1~dbeta (a1,be)
span<-0.03
span2<-span*span
span3<-span*span*span
b1<- -span+2*span*db1
db2~dbeta (a1,be)
b2<- -0.02+0.04*db2

ds1p~dbeta (a1,be)
s1p<- -span+2*span*ds1p
ds1j~dbeta (a1,be)
s1j<- -span+2*span*ds1j
ds1a~dbeta (a1,be)
s1a<- -span+2*span*ds1a
s1[1]<-s1p;s1[2]<-s1j;s1[3]<-s1j;s1[4]<-s1j;s1[5]<-s1a;s1[6]<-s1p;s1[7]<-
s1j;s1[8]<-s1j;s1[9]<-s1j;s1[10]<-s1a

ds2p~dbeta (a1,be)
s2p<- -0.02+0.04*ds2p
ds2j~dbeta (a1,be)
s2j<- -0.02+0.04*ds2j
ds2a~dbeta (a1,be)
s2a<- -0.02+0.04*ds2a
s2[1]<-s2p;s2[2]<-s2j;s2[3]<-s2j;s2[4]<-s2j;s2[5]<-s2a;s2[6]<-s2p;s2[7]<-
s2j;s2[8]<-s2j;s2[9]<-s2j;s2[10]<-s2a

# Shooting mortality
dmort~dbeta (a1,be)
mort<-0.05+dmort*0.15
strbe~dunif (0.40,0.60)
straf~dunif (0.05,0.15)
for(i in 1:11) {str[i]<-strbe}
for(i in 12:15) {str[i]<-1}
for(i in 16:33) {str[i]<-straf}

# Total mortality scalar (split between inner and outer Moray firth)
dsplit~dbeta (a1,be)
split<-1.99+0.02*dsplit

#Initial age structure
femI~dunif (200,1000)
cfd~dbeta (a1,be)
cf<-0.1+0.14*cfd
cm<-cf+0.03
malI<-femI*(1-exp(-cf))/(1-exp(-cm))
for(i in 1:4)
{
n[i,1]<-round(malI*(exp(-(i-1)*cm)-exp(-i*cm)))
n[i+5,1]<-round(femI*(exp(-(i-1)*cf)-exp(-i*cf)))
}
n[5,1]<-round(malI*exp(-4*cm))
n[10,1]<-round(femI*exp(-4*cf))

# Observation parameters
pobspg<-1 #Pup sightability from the ground
pobspa<-1 #Pup sightability from the air
for(i in 1:163)
{pobsp[i]<-pobspg*equals(sType[i],1)+pobspa*equals(sType[i],2)}

```



```

pobsag<-1 # Adultsightability from the ground
pobsaa<-1# Adult sightability from the air
for(i in 1:163)
{pobsa[i]<-pobsag*equals(sType[i],1)+pobsaa*equals(sType[i],2)}

```

Brora parameters

```

p0P~dnorm(-7.19340,0.4572912)
p1P~dnorm(0.21810,238.2967)

```

```

p0Ab~dnorm(-3.35128,12.64737)
p1Ab~dnorm(0.07658,5721.858)

```

```

poBroAdmd~dbeta(a1,be)
poBroAdm<-0.01+poBroAdmd*0.98

```

Assignment of observation CVs referring to 1st part of the time series

```

for(i in 1:11) {cvpops[i]<-0.2}

```

Assignment of observation CVs referring to 2nd part of the time series

```

for(i in 12:33) {cvpops[i]<-0.075}
}

```

DATA

```

list(
# Length of time series of states
tmax=33,
# Time lag to be used in demographic functions for each population class
dtsur=c(22,22,22,22,22,22,22,22,22,22,22),
# Independent population estimates
ntot = c(NA,NA,NA,NA,NA,NA,860,
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,497,NA,NA,NA,NA,NA,NA,NA,NA,
,NA,NA),
# Number of surveys conducted each year
noSurv=
c(3,7,3,2,4,10,4,7,7,6,8,7,10,8,8,7,4,7,12,6,7,5,6,5,5,5,0,0,0,0,0,0,0), #
Cumulative number of surveys from the start of the time series
totsurv=c(0,3,10,13,15,19,29,33,40,47,53,61,68,78,86,94,101,105,112,124,130
,137,142,148,153,158,163,163,163,163,163,163,163,163),
# Median number of reported shot seals
shot=c(NA,NA,NA,NA,NA,NA,136,136,132,124,142,231,178,177,184,29,34,NA,NA,NA
,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA),
#Season (1=breeding survey, 2=moult survey)
seas=c(1,1,2,1,1,1,1,1,1,2,
1,1,2,2,2,1,1,2,2,1,
1,1,1,1,1,1,1,2,2,1,
1,1,1,1,1,1,1,1,2,2,
1,1,1,1,1,2,2,1,1,1,
1,1,2,1,1,1,1,1,2,2,
2,1,1,1,1,1,2,2,1,1,
1,1,1,2,2,2,2,2,1,
1,1,1,1,2,2,2,1,1,1,
1,1,2,2,2,1,1,1,1,1,
2,2,1,1,2,2,1,

```

1,1,1,2,2,2,1,1,
1,1,1,1,1,1,1,1,2,2,
1,1,1,1,2,2,1,1,1,1,
1,2,2,1,1,1,1,2,1,1,
1,1,1,2,1,1,1,1,2,1,
1,1,1,2,1,1,1,1,2),

Observed number of pups in each survey
P_d=c(27, 21, 0, 29, 23, 34, 31, 29, 25, 0,
0, 6, 0, 0, 0, 62, 85, 0, 0, 26,
134, 136, 116, 70, 85, 63, 33, 0, 0, 121,
63, 53, 24, 17, 34, 100, 113, 90, 0, 0,
20, 81, 109, 104, 55, 0, 0, 40, 60, 51,
59, 61, 0, 45, 108, 123, 91, 44, 0, 0,
0, 11, 36, 128, 78, 78, 0, 0, 79, 90,
123, 72, 61, 0, 0, 0, 0, 0, 61,
130, 106, 95, 74, 0, 0, 0, 20, 107, 123,
76, 63, 0, 0, 0, 81, 86, 69, 56, 25,
0, 0, 89, 115, 0, 0, 21,
58, 33, 25, 0, 0, 0, 22, 49,
77, 53, 43, 17, 60, 84, 76, 57, 0, 0,
28, 85, 69, 54, 0, 0, 53, 89, 77, 87,
33, 0, 0, 91, 168, 150, 118, 0, 72, 162,
150, 141, 61, 0, 34, 132, 150, 101, 0, 34,
113, 136, 69, 0, 15, 119, 130, 99, 0),

Observed number of adults in each survey
A_d=c(
528, 513, 542, 443, 183, 156, 148, 135, 330, 363,
357, 385, 453, 437, 327, 468, 363, 590, 441, 489,
556, 532, 642, 528, 489, 562, 582, 656, 614, 534,
380, 449, 388, 343, 380, 497, 547, 411, 511, 464,
419, 531, 428, 401, 421, 415, 405, 293, 427, 331,
243, 253, 834, 379, 479, 470, 462, 226, 521, 472, 399,
518, 363, 451, 374, 333, 262, 446, 437, 408, 417,
282, 247, 328, 318, 325, 317, 335, 338, 435, 423,
396, 348, 280, 373, 365, 306, 378, 374, 349, 275, 470,
302, 336, 349, 410, 266, 302, 213, 272, 206, 330,
326, 313, 294, 266, 230, 231, 226, 445, 295, 240, 195,
209, 207, 213, 134, 219, 283, 189, 268, 190, 491,
481, 218, 234, 223, 199, 174, 386, 257, 229, 183,
282, 184, 349, 250, 358, 305, 296, 230, 250, 297,
292, 271, 295, 203, 434, 207, 296, 319, 259, 408,
305, 261, 340, 276, 392, 235, 306, 285, 257, 418),
Type of survey methodology: 1=ground, 2=aerial

sType=c(1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,
1,1,2,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,
1,1,2,1,1,1,1,1,1,
1,1,1,1,1,1,1,
1,1,1,2,1,1,1,1,1,

```
1,1,1,2,2,2,2,2,2,2,  
2,2,2,2,2,2,2,2,2,2,  
2,2,2,2,2,2,2,2,2,2,  
2,2,2,2,2,2,2,2,2,2,  
2,2,2,2,2,2,2,2,2,2),
```

```
AdBrora=c (NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,22,NA,NA,28,123,86,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,214,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,91,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,188,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,34,  
NA,113,NA,NA,NA,NA,  
NA,NA,NA,28,49,8,32,19,163,264,  
40,37,23,28,18,90,28,16,33,71,  
32,102,43,78,42,49,39,19,23,33,  
34,65,68,101,18,38,42,48,87,66,  
58,62,70,102,54,57,51,29,70),
```

```
Brora=c (NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,0,NA,NA,0,0,0,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,0,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,0,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,0,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,  
NA,NA,NA,NA,NA,NA,NA,NA,2,NA,0,  
NA,NA,NA,NA,NA,NA,NA,NA,0,1,0,  
1,2,0,0,1,7,1,0,0,0,  
1,0,12,24,0,0,0,5,17,20,  
15,0,0,12,13,17,20,0,0,10,  
12,17,0,0,13,20,18,0,0,11,17,16,0)  
)
```

EXAMPLE INITIAL VALUES (Automatically generated initial values work as well)

```
list(dbfec0=0.8, db1= 0.5, dsurvp= 0.5, dsurvj=0.5, dsurvm= 0.5 , dsurfv=  
0.5 , ds1a=0.5 , db2=0.5, ds2j=0.5, ds2a=0.5,  
femI=500, dmort=0.5, dsplit=0.5,  
cfd=0.8
```

)

```
list(dbfec0=0.4, db1= 0.5, dsurvp= 0.5, dsurvj=0.5001,dsurvm= 0.54 ,  
dsurvf= 0.5 , ds1a= 0.5 , db2=0.5, ds2j=0.85, ds2a=0.4,  
femI=350, dmort=0.55,dsplit=0.5,  
cfd=0.7
```

)