# Appendix S2: Supplemental material for “The sensitivity of seabird populations to density-dependence, environmental stochasticity and anthropogenic mortality”

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## S1 Read in files for population data:

Kittiwake and Guillemot from Newell et al. 2016, Gannet from JNCC 2017.

Kittiwake<-c(4801,6765,7638,7564,8129,6535,6916,7009,3751,

 7603,6269,6518,4306,4196,4618,3639,3666,3335,3876,3790,3167,3424,3354,2316,NA)

Gannet<-c(21591,NA,NA,NA,NA,NA,NA,NA,NA,34397,NA,

 NA,NA,44110,NA,NA,NA,NA,48065,NA,NA,NA,NA,NA,NA,NA,NA,NA,75259,NA)

Guillemot<-c(3360,3920,3880,3790,NA,NA,NA,NA,11250,NA,14750,13000,

 13000,13700,11680,11223,12736,12632,11440,11511,12418,13843,15326,

 14500,17340,17384,16933,17979,18442,20185,19519,20332,18858,15578,

 15536,15036,14143,15029,14955,14100,13349,14248,15945,16132, NA)

## S1 JAGS code: example model, guillemots.

IOMGUpopmodel<-"model{

bmax<-0.45 #female only post breeding census productivity

s1<- 0.56 #vital rate for each age class

s2<-0.792

s3<-0.917

s4<-0.939

s5<-0.939

s6<-0.939

a0<-log(bmax/(1-bmax)) #natural log transformation

s1a0<-log(s1/(1-s1))

s2a0<-log(s2/(1-s2))

s3a0<-log(s3/(1-s3))

s4a0<-log(s4/(1-s4))

s5a0<-log(s5/(1-s5))

s6a0<-log(s6/(1-s6))

# fixed species specific values for scalar

scalar1<-0.977

scalar2<-0.741

scalar3<-0.547

scalar4<-0.556

scalar5<-0.584

scalar6<-0.584

obsR<-0.01#observation error

#\_\_\_\_\_\_\_\_\_\_\_\_\_\_time loop\_\_\_\_\_\_\_\_\_\_\_\_\_\_

for (t in 1:(tmax-1))

{

 ntot[t]<-sum(n[,t]) # Total density

 eps1[t]~dnorm(0, prec) #full impact of environmental stochasticity

 eps2[t]<-scalar1\*eps1[t] #relative impact as scaled by each age class relationship to productivity

 eps3[t]<-scalar2\*eps1[t]

 eps4[t]<-scalar3\*eps1[t]

 eps5[t]<-scalar4\*eps1[t]

 eps6[t]<-scalar5\*eps1[t]

 eps7[t]<-scalar6\*eps1[t]

 lt[t]<-a0-a1\*ntot[t]+eps1[t] # Linear predictor for productivity, with density-dependence and environmental stochasticity

 logit(b[t])<-lt[t] # logit of Lt, representing proportion of maximum vital rate that is actually realised

 lts1[t]<-s1a0+eps2[t] #probability of survival at each age class on logit scale with environment

 logit(s1E[t])<-lts1[t]

 lts2[t]<-s2a0+eps3[t]

 logit(s2E[t])<-lts2[t]

 lts3[t]<-s3a0+eps4[t]

 logit(s3E[t])<-lts3[t]

 lts4[t]<-s4a0+eps5[t]

 logit(s4E[t])<-lts4[t]

 lts5[t]<-s5a0+eps6[t]

 logit(s5E[t])<-lts5[t]

 lts6[t]<-s6a0+eps7[t]

 logit(s6E[t])<-lts6[t]

#update rules for process model, with demographic stochasticity included as binomial distribution

 n[1,t+1]~dbin(b[t],n[6,t])

 n[2,t+1]~dbin(s1E[t],n[1,t])

 n[3,t+1]~dbin(s2E[t],n[2,t])

 n[4,t+1]~dbin(s3E[t],n[3,t])

 n[5,t+1]~dbin(s4E[t],n[4,t])

 nnew[t]~dbin(s5E[t],n[5,t])

 nold[t]~dbin(s6E[t],n[6,t])

 n[6,t+1]<-nnew[t]+nold[t]

#observation error

 obsR<-0.01

 ObsV[t]<-obsR\*n[6,t]

 ObsTau[t]<-1/ObsV[t]^2

 nDat[t]~dnorm(n[6,t], ObsTau[t])

#eigenvector for initialisation

 EV<-(c( 0.20, 0.10, 0.08, 0.07, 0.07, 0.48))

#data points to monitor

 expectNests[t]<-n[6,t]

}

# PRIORS ------

prec<-1/sigma^2

# Prior for density-dependence

mu1<-0.0000001

sd<-0.0001

s<-mu1^2/sd^2

r<-mu1/sd^2

a1~dgamma(s,r) T(0.00000000001,0.001) # Truncation as searching incomputable lower values

#Prior for environmental stochasticity

prec<-1/sigma^2

mu<-2

sdi<-0.5

p<-mu^2/sdi^2

q<-mu/sdi^2

sigma~dgamma(p,q)

popstart<-7024 #initial starting population size scaled to each stage

n[6,1]~dpois(EV[6]\*popstart)

n[1,1]~dpois(EV[1]\*popstart)

n[2,1]~dpois(EV[2]\*popstart)

n[3,1]~dpois(EV[3]\*popstart)

n[4,1]~dpois(EV[4]\*popstart)

n[5,1]~dpois(EV[5]\*popstart)

#data# tmax, nDat

#monitor# expectNests,a1, sigma,

}"

##DATA

#Length of time series

tmax<-45

#Nest observations

nDat<-c(3360,3920,3880,3790,NA,NA,NA,NA,11250,NA,14750,13000,

 13000,13700,11680,11223,12736,12632,11440,11511,12418,13843,15326,

 14500,17340,17384,16933,17979,18442,20185,19519,20332,18858,15578,

 15536,15036,14143,15029,14955,14100,13349,14248,15945,16132,NA)

## S2 Fixed Parameters in model fitting

### Vital rates for each species at each life stage (productivity adjusted for female only post breeding census in bold). All data acquiesced from colony specific citation from Horswill and Robinson 2015 (e.g. Harris,Frederiksen & Wanless 1997) and/or Newell *et al.* 2016.

|  |
| --- |
| Table SI1 Gannet Vital Rates |
| S1 | S2 | S3 | S4 | S5 |
|  |  |  |  | **0.47** |
| 0.542 |  |  |  |  |
|  | 0.779 |  |  |  |
|  |  | 0.859 |  |  |
|  |  |  | 0.869 | 0.916 |

|  |
| --- |
| Table SI2 Kittiwake Vital Rates |
| S1 | S2 | S3 | S4 |
|  |  |  | **0.68** |
| 0.76 |  |  |  |
|  | 0.85 |  |  |
|  |  | 0.87 | 0.882 |

|  |  |
| --- | --- |
| Table SI 3 Guillemot Vital Rates |  |
| S1 | S2 | S3 | S4 | S5 | S6 |
|  |  |  |  |  | **0.45** |
| 0.56 |  |  |  |  |  |
|  | 0.792 |  |  |  |  |
|  |  | 0.917 |  |  |  |
|  |  |  | 0.939 |  |  |
|  |  |  |  | 0.939 | 0.939 |

Table SI 4 Fixed parameters

| Variable | Description | Parameter | Value |
| --- | --- | --- | --- |
| Productivity | Number female chicks fledged per nest | bmax | See tables SI1-SI3 |
| Survival | Probability of survival at each life stage | S | See tables SI1-SI3 |
| Observation error | Observational error in nest counts | obsR | 0.01 |
| Observation Variance | The variance around a nest count | ObsV | 0.01\*adult population |
| Observation precision | Precision in the observed nest distribution | ObsTau | 1/ObsV2 |
| Scalar for each life stage | Coefficient for environmental impact at each life stage | Scalar(x) | See section: Scalar |
| Initial population size | Population starting size | Popstart | First data point multiplied by last age class dominant eigenvalue |

## S3 Stochastic parameters in model fitting

Table SI 5 Stochastic parameters

| Variable | Parameter | JAGS code | Distribution | Prior | Mean/Variance |
| --- | --- | --- | --- | --- | --- |
| Density-dependence | ϕ |  a1 | Gamma | See Table 2 Appendix |
| Environmental Stochasticity | Eps1 | Eps1 | Normal | (0,prec) | (0, 1/σ2) |
| Environmental perturbation magnitude | σ | sigma | Gamma | See Table Appendix |
| Initial population size each age class | n[6,1] etc. | N[6,1]etc. | Poisson | (Dominant eigen value\*popstart) | (Resulting value) |
| Demographic stochasiticty in process model | N[1,t+1] etc. | N[1,t+1] etc. | Binomial | (dbin(b[t],n[6,t]) etc. | Probability of survival/productivity, population size of dependent life stage) |

## S4 JAGS code: PVA/PBR simulation, example guillemots

#COMMON GUILLEMOT

#Model data based on Isle of May

IOMGUpopmodel<-function (a1, sigma, tmax, tinit,tmed, FRi){

 bmax<- 0.45 s1<- 0.56 #Harris et al. 2007

 s2<-0.792 #Harris et al.2007

 s3<-0.917 #Harries et al. 2007

 s4<-0.939 #Harris et al. 2007

 s5<-0.939 #Harris et al.2007

 s6<-0.939 #Harris et al. 2007

 a0<-log(bmax/(1-bmax)) # Intercept representing fecundity when there is no DD and eps is zero

 s1a0<-log(s1/(1-s1))

 s2a0<-log(s2/(1-s2))

 s3a0<-log(s3/(1-s3))

 s4a0<-log(s4/(1-s4))

 s5a0<-log(s5/(1-s5))

 s6a0<-log(s6/(1-s6))

 n<-array(0,dim=c(6,tmax)) # Population data

 L<-matrix(0, 6,6) # The Leslie matrix

 EV<-(c(0.20, 0.10, 0.08, 0.07, 0.07 ,0.48))

 popUpper<-10^9 #ceiling to allow for computation when density-dependence values very low and environmental favourable

 popstart<-42502.34

 n[6,1]<-round(EV[6]\*popstart)

 n[1,1]<-round(EV[1]\*popstart)

 n[2,1]<-round(EV[2]\*popstart)

 n[3,1]<-round(EV[3]\*popstart)

 n[4,1]<-round(EV[4]\*popstart)

 n[5,1]<-round(EV[5]\*popstart)

 # Main time loop/ PVA

 for (t in 2:tmax)

 {

 ntot<-sum(n[,t-1]) # Total density

 scalar1<-0.977

 scalar2<-0.741

 scalar3<-0.547

 scalar4<-0.556

 scalar5<-0.584

 scalar6<-0.584

 eps1<-rnorm(1,0,sigma)

 eps2<-scalar1\*eps1

 eps3<-scalar2\*eps1

 eps4<-scalar3\*eps1

 eps5<-scalar4\*eps1

 eps6<-scalar5\*eps1

 eps7<-scalar6\*eps1

 lt<-a0-a1\*ntot+eps1 # Linear predictor

 b<-inv.logit(lt) # logit of L, representing proportion of maximum vital rate that is actually realised

 lts1<-s1a0+eps2

 s1E<-inv.logit(lts1)

 lts2<-s2a0+eps3

 s2E<-inv.logit(lts2)

 lts3<-s3a0+eps4

 s3E<-inv.logit(lts3)

 lts4<-s4a0+eps5

 s4E<-inv.logit(lts4)

 lts5<-s5a0+eps6

 s5E<-inv.logit(lts5)

 lts6<-s6a0+eps7

 s6E<-inv.logit(lts6)

 n[1,t]<-min(popUpper,rbinom(1,n[6,t-1],b))

 n[2,t]<-min(popUpper,rbinom(1,n[1,t-1],s1E))

 n[3,t]<-min(popUpper,rbinom(1,n[2,t-1],s2E))

 n[4,t]<-min(popUpper,rbinom(1,n[3,t-1],s3E))

 n[5,t]<-min(popUpper,rbinom(1,n[4,t-1],s4E))

 n[6,t]<-min(popUpper,rbinom(1,n[5,t-1],s5E))+min(popUpper,rbinom(1,n[6,t-1],s6E))

 if(t==tmed){

 Nhat<-sum((n[6,t]\*2))

 harvest<-PBRGU(Nhat,FRi)

 }

 if(t>tmed) {

 har<-min(harvest, sum(n[,t]))

 n[,t]<-round(n[,t]-har\*n[,t]/sum(n[,t]))

 }

 if(is.na(sum(n[,t])==0)) break()

 }

 return(n)

}

####GUILLEMOT

PBRGU<-function (Nhat, FR){

 #Nmin: the minimum population estimate

 Zp<-qnorm(0.2,0,1) #The pth standard normal variate. Wade 1998 suggest lower 60th percentile 0.2 on sensitivity

 CVnhat<-0.1 #estimate of coefficient of variation for Nhat : Dillingham and Fletcher 2008

 Nmin<-Nhat\*exp(Zp\*CVnhat)

 ## Rmax: the maximum net recruitment rate formula from Neil & Lebreton 2005

 # parameters

 s<-0.939 #adult survival

 a<-6 #age at first breeding

 Rmax <- (((s\*a - s + a +1) + (((s-s\*a-a-1)^2) - (4 \*s \* a^2))^0.5) / (2 \* a))-1

 PBR<-Nmin\*(Rmax/2)\*FR

 return(PBR)

}

##################################################################################

PVA and PBR Model

############################################################

### PVA model coding for comparison of the effect of stochasticity, both environmental and

### demographic, with varying strengths of density dependence to a named population without and

### then with a mortality regime. Regulation is manipulated via the a1 and sigma terms.

### The mortality regime is called from a function where

### all values are set save for the FR (recovery factor). This allows for varied levels of

### precaution to be assessed.

maxa1<-0.000000607929#highest/lowest value of a1

mina1<-0.0000000000100023

incra1<-(maxa1-mina1)/50 #increments by which we reach a1

maxsigma<-3.01154 #highest value of sigma

minsigma<-1.80446#1.83669

incrsigma<-(maxsigma-minsigma)/50 #increments by which we reach highest sigma

tmax<-300 #maximum number of years

tinit<-100 # Settling time

tmed<-200 # Allows for no influence of initial conditions and allows for the system to reach a steadier state in the face of stochasticity. Allowing for baseline comparisons of populations under regulation that can still persist against the impact of additional mortality

a1Range<-seq(mina1,maxa1,incra1)

sigmaRange<-seq(minsigma, maxsigma, incrsigma)

FR<-c(0,0.1,0.3,0.5,1.0) #adjusted recovery factor for amount of mortality applied

maxreps<-50 #number of times to repeat loop for values

data<-array(0, dim=c(c(length(a1Range)\*length(sigmaRange)),6,5))#data store

##\_\_\_\_\_\_\_\_\_\_\_\_\_simulate\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

for(i in 1:length(FR))

{

 j<-0

 for (a1 in a1Range)

 {

 print(a1) #sense check working through

 for(sigma in sigmaRange)

 {

 estT<-SDT<-DropT<-rep(0,maxreps)

 for(rep in 1:maxreps)

 {

 pops<-IOMGUpopmodel(a1, sigma, tmax, tinit, tmed, FR[i])

 pop<-colSums(pops) #total population size

 estT[rep]<-mean(pop[(tmax-100):(tmax-75)])#years 200-225 (mortality applied)

 SDT[rep]<-sd(pop[(tmax-100):(tmax-75)])#years 200-225 (mortality applied)

 DropT[rep]<-(mean(pop[(tmed-25):tmed])-mean(pop[(tmax-100):(tmax-75)]))/mean(pop[(tmed-25):tmed]) # population change years 175-200 and years 200-225

 }

 j<-j+1 #counter for data storage

 data[j,1,i]<-a1

 data[j,2,i]<-sigma

 data[j,3,i]<-mean(estT)

 data[j,4,i]<-mean(SDT)

 data[j,5,i]<-mean(DropT) #comparison of mean pop size, pre/post treatment

 data[j,6,i]<-sd(DropT)

 }

 }

}

## References

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