Wildlife Biology

Appendix 1

Number of common pochards annually ringed in Switzerland, the United Kingdom and France by sex and age (hatch-year versu adults).
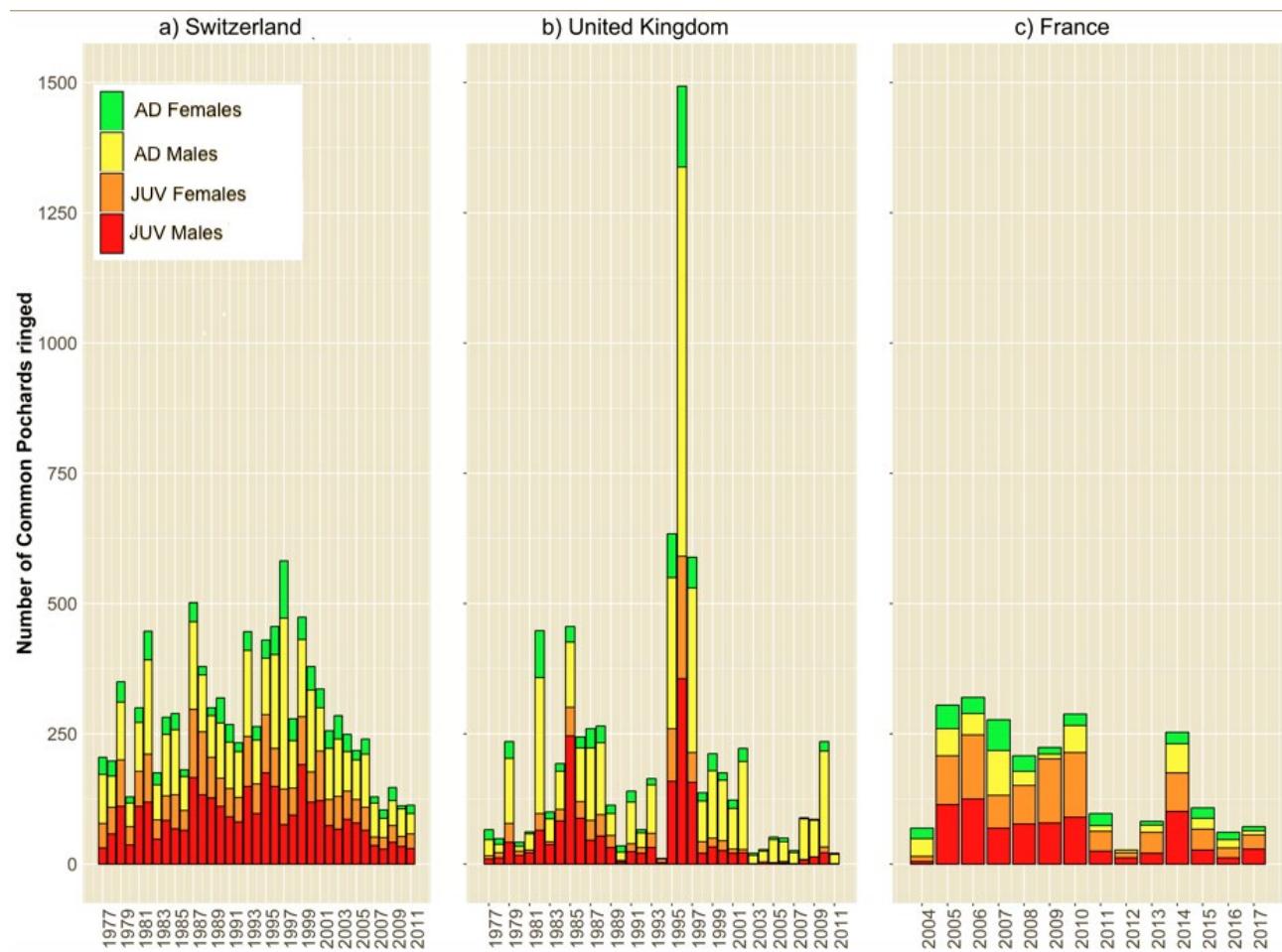
Appendix 2

Summary table of the transition (a) and event (b) matrices used for model parameterisation. S stands for survival probability, p for the probability to re-encounter an individual alive, by a physical or visual recapture, and r for the probability of dead-recovery. A, ND and D mean Alive, Newly Dead and Dead, respectively. p was equal to 0 for modelling the UK and CH datasets, which did not include live resightings.

a)

Transition matrix(S)	A	ND	D
A	S	S-1	0
ND	0	0	1
D	0	0	1

b)

| Event matrix (E)	Not seen	Seen Alive	Seen Dead
A	1-p	p	0
ND	1-r	0	r
D	1	0	0

Appendix 3

Summary of GOF tests (transience 3G, trap-dependence M and combined) for capture-mark-recaptures/recovery of common pochards ringed on Grand-lieu lake (France) between 2004 and 2017. $\hat{c}$ indicates the variance inflation factor used in the analyses.

GOF	Adult females			Juvenile females			Adult males			Juvenile males		
	χ^2	df	p	χ^2	df	p	χ^2	df	p	χ^2	df	p
3G Test	5.32	16	0.99	16.01	23	0.85	12.07	19	0.88	9.56	21	0.98
M Test	37.99	22	0.01	54.6	39	0.05	30.56	35	0.68	68.79	43	0.01
Overall test	43.31	38	0.26	70.65	62	0.21	42.62	54	0.87	78.35	64	0.11
$\hat{c}$		1.14			1.14			0.79			1.22	
Global $\hat{c}$	1.08											

Appendix 4

Changes in the proportions of male common pochards derived from a two-age structured two-sex matrix population model (see model structure and parameters below) when survival of adult males (0.81) > survival of adult females (0.69) and under incremental variations of juvenile survival of 0.02 from 0.1 (top curve) to 0.2 (bottom curve). One can notice that: 1) sex-ratio remains constant once the stable sex and age distributions are reached, and 2) an increasing proportion of males systematically follows decreasing juvenile survival (both sexes affected in the same manner). Outputs for the bottom curve model (Sj = 0.2): SR=60.1%, Lambda =1.07. Outputs for the top curve model (Sj = 0.1): SR=74%, Lambda =0.89.
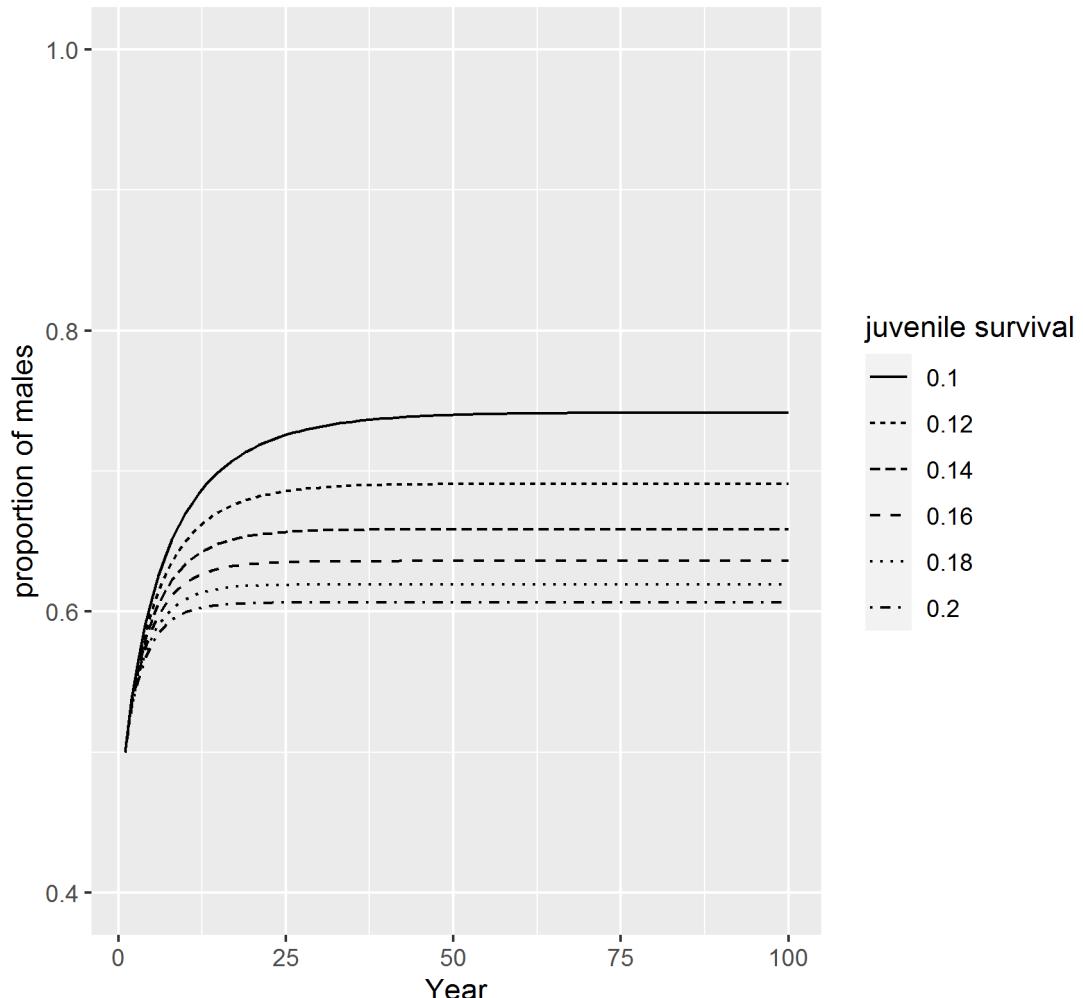
Code for simulating a population of male and female pochards with two age classes in R software

```
# 2 age-classes sex-dependent population matrix
# N[1,] = number of first-year female
# N[2,] = number of adult female
# N[1,] = number of first-year male
# N[1,] = number of adult male

# defining all parameters of the matrix
## productivity assuming a 1:1 sex-ratio
# number of female eggs produced per first year female
fj1=4.15
# number of female eggs produced per adult female
fa1=4.6
# number of male eggs produced by first year females
fj2=4.15
# number of male eggs produced by adult females
fa2=4.6
```

```
# survival of nests of first year females
snj=0.3
# survival of nests of adult females
sna=0.53
## sex and age specific survival rate
# juvenile survival
sj=0.20
# juvenile survival of female
sj1=0.15
# juvenile survival of male
sj2=0.20
# survival of adult females
sa1=0.67
# survival of adult males
sa2=0.81

## defining the matrix
# Mat, equal juvenile survival of male and female
Mat <- matrix(c(
 fj1*snj*sj, fa1*sna*sj, 0, 0,
 sa1    , sa1    , 0, 0,
 fj2*snj*sj, fa2*sna*sj, 0, 0,
 0    , 0    , sa2, sa2),ncol=4,byrow = T)

Mat.exp <- expression(fj1*snj*sj, fa1*sna*sj, 0, 0,
              sa1    , sa1    , 0, 0,
              fj2*snj*sj, fa2*sna*sj, 0, 0,
              0    , 0    , sa2, sa2)
Mat.vr <- list(fj1 = fj1, snj = snj, sj = sj, fa1 = fa1, sna = sna, sa1 = sa1, fj2 = fj2, fa2 = fa2, sa2 = sa2)
# Mats, different juvenile survival of male (0.2) and female (0.1)
Mat2 <- matrix(c(
 fj1*snj*sj1, fa1*sna*sj1, 0, 0,
 sa1    , sa1    , 0, 0,
 fj2*snj*sj2, fa2*sna*sj2, 0, 0,
 0    , 0    , sa2, sa2),ncol=4,byrow = T)

Mat2.exp <- expression(fj1*snj*sj1, fa1*sna*sj1, 0, 0,
              sa1    , sa1    , 0, 0,
              fj2*snj*sj2, fa2*sna*sj2, 0, 0,
              0    , 0    , sa2, sa2)
Mat2.vr <- list(fj1 = fj1, snj = snj, sj1 = sj1, fa1 = fa1, sna = sna, sa1 = sa1, fj2 = fj2, sj2 = sj2, fa2 = fa2, sa2 =
sa2)

# using the package popbio to run the matrix model
require(popbio)
# computing population growth rate of the projection matrix ####
lambda(Mat) # 1.0686
lambda(Mat2) # 0.9791941

# generation time ####
generation.time(Mat) # 4.163966
generation.time(Mat2) # 4.330003

## sensitivity and elasticy of each cell of the matrix ####
elasticity(Mat)
#          [,1]     [,2] [,3] [,4]
# [1,] 0.07624351 0.2509604   0   0
# [2,] 0.25096043 0.4218356   0   0
# [3,] 0.00000000 0.0000000   0   0
# [4,] 0.00000000 0.0000000   0   0

elasticity(Mat2)
#          [,1]     [,2] [,3] [,4]
# [1,] 0.05352837 0.2271392   0   0
# [2,] 0.22713917 0.4921933   0   0
```

```
# [3,] 0.00000000 0.0000000   0   0
# [4,] 0.00000000 0.0000000   0   0


## sensitivity and elasticity of each parameter ####
vitalsens(Mat.exp,Mat.vr)
#     estimate sensitivity elasticity
# fj1    4.15  0.01963224 0.07624351
# snj    0.30  0.27157927 0.07624351
# sj     0.20  1.74824991 0.32720394
# fa1    4.60  0.05829917 0.25096043
# sna    0.53  0.50599283 0.25096043
# sa1    0.67  1.07305904 0.67279606
# fj2    4.15  0.00000000 0.00000000
# fa2    4.60  0.00000000 0.00000000
# sa2    0.81  0.00000000 0.00000000

vitalsens(Mat2.exp,Mat2.vr)
#     estimate sensitivity elasticity
# fj1    4.15  0.01263004 0.05352837
# snj    0.30  0.17471554 0.05352837
# sj1    0.15  1.83218660 0.28066754
# fa1    4.60  0.04835072 0.22713917
# sna    0.53  0.41964779 0.22713917
# sa1    0.67  1.05129265 0.71933246
# fj2    4.15  0.00000000 0.00000000
# sj2    0.20  0.00000000 0.00000000
# fa2    4.60  0.00000000 0.00000000
# sa2    0.81  0.00000000 0.00000000


# simulation: projection over 100 years
sj <- seq(0.2,0.1,-0.02)
Mat.sim <- NULL
ratioM.sim <- matrix(NA,ncol = 100,nrow = length(sj1))
for (i in 1:length(sj1)){
 Mat.sim <- matrix(c(
   fj1*snj*sj[i], fa1*sna*sj[i], 0, 0,
   sa1    , sa1   , 0, 0,
   fj2*snj*sj[i], fa2*sna*sj[i], 0, 0,
   0   , 0   , sa2, sa2),ncol=4,byrow = T)
 proj <- pop.projection(A = Mat.sim,n = c(rep(10000,4)),iterations = 100)
 ratioM.sim[i,] <- apply(proj$stage.vectors[3:4,],2,sum)/proj$pop.sizes
}

require(tidyverse)
ratio.sim <- ratioM.sim %>%
 t(.) %>%
 as_tibble(.) %>%
 `colnames<-`(paste("sj_",sj,sep="")) %>%
 mutate(time = c(1:100)) %>%
 pivot_longer(cols = starts_with("sj_"),names_prefix = "sj_",names_to = "sj",values_to = "ratio")

sj_plot <- ggplot(ratio.sim,aes(x = time,y = ratio))+
 geom_line(aes(linetype=sj)) +
 scale_y_continuous(limits = c(0.4,1.0)) +
 ylab(label = "proportion of males") + xlab(label = "Year") +
 labs(linetype = "juvenile survival")
ggsave("sj_plot.tiff",dpi=300)
```