##CROSLO##

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### STEP 1: GETTING POPULATION STRUCTURE FOR NON-HUNTED POPULATIONS

### LARGELY BASED ON BISCHOFF ET AL. ETC

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library(popbio)

A <- matrix(ncol=42, nrow=42, 0)

sim <- 1000

res\_lamA <- matrix(ncol=1, nrow=sim)

res\_ageA <- matrix(ncol=42, nrow=sim)

## Mean demographic rates

N <- 1558#960#1378#1738

LS = 1.92

#wlr <- c(0.05, 0.10, 0.125, 0.15, 0.20, 0.21, 0.25)

#ilir <- c(2.094, 2.008, 1.965, 1.922, 1.836, 1.82, 1.75)

wlr <- 0.21 #Whole litters loss; Ofelia,Švigelj, Hristianenko, Groff, Jerina

ilir <- 1.82 # Zedrosser

Socoy <- 0.873

#Bischof

Sof1 <-0.82

Sof2\_4<-0.94

Sof5\_19<-0.93

Sof20<-0

#Bischof

Som1<-0.91

Som2\_4<-0.82

Som5\_19<-0.89

Som20<-0

## Stochastic simulations;

for(i in 1:sim){

n <- rnorm(1, N,55)#rnorm(1, N, 1)

WL <- 1-(betaval(wlr, sdev=0.03))

ILI <- rnorm(1, ilir, 0.05)

F1 <- rnorm(1, LS, 0.03)

F = F1/2/ILI

#female survival

A[2,1] <- betaval(Socoy, sdev=0.03)\*WL

A[3,2] <- (betaval(Sof1, sdev=0.03))

A[4,3] <- (betaval(Sof2\_4, sdev=0.03))

A[5,4] <- (betaval(Sof2\_4, sdev=0.03))

A[6,5] <- (betaval(Sof2\_4, sdev=0.03))

A[7,6] <- (betaval(Sof5\_19, sdev=0.03))

A[8,7] <- (betaval(Sof5\_19, sdev=0.03))

A[9,8] <- (betaval(Sof5\_19, sdev=0.03))

A[10,9] <- (betaval(Sof5\_19, sdev=0.03))

A[11,10] <- (betaval(Sof5\_19, sdev=0.03))

A[12,11] <- (betaval(Sof5\_19, sdev=0.03))

A[13,12] <- (betaval(Sof5\_19, sdev=0.03))

A[14,13] <- (betaval(Sof5\_19, sdev=0.03))

A[15,14] <- (betaval(Sof5\_19, sdev=0.03))

A[16,15] <- (betaval(Sof5\_19, sdev=0.03))

A[17,16] <- (betaval(Sof5\_19, sdev=0.03))

A[18,17] <- (betaval(Sof5\_19, sdev=0.03))

A[19,18] <- (betaval(Sof5\_19, sdev=0.03))

A[20,19] <- (betaval(Sof5\_19, sdev=0.03))

A[21,20] <- (betaval(Sof5\_19, sdev=0.03))

A[21,21] <- Sof20

#male survival

A[23,22] <- betaval(Socoy, sdev=0.03)\*WL

A[24,23] <- (betaval(Som1, sdev=0.03))

A[25,24] <- (betaval(Som2\_4, sdev=0.03))

A[26,25] <- (betaval(Som2\_4, sdev=0.03))

A[27,26] <- (betaval(Som2\_4, sdev=0.03))

A[28,27] <- (betaval(Som5\_19, sdev=0.03))

A[29,28] <- (betaval(Som5\_19, sdev=0.03))

A[30,29] <- (betaval(Som5\_19, sdev=0.03))

A[31,30] <- (betaval(Som5\_19, sdev=0.03))

A[32,31] <- (betaval(Som5\_19, sdev=0.03))

A[33,32] <- (betaval(Som5\_19, sdev=0.03))

A[34,33] <- (betaval(Som5\_19, sdev=0.03))

A[35,34] <- (betaval(Som5\_19, sdev=0.03))

A[36,35] <- (betaval(Som5\_19, sdev=0.03))

A[37,36] <- (betaval(Som5\_19, sdev=0.03))

A[38,37] <- (betaval(Som5\_19, sdev=0.03))

A[39,38] <- (betaval(Som5\_19, sdev=0.03))

A[40,39] <- (betaval(Som5\_19, sdev=0.03))

A[41,40] <- (betaval(Som5\_19, sdev=0.03))

A[42,41] <- (betaval(Som5\_19, sdev=0.03))

A[42,42] <- Som20

A[c(1,22),c(3,4)] <- Sof2\_4\*F\*betaval(0.25, sdev=0.1)

A[c(1,22),c(4,5)] <- Sof2\_4\*F

A[c(1,22),c(6:16)] <- Sof5\_19\*F

A[c(1,22),c(17:20)]<- Sof5\_19\*F\*betaval(0.925,sdev=0.01) #Schwartz

A[c(1,22),c(21)]<- Sof5\_19\*F\*0.848 #Schwartz

res\_lamA[i] <- eigen.analysis(A)$lambda

res\_ageA[i,] = eigen.analysis(A)$stable.stage

}

mean\_lam <- exp(mean(log(res\_lamA)))

sd\_lam <- sd(res\_lamA)

table2 <- matrix(ncol=2, nrow=42)

for(i in 1:42){

temp <- res\_ageA[,i]

table2[i,1] <- mean(temp)

table2[i,2] <- sd(temp)

}

par(mfrow=c(1,2))

barplot(table2[,1], beside=T, xlab="Initial population size and structure\_Cro+Slo", ylab="Proportions", col=c(rep(grey(1), 21), rep(grey(0.7), 21)))

text(c("f", "m"), x=c(3, 29), y=0.11)

text("Population size", x=43, y=0.1)

text(x=43, y=0.09, paste("n=",N))

table2

table3<-matrix(ncol=1,nrow=42)

table3[1:21]<-table2[1:21,1]\*1/(sum(table2[1:21,1]))\*0.595 ##adjusting to real sex ratio

table3[22:42]<-table2[22:42,1]\*1/(sum(table2[22:42,1]))\*0.405 ##adjusting to real sex ratio

sum(table3[1:21])

sum(table3[22:42])

sum (table3)

table3

mean\_lam

sd\_lam

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

### STEP 2; START WITH STRUCTURE FROM BISCHOFF ET AL. AND INCLUDE REAL HARVEST

### CHANGE ESTIMATED POPULATION SIZE TO SEE THE EFFECT ON POPULATION SIZE AND SEX/AGE ###STRUCTURE IN THE FUTURE AND RUN FOR n.years number of years and sim=number of ###simulations

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## Here you control initial popualtion size for step 2

#Hsq <- c(7,30,54,34,7,5,5,3,4,1,1,3,3,2,1,1,0,0,0,0,0,9,54,60,52,22,7,8,2,4,1,4,3,2,2,0,0,0,0,0,0,0)

Hsh <- c(0,46,65,39,9,6,5,4,6,1,1,5,3,2,1,1,1,0,0,0,0,0,74,67,53,22,8,9,3,4,2,4,4,2,2,0,0,0,0,0,0,0) #with excluding of removals of COYs (this is calculated in the survival rate of COYs and litter losses(WL)

#Hcq <- c(0,7,8,10,15,7,5,10,10,1,4,1,1,0,1,0,1,0,0,0,0,0,12,44,52,47,28,18,26,16,6,15,5,1,1,1,4,2,1,1,1,0)

Hch <- c(0,9,9,13,19,8,7,13,10,1,4,1,1,0,1,0,1,0,0,0,0,0,13,50,52,50,28,18,27,16,6,15,5,1,1,1,4,2,1,1,1,0)

Hcsh<-Hsh+Hch

#(0,55,74,52,28,14,12,17,16,2,5,6,4,2,2,1,2,0,0,0,0,0,87,117,105,72,36,27,30,20,8,19,9,3,3,1,4,2,1,1,1,0)#

# Harvest ###Legal hunting + intervention

Ht<- Hcsh/6

## Control variables for step 2;

n.years=5 #####5, 10, 15 years

N10 <- matrix(ncol=n.years, nrow=42)

B <- matrix(ncol=42, nrow=42, 0)

res <- matrix(ncol=sim, nrow=42)

ni<- matrix (ncol=sim, nrow=1)

for(i in 1:sim){

n <- rnorm(1, N, 55) # rnorm(1, N, 1)

N10[,1] <- table3\*n

for(j in 1: (n.years-1)){

WL <- 1-(betaval(wlr, sdev=0.03))

ILI <- rnorm(1, ilir, 0.05)

F1 <- rnorm(1, LS, 0.03)

F = F1/2/ILI

#female survival

B[2,1] <- betaval(Socoy, sdev=0.03)\*WL

B[3,2] <- (betaval(Sof1, sdev=0.03))

B[4,3] <- (betaval(Sof2\_4, sdev=0.03))

B[5,4] <- (betaval(Sof2\_4, sdev=0.03))

B[6,5] <- (betaval(Sof2\_4, sdev=0.03))

B[7,6] <- (betaval(Sof5\_19, sdev=0.03))

B[8,7] <- (betaval(Sof5\_19, sdev=0.03))

B[9,8] <- (betaval(Sof5\_19, sdev=0.03))

B[10,9] <- (betaval(Sof5\_19, sdev=0.03))

B[11,10] <- (betaval(Sof5\_19, sdev=0.03))

B[12,11] <- (betaval(Sof5\_19, sdev=0.03))

B[13,12] <- (betaval(Sof5\_19, sdev=0.03))

B[14,13] <- (betaval(Sof5\_19, sdev=0.03))

B[15,14] <- (betaval(Sof5\_19, sdev=0.03))

B[16,15] <- (betaval(Sof5\_19, sdev=0.03))

B[17,16] <- (betaval(Sof5\_19, sdev=0.03))

B[18,17] <- (betaval(Sof5\_19, sdev=0.03))

B[19,18] <- (betaval(Sof5\_19, sdev=0.03))

B[20,19] <- (betaval(Sof5\_19, sdev=0.03))

B[21,20] <- (betaval(Sof5\_19, sdev=0.03))

B[21,21] <- Sof20

#male survival

B[23,22] <- betaval(Socoy, sdev=0.03)\*WL

B[24,23] <- (betaval(Som1, sdev=0.03))

B[25,24] <- (betaval(Som2\_4, sdev=0.03))

B[26,25] <- (betaval(Som2\_4, sdev=0.03))

B[27,26] <- (betaval(Som2\_4, sdev=0.03))

B[28,27] <- (betaval(Som5\_19, sdev=0.03))

B[29,28] <- (betaval(Som5\_19, sdev=0.03))

B[30,29] <- (betaval(Som5\_19, sdev=0.03))

B[31,30] <- (betaval(Som5\_19, sdev=0.03))

B[32,31] <- (betaval(Som5\_19, sdev=0.03))

B[33,32] <- (betaval(Som5\_19, sdev=0.03))

B[34,33] <- (betaval(Som5\_19, sdev=0.03))

B[35,34] <- (betaval(Som5\_19, sdev=0.03))

B[36,35] <- (betaval(Som5\_19, sdev=0.03))

B[37,36] <- (betaval(Som5\_19, sdev=0.03))

B[38,37] <- (betaval(Som5\_19, sdev=0.03))

B[39,38] <- (betaval(Som5\_19, sdev=0.03))

B[40,39] <- (betaval(Som5\_19, sdev=0.03))

B[41,40] <- (betaval(Som5\_19, sdev=0.03))

B[42,41] <- (betaval(Som5\_19, sdev=0.03))

B[42,42] <- Som20

B[c(1,22),c(3,4)] <- Sof2\_4\*F\*betaval(0.25, sdev=0.1)

B[c(1,22),c(4,5)] <- Sof2\_4\*F

B[c(1,22),c(6:16)] <- Sof5\_19\*F

B[c(1,22),c(17:20)]<- Sof5\_19\*F\* betaval(0.925,sdev=0.01) #Schwartz

B[c(1,22),c(21)]<- Sof5\_19\*F\*0.848 #Schwartz

temp <- N10[,j]-Ht

temp <- transform(temp, temp=ifelse(temp<0, 0, temp))

N10[,j+1] <- (B%\*%temp[,2])

}

res[,i] <- N10[,n.years]

ni[,i] <- n

}

N10\_sum <- colSums(res)

mean\_N10 <- mean(N10\_sum)

mean\_St1 <- matrix(ncol=1, nrow=42)

for(i in 1:42){

mean\_St1[i] <- mean(res[i,])

}

trf<- ((sum(mean\_St1[3,1]))/2)+(sum(mean\_St1[4:21,1]))

trm<-((sum(mean\_St1[24,1]))/2)+(sum(mean\_St1[25:42,1]))

sr<-trf/trm

trf

trm

sr

srfp<-trf/(trf+trm)

srfp

sum(mean\_St1[1:21,1])/(sum(mean\_St1[1:21,1])+ sum(mean\_St1[22:42,1]))

mean\_St10s <- mean\_St1/sum(mean\_St1)

barplot(mean\_St10s, beside=T, xlab="Population size and structure after 5 years\_Cro+Slo", col=c(rep(grey(1), 21), rep(grey(0.7), 21)))

text(c("f", "m"), x=c(4, 25.5), y=0.12)

text("Population size", x=37, y=0.11)

text(x=37, y=0.10, paste("n=",round(colSums(mean\_St1))))

min(ni)

max(ni)

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#LAMBDA and graphics

lambda\_final<-(colSums(res)/as.matrix(ni))\*\*(1/n.years)

mean(lambda\_final)

sd(lambda\_final)

par(mfrow=c(1,1))

hist(lambda\_final)

z<-hist(lambda\_final)

barplot(z$counts/sum(z$counts), ylab="Frequency", xlab="Lambda (λ)", main="Distribution of lambda values\_Croatia+Slovenia")

axis(1,seq(0,11,1.2),seq(0.98,1.025,0.005),tick=TRUE,lwd.ticks=1)

text(x=7.75, y=0.275, paste("λ=",round(mean(lambda\_final),3)))

text(x=8.75, y=0.275, paste("±",round(sd(lambda\_final),3)))