### Exercise

#### Vildsvinegruppen

2023-04-18

#### Question

How large is the maximal sustainable hunting pressure on wild boars in Tofte Skov?

#### **Phenology Parameters**

From article (REF):

```
Fecundity <- list(distribution = "Gamma", parameters = c(47.4, 8.66))

SexRatio <- list(distribution = "Beta", parameters = c(31.2, 29.2))

SurvivalFemale <- list(distribution = "Beta", parameters = c(2.89, 1.46))

SurvivalJuveniles <- list(distribution = "Beta", parameters = c(1.92, 1.54))

SurvivalMale <- list(distribution = "Beta", parameters = c(2.82, 1.55))
```

## **Population Transition Matrix**

Formulas from article (REF):

```
constructMatrix <- function(Pop, Fec, SR, Sj, Sf, Sm, K, h) {
    ## Pop: Population structure after removal
    ## Fec: Fecundity
    ## SR : Sex Ratio
    ## Sj : Survival juveniles
    ## Sf : Survival female
    ## Sm : survival male
    ## K : Carrying capacity

TM <- matrix(0, nrow = 3, ncol = 3)

# Juveniles born
TM[1, 2] <- Sf * Fec * exp(-sum(Pop)/K)

# Juveniles maturing to females
TM[2, 1] <- Sj * SR

# Juveniles maturing to males
TM[3, 1] <- Sj * (1 - SR)</pre>
```

```
# Adult female surval
TM[2, 2] <- Sf

# Adult male survival
TM[3, 3] <- Sm

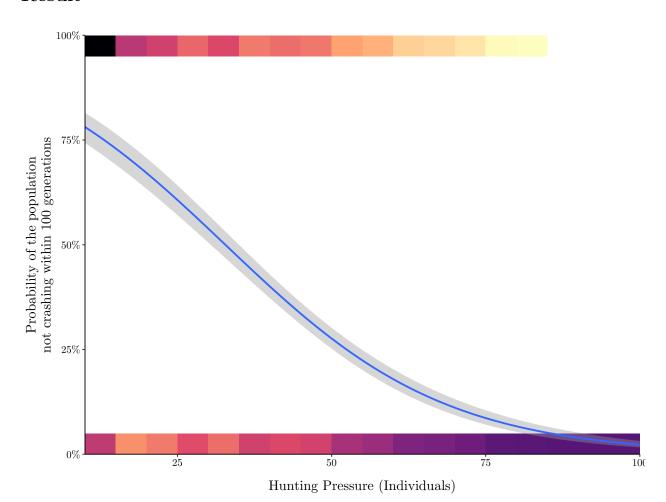
if (!missing(h)) {
   TM - matrix(rep(h, 3), ncol = 3)
}
else {
   TM
}</pre>
```

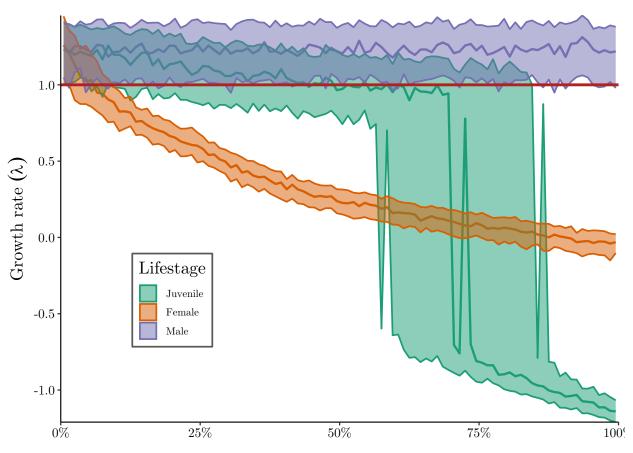
#### Simulation loop

```
results <- lapply(rep(seq(10, 100, 5), each = 100), function(R) {
  phenologyParameters <- list(</pre>
    Fec = Fecundity %>%
      sampleFromDist,
    SR = SexRatio %>%
      sampleFromDist,
    Sf = SurvivalFemale %>%
     sampleFromDist,
    Sm = SurvivalMale %>%
     sampleFromDist,
    Sj = 0.364#SurvivalJuveniles %>%
    #sampleFromDist,
    K = 4*800.
    Pop = c(50, 70, 30)
  populationHistory <- matrix(ncol = 3, nrow = 0)</pre>
 for (i in seq(100)) {
    phenologyParameters$Pop <- phenologyParameters$Pop -</pre>
      as.vector(table(factor(sample.int(3, R, T), levels = c("1", "2", "3"))))
    PopMatrix <- do.call(constructMatrix, phenologyParameters)</pre>
    phenologyParameters$Pop <- as.vector(PopMatrix %*% phenologyParameters$Pop)</pre>
    phenologyParameters$Pop[phenologyParameters$Pop < 0] <- 0</pre>
    populationHistory <- rbind(populationHistory, phenologyParameters$Pop)</pre>
```

```
populationHistory %>%
  set_colnames(c("Juveniles", "Females", "Males")) %>%
  as_tibble() %>%
  mutate(
    Generation = row_number(),
    HuntingPressure = R
  )
}) %>%
bind_rows()
```

# Result





% Individuals culled per generation