# Exercise

## Vildsvinegruppen

## 2023-04-25

## Question

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

### Phenology Parameters

We use the phenological parameters from the [?]:

```
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

As well as the transition matrix formulation:

$$\mathbf{A}_t = \begin{bmatrix} 0 & s_2 F_t & 0 \\ s_1 m & s_2 & 0 \\ s_1(1-m) & 0 & s_2 \end{bmatrix}$$

where $s_1, s_2, s_3$ are juvenile, female & male survival rates respectively, while $m$ is the sex-ratio and $F_t$ is the fecundity at time $t$. If fecundity is density dependent (as in [?]) then:

$$F_t = f_0 e^{\frac{-\sum \frac{(\mathbf{n}-\mathbf{r})_t}{k}}}$$

otherwise:

$$F_t = f_0$$

We also adapt the formulation of stochastic growth as [?]:

$$\log(\mathbf{n}_{t+1}) \sim N\left(\log\left(\mathbf{A}_t(\mathbf{n}-\mathbf{r})_t\right), \sigma_i^2\right)$$

Where the cohort stratified population size is sampled from an essentially quasi-poisson distribution.

The code for constructing the matrix:

```r
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
  ## h  ; hunting pressure

  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)

  # 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
  }
}

sampleParam <- function(Pop = c(50, 70, 30), K = 4*800, h = c(0, 0, 0)) {
  list(
    Fec = Fecundity %>%
      sampleFromDist,
    SR = SexRatio %>%
      sampleFromDist,
    Sf = SurvivalFemale %>%
      sampleFromDist,
    Sm = SurvivalMale %>%
      sampleFromDist,
    Sj = 0.364#SurvivalJuveniles %>%
    #sampleFromDist,
    ,
    Pop = Pop,
    K = K,
    h = h
  )
}
```

# Non-Stochastic Growth