

# Matrix Modelling Exercise

Vildsvinegruppen

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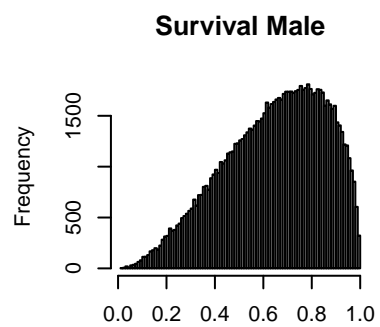
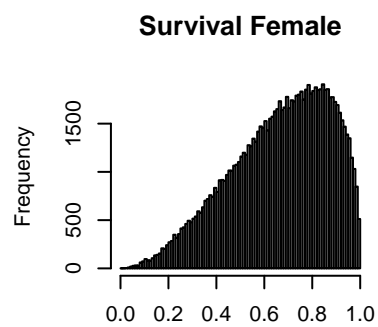
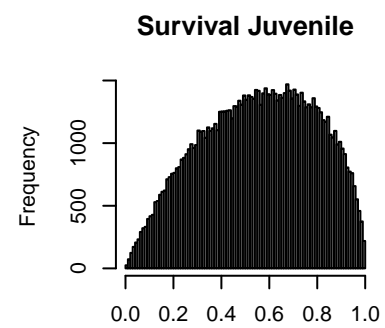
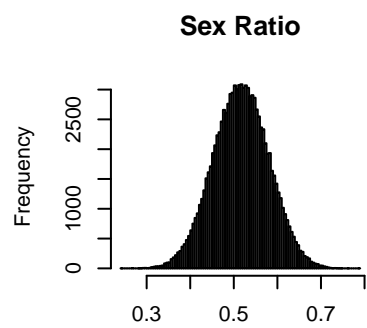
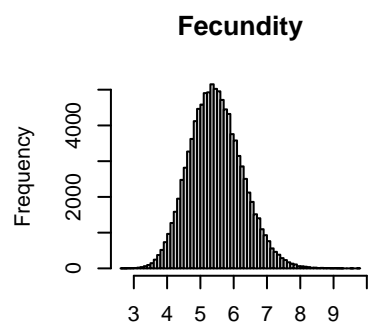
## 1 Question

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

## 2 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))
```



### 3 Population Transition Matrix

Formulas from article (REF):

```
constructMatrix <- function(Pop, Fec, SR, Sj, Sf, Sm, K) {  
  ## 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)  
  
  # Adult female survival  
  TM[2, 2] <- Sf  
  
  # Adult male survival  
  TM[3, 3] <- Sm  
  
  TM  
}
```

## 4 Simulation loop

```
results <- lapply(rep(seq(10, 100, 5), each = 100), function(R) {
  phenologyParameters <- list(
    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)

  for (i in seq(100)) {

    phenologyParameters$Pop <- phenologyParameters$Pop -
      as.vector(table(factor(sample.int(3, R, T), levels = c("1", "2", "3"))))

    PopMatrix <- do.call(constructMatrix, phenologyParameters)

    phenologyParameters$Pop <- as.vector(PopMatrix %*% phenologyParameters$Pop)

    phenologyParameters$Pop[phenologyParameters$Pop < 0] <- 0

    populationHistory <- rbind(populationHistory, phenologyParameters$Pop)
  }

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

## 5 Result

