Amami Rabbit Management Plan

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Matrix Modelling

In this section I will be using the results from the "Estimating Amami Rabbit Survival" and "Estimating Amami Rabbit Population Size" sections to build a population matrix projection model (MPM) for the Amami Rabbit. This will allow me to determine the current population growth rate of the species and which age-stages have vital rates that are most sensitive to changes in parameter values. I can then explore the effects various conservation interventions will have on the population as a whole.

The information I require to construct the Amami Rabbit MPM are the age-structured population sizes for 2021 (the year of the most recent study) and the age-structured survival rates which I estimated using closed-CMR and open-CMR analyses respectively. Additionally, I require age-structured fecundity rates which I was not able to collect data on so attempted to find them from the literature. All data was collected pre-breeding season, as such in order to calculate fecundity rates using literature values I needed to find data on the average number of offspring produced per individual (m), the Amami rabbit sex ratio, and the survival rates for 1yr olds and 2yr olds (which I have estimated). However, after scanning the literature I could not find a sex ratio for the Amami rabbit or a recent sex ratio estimate of the species' two closest relatives. I was able to obtain a recent estimate for the sex ratio of the third closest relative to the Amami rabbit, the pygmy rabbit (*brachylagus idahoensis*). It is also unknown at what age Amami rabbits become sexually mature but as only data on the average offspring per adult individual could be found, I will assume 2yr olds are not sexually mature. Estimates for all parameters are given below with 95%CI estimates in brackets:

- N_1yr: 66 (64,69)
- N_2yr: 47 (43,59)
- N_adults: 105 (94,126)
- phi_1yr : 0.49 (0.66,0.86)
- phi_2yr : 0.67 (0.28,0.94)
- phi_adults : 0.72 (0.76,0.99)
- m : 1.10 (0.51,1.69)
- sigma : 1.02 (NA,NA)

One final note is that 1yr old and 2yr old Amami rabbits cannot stay this age for more than 1 year but adults stay adults until their death. This type of age-stage classification requires the transition matrix to be constructed in such a way that makes it not truly age or stage based but a combination of the 2. This type of MPM is commonly known as a pseudo-stage structured population matrix projection model.

For matrix modelling there are several possible R packages available but I will be using **popdemo**.

```
library(popdemo)
```

```
## Warning: package 'popdemo' was built under R version 4.1.2
```

```
## Welcome to popdemo! This is version 1.3-0
## Use ?popdemo for an intro, or browseVignettes('popdemo') for vignettes
## Citation for popdemo is here: doi.org/10.1111/j.2041-210X.2012.00222.x
## Development and legacy versions are here: github.com/iainmstott/popdemo
```

Current State of the Population

First, I will store the parameter values as variablesto make it easier to manipulate them when it comes to testing conservation stratagies.

```
# Age-structured population sizes
## Mean average (avg) values
N_1yr.avg = 66
N_2yr.avg = 47
N_adults.avg = 105
pop_vec.avg = c(N_1yr.avg, N_2yr.avg, N_adults.avg)

## Lower (lwr) estimates
N_1yr.lwr = 64
N_2yr.lwr = 43
N_adults.lwr = 94
pop_vec.lwr = c(N_1yr.lwr, N_2yr.lwr, N_adults.lwr)

## Upper (upr) estimates
N_1yr.upr = 69
N_2yr.upr = 59
N_adults.upr = 126
pop_vec.upr = c(N_1yr.upr, N_2yr.upr, N_adults.upr)

# Age-structured survival rates
## Mean average (avg) values
phi_1yr.avg = 0.49
phi_2yr.avg = 0.67
phi_adults.avg = 0.72

## Lower (lwr) estimates
phi_1yr.lwr = 0.45
phi_2yr.lwr = 0.63
phi_adults.lwr = 0.68

## Upper (upr) estimates
phi_1yr.upr = 0.53
phi_2yr.upr = 0.71
phi_adults.upr = 0.78

# Fecundity components
m.avg = 1.10
m.lwr = 0.51
m.upr = 1.69
sigma = 1.02
```

Now I will use the fecundity component variables to calculate the age-structured fecundity rates.

```
F_adult.avg = round(m.avg*phi_1yr.avg*sigma, digits = 2)
F_adult.lwr = round(m.lwr*phi_1yr.lwr*sigma, digits = 2)
F_adult.upr = round(m.upr*phi_1yr.upr*sigma, digits = 2)
```

Next, I will create the transition matrices using mean average, lower 95%CI and upper 95%CI values for the vital rates.

```
# Mean average values
A.avg = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.avg, 0),
    Two.yr_old = c(0, 0, phi_2yr.avg),
    adults = c(F_adult.avg, 0, phi_adults.avg)
  )
)
row.names(A.avg) = colnames(A.avg)

# Lower (lwr) estimated values
A.lwr = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.lwr, 0),
    Two.yr_old = c(0, 0, phi_2yr.lwr),
    adults = c(F_adult.lwr, 0, phi_adults.lwr)
  )
)
row.names(A.lwr) = colnames(A.lwr)

# Upper (upr) estimated values
A.upr = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.upr, 0),
    Two.yr_old = c(0, 0, phi_2yr.upr),
    adults = c(F_adult.upr, 0, phi_adults.upr)
  )
)
row.names(A.upr) = colnames(A.upr)

# Check the matrices are correct
A.avg
```

```
##            One.yr_old Two.yr_old adults
## One.yr_old       0.00       0.00   0.55
## Two.yr_old       0.49       0.00   0.00
## adults           0.00       0.67   0.72
```

```
A.lwr
```

```
##            One.yr_old Two.yr_old adults
## One.yr_old       0.00       0.00   0.23
## Two.yr_old       0.45       0.00   0.00
## adults           0.00       0.63   0.68
```

```
A.upr
```

```
##             One.yr_old Two.yr_old adults
## One.yr_old       0.00       0.00   0.91
## Two.yr_old       0.53       0.00   0.00
## adults           0.00       0.71   0.78
```

Every entry in the matrices look like they are in the correct place. Now for some actual analysis! First, I will calculate the finite rate of increase/population growth rate (lambda). To do this I will use the *eigs()* function with the *what* argument set to "lambda".

```
lambda.avg = eigs(A.avg, what = "lambda")
lambda.lwr = eigs(A.lwr, what = "lambda")
lambda.upr = eigs(A.upr, what = "lambda")

round(lambda.avg, digits = 2)
```

```
## [1] 0.93
```

```
round(lambda.lwr, digits = 2)
```

```
## [1] 0.79
```

```
round(lambda.upr, digits = 2)
```

```
## [1] 1.08
```

The mean average population growth rate is 0.93 with the lower 95%CI being 0.79 and the upper 95%CI being 1.08. Thus the population could be decreasing as much as 19% per year or increasing as much as 51% per. What is more informative from the estimate of uncertanty is that we cannot be confident that the Amami rabbit population is not decling (rather our closed-CMR analysis strongly suggests that the population has been decreasing). To be confident that the population is no longer decreasing we need the lower estimate of lambda to be greater than or equal to 1.

Some more useful information that we can get using the *eigs()* function is the relative proportion of each pseudo-stage there is in a stable population (the stable stage distribution) and the relative contribution to population growth of each pseudo-stage (the reproductive value).

```
# Stable Stage Distribution
ss.avg = eigs(A.avg, what = "ss")
ss.lwr = eigs(A.lwr, what = "ss")
ss.upr = eigs(A.upr, what = "ss")

round(ss.avg, digits = 2)
```

```
## [1] 0.31 0.16 0.53
```

```
round(ss.lwr, digits = 2)
```

```
## [1] 0.20 0.11 0.68
```

```
round(ss.upr, digits = 2)
```

```
## [1] 0.37 0.18 0.44
```

```
# Reproductive Values
rv.avg = eigs(A.avg, what = "rv")
rv.lwr = eigs(A.lwr, what = "rv")
rv.upr = eigs(A.upr, what = "rv")

round(rv.avg, digits = 2)
```

```
## [1] 0.50 0.95 1.31
```

```
round(rv.lwr, digits = 2)
```

```
## [1] 0.53 0.92 1.15
```

```
round(rv.upr, digits = 2)
```

```
## [1] 0.47 0.96 1.46
```

The analysis for the stable stage distribution suggests that on average 1 year olds make up 33% (lwr = 23%, upr = 39%) of the total population whilst 2 year olds make up 21% (lwr = 18%, upr = 22%) of the total population and adults make up 45% (lwr = 39%, upr = 58%) of the total population.

As for the reproductive values, adults contribute the most to population growth (mean = 1.47, lwr = 1.42, upr = 1.50), then 2 year olds (mean = 0.77, lwr = 0.47, upr = 0.93) and then 1 year olds (mean = 0.50, lwr = 0.37, upr = 0.53).

Finally, to see what vital rate is most affected by changes in its mean value we can do an elasticity analysis. This is where we make a proportional change to each vital rate and measure the effect it has on the population growth rate. The larger the elasticity value, the more elastic the parameter is to change, and the smaller the elasticity value, the less elastic the parameter is to change.

```
elasticity.avg = elas(A.avg)
elasticity.lwr = elas(A.lwr)
elasticity.upr = elas(A.upr)
round(elasticity.avg, digits = 2)
```

```
##            One.yr_old Two.yr_old adults
## One.yr_old       0.00       0.00   0.16
## Two.yr_old       0.16       0.00   0.00
## adults           0.00       0.16   0.53
```

```
round(elasticity.lwr, digits = 2)
```

```
##            One.yr_old Two.yr_old adults
## One.yr_old       0.00       0.00   0.11
## Two.yr_old       0.11       0.00   0.00
## adults           0.00       0.11   0.68
```

```
round(elasticity.upr, digits = 2)
```

```
##           One.yr_old Two.yr_old adults
## One.yr_old      0.00        0.00   0.18
## Two.yr_old      0.18        0.00   0.00
## adults          0.00        0.18   0.47
```

The elasticity analysis has shown that adult survival is the most elastic parameter (mean = 0.50, lwr = 0.39, upr = 0.74) relative to all others (mean = 0.17, lwr = 0.09, upr = 0.20 for all parameters). Thus, this vital rate should be the main focus of conservation efforts for the species based on the data used in this analysis.

We can get an estimate of extinction time for the population if we use the lower estimate of lambda (as its the only one less than 1) ny using the *project()* function. All we need to supply the function with is the intital population size vector, the projection matrix and the length of time we want to project into.

```
#Do the projection
current = project(A.avg, vector = pop_vec.avg, time = 25, return.vec = TRUE)

#Plot on the original scale
plot(current)
```
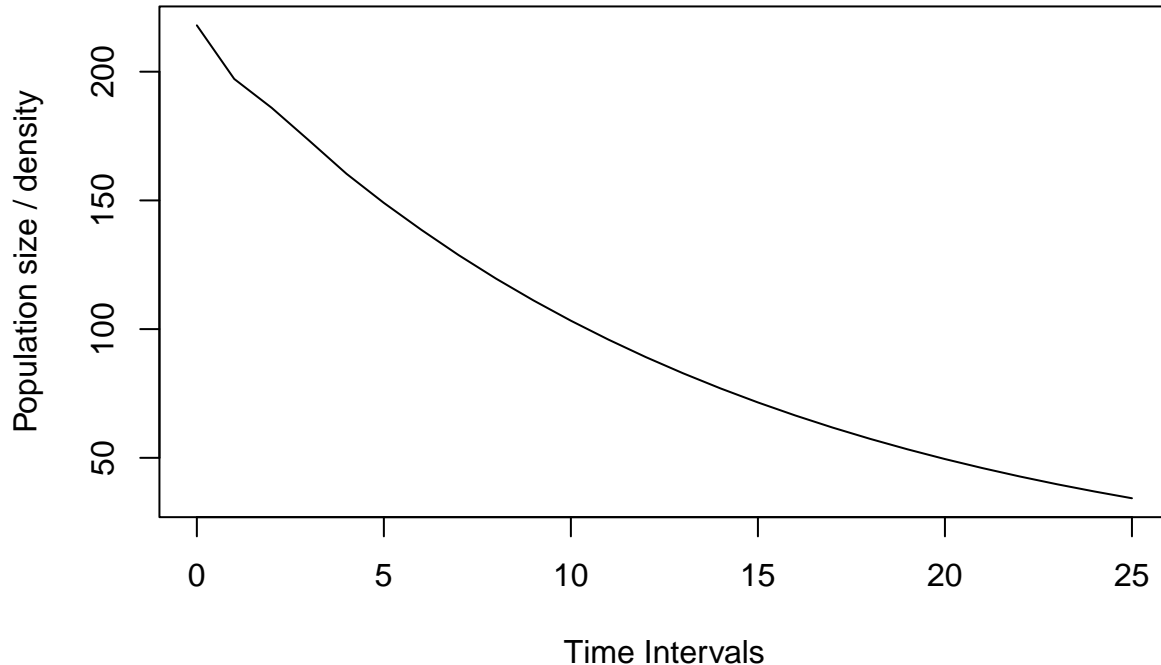


```
#Plot on the natural log scale
plot(current, log = "y", xlim = c(0,35))
```
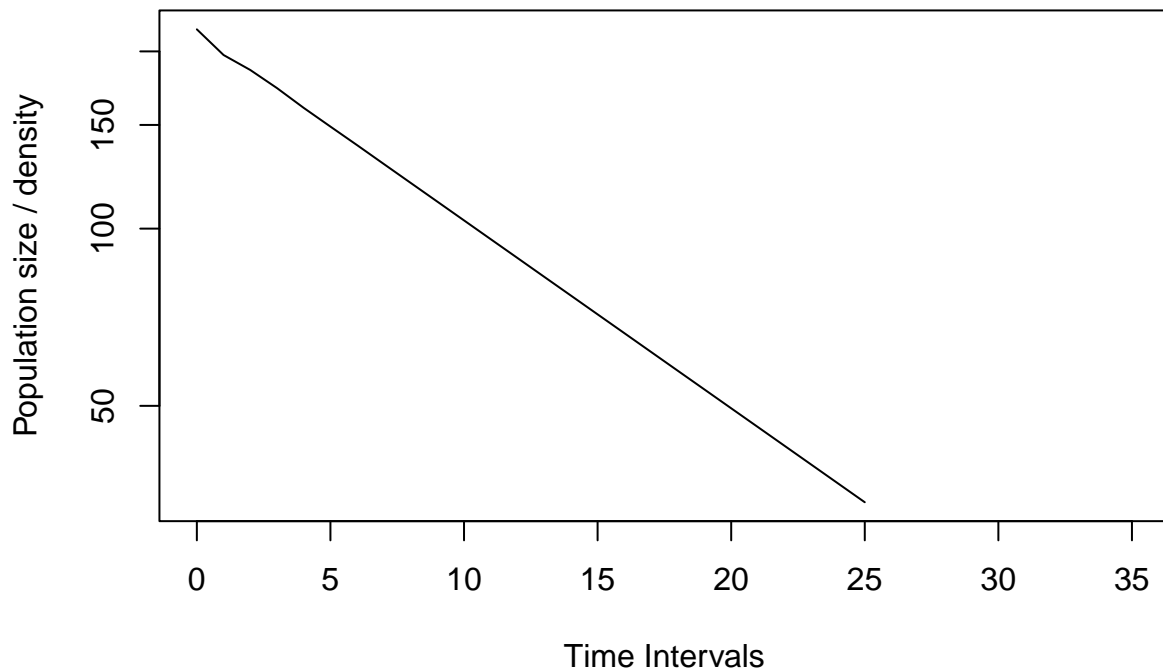
The plot suggests that the Amami rabbit population will go extinct in between 25 and 28 years. To narrow this further we can pull out data to manually calculate the slope of the straight-line, construct the equation of the straight line and use it to solve for t when y is 0. In order to estimate the gradient of the line properly we will calculate it for multiple points then take the mean average

```
y = c(current@.Data[2],current@.Data[3], current@.Data[4], current@.Data[5], current@.Data[6],
      current@.Data[7],current@.Data[8], current@.Data[9], current@.Data[10], current@.Data[11],
      current@.Data[12],current@.Data[13], current@.Data[14], current@.Data[15], current@.Data[16],
      current@.Data[17],current@.Data[18], current@.Data[19], current@.Data[20], current@.Data[21],
      current@.Data[22],current@.Data[23], current@.Data[24], current@.Data[25], current@.Data[26])
x = seq(from = 1, to = 25, by = 1)
dat = data.frame(y = log(y), x = x)
summary(lm(y ~ x, data = dat))
```

```
##
## Call:
## lm(formula = y ~ x, data = dat)
##
## Residuals:
##         Min          1Q      Median          3Q         Max
## -0.0126726  -0.0003141   0.0003660   0.0008594   0.0047518
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.370e+00  1.213e-03  4425.4   <2e-16 ***
## x           -7.337e-02  8.163e-05  -898.8   <2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.002943 on 23 degrees of freedom
## Multiple R-squared:     1,  Adjusted R-squared:     1
## F-statistic: 8.079e+05 on 1 and 23 DF,  p-value: < 2.2e-16
```

The model suggests that the slope is approximately -5.1497 +/- 0.5557. Now I can calculate the extinction time with 95% confidence intervals.

```
t = 5.276/0.07335
t.se = t*sqrt(((0.00123/5.276)^2) + ((0.00008/-5.1497)^2))
t.avg = t
t.lwr = t - 1.96*t.se
t.upr = t + 1.96*t.se
t.avg
```

```
## [1] 71.92911
```

```
t.lwr
```

```
## [1] 71.89617
```

```
t.upr
```

```
## [1] 71.96205
```

The mean extinction time based on the lower lambda confidence interval is 31.26 years with 95% CIs of (31.20, 31.31) years.

Testing Conservation Stratagies

Using the survival function for adult Amami rabbits we can test several scenarios that we could implement in an attempt to save the species. Two possible actions to take are detailed below:

- The java mongoose is eradicated from the islands where Amamai rabbits are found and houses stay the 20221 mean average distance (3.5 metres) away from Amami rabbit habitat (1)
- The java mongoose is eradicated from the islands where Amami rabbits are found and house building is allowed to continue closer to Amami rabbit habitat (2)

Recall the survival function: logit(phi) = 0.145 + 0.784*2-yr-olds* + *1.013*adults + 0.014*house* - *0.151*mongoose

To calculate adult survival for scenario (1) is relatively straight forward.

```
phi_adults_1 = 0.145 + 1.013*1 + 0.014*(3.5) - 0.151*0
plogis(phi_adults_1)
```

```
## [1] 0.7697677
```

Under this scenario adult survival increases suggesting that it will not positively impact the growth rate of the population. The same is true if house building is allowed to continue.

```
house = seq(from = -3.5, to = 0, by = 0.5)
phi_adults_2 = 0.145 + 1.013*1 + 0.014*house - 0.151*0
plogis(phi_adults_2)
```

```
## [1] 0.7519426 0.7532460 0.7545448 0.7558389 0.7571284 0.7584133 0.7596935
## [8] 0.7609691
```

```
# Action 1
A1.avg = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.avg, 0),
    Two.yr_old = c(0, 0, phi_2yr.avg),
    adults = c(F_adult.avg, 0, 0.76)
  )
)
row.names(A1.avg) = colnames(A.avg)

A1.lwr = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.lwr, 0),
    Two.yr_old = c(0, 0, phi_2yr.lwr),
    adults = c(F_adult.lwr, 0, 0.72)
  )
)
row.names(A1.lwr) = colnames(A1.lwr)

A1.upr = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.upr, 0),
    Two.yr_old = c(0, 0, phi_2yr.upr),
    adults = c(F_adult.upr, 0, 0.80)
  )
)
row.names(A1.upr) = colnames(A1.upr)

# Action 2
A2.avg = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.avg, 0),
    Two.yr_old = c(0, 0, phi_2yr.avg),
    adults = c(F_adult.avg, 0, 0.76)
  )
)
row.names(A2.avg) = colnames(A2.avg)

# Lower (lwr) estimated values
A2.lwr = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.lwr, 0),
    Two.yr_old = c(0, 0, phi_2yr.lwr),
    adults = c(F_adult.lwr, 0, 0.72)
  )
)
```

```r
row.names(A2.lwr) = colnames(A2.lwr)

A2.upr = as.matrix(
  data.frame(
    One.yr_old = c(0, phi_1yr.upr, 0),
    Two.yr_old = c(0, 0, phi_2yr.upr),
    adults = c(F_adult.upr, 0, 0.80)
  )
)
row.names(A2.upr) = colnames(A2.upr)

# The plots
#png("Matrix Model.png")
#par(mfrow = c(1,3))
#current = project(A.avg, vector = pop_vec.avg, time = 25)
#plot(action1, log = "y", xlim = c(0,30))
#action1 = project(A1.avg, vector = pop_vec.avg, time = 25)
#plot(action1, log = "y", xlim = c(0,30))
#action2 = project(A2.avg, vector = pop_vec.avg, time = 25)
#plot(action2, log = "y", xlim = c(0,30))
#dev.off()
```

An additional option would be to re-forest the island but this will increase the colonisation rate of the java mongoose. As such it would require a continued mongoose buisting operation in order to keep the mongoose eradicated. Further work would also bee needed to look at the effect of forest cover on Amami rabbit occupancy dynamics.