Vulture_Metapopulation_pseudo-extinction_probability.R

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```r
# Vulture Metapopulation pseudo-extinction probability
```

```r
# useful link http://www.mbr-pwrc.usgs.gov/workshops/uf2016/
```

```r
# clean everything first
rm(list=ls())
```

```r
# load required packages
library(popbio)
library(diagram)
```

```
## Loading required package: shape
```

```r
# PARAMETERS
```

```r
# fecundity calculation, (Gauthier & Lebreton (2004) Population models for Greater Snow Geese)
bp <- 0.8 # breeding propensity
cs <- 1 # clutch size
hs <- 0.76 # hatching success
fs <- 0.6 # fledging success
f1 <- bp * (cs/2) * hs * fs # divide by 2 to get females only


# survival
s0 <- 0.42 # first year survival # this value should probably be modified to account for
# lower adult survival in KZN
s1Kr <- 0.82 # juvenile survival Kruger
s2Kr <- 0.89 # subadult survival Kruger
s3Kr <- 1.0 # adult survival Kruger
```

```r
# KRUGER PRE-BREEDING CENSUS
```

```r
MKrpre <- c(0,0,0,0,s0*f1,
            s1Kr,0,0,0,0,
            0,s1Kr,0,0,0,
            0,0,s2Kr,0,0,
            0,0,0,s2Kr,s3Kr)
MKrpre <- matrix ((MKrpre), ncol=5, byrow = TRUE)

lambda(MKrpre)
```

```
## [1] 1.035489
```

```r
eigen.analysis(MKrpre)
```

```
## $lambda1
## [1] 1.035489
##
## $stable.stage
```

```
## [1] 0.06069909 0.04806737 0.03806436 0.03271620 0.82045299
##
## $sensitivities
##            [,1]       [,2]       [,3]       [,4]      [,5]
## [1,] 0.00000000 0.00000000 0.00000000 0.00000000 0.4074077
## [2,] 0.03806182 0.00000000 0.00000000 0.00000000 0.0000000
## [3,] 0.00000000 0.03806182 0.00000000 0.00000000 0.0000000
## [4,] 0.00000000 0.00000000 0.03506819 0.00000000 0.0000000
## [5,] 0.00000000 0.00000000 0.00000000 0.03506819 0.8794360
##
## $elasticities
##          [,1]     [,2]     [,3]     [,4]     [,5]
## [1,] 0.000000 0.000000 0.000000 0.000000 0.030141
## [2,] 0.030141 0.000000 0.000000 0.000000 0.000000
## [3,] 0.000000 0.030141 0.000000 0.000000 0.000000
## [4,] 0.000000 0.000000 0.030141 0.000000 0.000000
## [5,] 0.000000 0.000000 0.000000 0.030141 0.849295
##
## $repro.value
## [1] 1.000000 1.262792 1.594644 1.855322 2.158614
##
## $damping.ratio
## [1] 2.179107
```

```r
# KZN SURVIVAL RATES
```

```r
s1Kz <-  0.86 # juvenile survival KZN
s2Kz <- 0.51 # subadult survival KZN
s3Kz <- 0.57 # adult survival KZN
```

```r
# KZN PRE-BREEDING CENSUS
```

```r
MKZpre <- c(0,0,0,0,s0*f1,
           s1Kz,0,0,0,0,
           0,s1Kz,0,0,0,
           0,0,s2Kz,0,0,
           0,0,0,s2Kz,s3Kz)
MKZpre <- matrix ((MKZpre), ncol=5, byrow = TRUE)

lambda(MKZpre)
```

```
## [1] 0.6516998
```

```r
eigen.analysis(MKZpre)
```

```
## $lambda1
## [1] 0.6516998
##
## $stable.stage
## [1] 0.07178361 0.09472752 0.12500490 0.09782495 0.61065902
##
## $sensitivities
##            [,1]       [,2]      [,3]      [,4]      [,5]
## [1,] 0.00000000 0.00000000 0.0000000 0.0000000 0.7102874
## [2,] 0.06327174 0.00000000 0.0000000 0.0000000 0.0000000
## [3,] 0.00000000 0.06327174 0.0000000 0.0000000 0.0000000
## [4,] 0.00000000 0.00000000 0.1066935 0.0000000 0.0000000
```

```
## [5,] 0.00000000 0.00000000 0.0000000 0.1066935 0.6660199
##
## $elasticities
##             [,1]        [,2]        [,3]        [,4]        [,5]
## [1,] 0.00000000 0.00000000 0.00000000 0.00000000 0.08349503
## [2,] 0.08349503 0.00000000 0.00000000 0.00000000 0.00000000
## [3,] 0.00000000 0.08349503 0.00000000 0.00000000 0.00000000
## [4,] 0.00000000 0.00000000 0.08349503 0.00000000 0.00000000
## [5,] 0.00000000 0.00000000 0.00000000 0.08349503 0.58252485
##
## $repro.value
## [1] 1.0000000 0.7577905 0.5742464 0.7337966 0.9376767
##
## $damping.ratio
## [1] 1.561557
```

```r
# METAPOPULATION MATRIX

f1 <- 0.1824 * 0.42 # fecundity * first year survival s0
gb0 <- 0.05 # migration rates from Kruger to KZN for ages < 1
bg0 <- 0.05 # migration rates from KZN to Kruger for ages < 1
gb <- 0.02 # migration rates from Kruger to KZN for ages > 1
bg <- 0.02 # migration rates from KZN to Kruger for ages > 1
s1Kz <- 0.86 # juvenile survival KZN
s2Kz <- 0.51 # Subadult survival KZN
s3Kz <- 0.57 # adult survival KZN
s1Kr <- 0.82 # juvenile survival Kruger
s2Kr <- 0.89 # Kruger subadult survival
s3Kr <- 1 # Kruger adult survival

metaA <- matrix(c(
  # Kruger                                        # KZN
  0,  0,  0,  0,  f1*(1-gb0),                      0,  0,  0,  0, f1*bg0,
  s1Kr*(1-gb), 0, 0, 0, 0,                        s1Kz*bg, 0, 0, 0, 0,
  0, s1Kr*(1-gb), 0, 0, 0,                        0, s1Kz*bg, 0, 0, 0,
  0, 0, s2Kr*(1-gb), 0, 0,                        0, 0, s2Kz*bg, 0, 0,
  0, 0, 0, s2Kr*(1-gb), s3Kr*(1-gb),              0, 0, 0, s2Kz*bg, s3Kz*bg,

  0, 0, 0, 0, f1*gb0,                              0, 0, 0, 0, f1*(1-bg0),
  s1Kr*gb, 0, 0, 0, 0,                            s1Kz*(1-bg), 0, 0, 0, 0,
  0, s1Kr*gb, 0, 0, 0,                            0, s1Kz*(1-bg), 0, 0, 0,
  0, 0, s2Kr*gb, 0, 0,                            0, 0, s2Kz*(1-bg), 0, 0,
  0, 0, 0, s2Kr*gb, s3Kr*gb,                      0, 0, 0, s2Kz*(1-bg), s3Kz*(1-bg)),

  nrow = 10, byrow = TRUE)

lambda(metaA)
```

```
## [1] 1.014661
```

```r
# SENSITIVITY AND ELASTICITY ANALYSIS

# Conduct a sensitivity and elasticity analysis for the lower-level vital rates
# (i.e, those that make up the matrix elements) using the popbio package.
# Just put the vital rates in a list, and write the matrix as an expression
```

```r
vulture.vr <- list(f1 = 0.076608, # fecundity * first year survival s0 = 0.1824 * 0.42
                   gb0 = 0.05, # migration rates from Kruger to KZN for ages < 1
                   bg0 = 0.05, # migration rates from KZN to Kruger for ages < 1
                   gb = 0.02, # migration rates from Kruger to KZN for ages > 1
                   bg = 0.02, # migration rates from KZN to Kruger for ages > 1
                   s1Kz = 0.86, # juvenile survival KZN
                   s2Kz = 0.51, # Subadult survival KZN
                   s3Kz = 0.57, # adult survival KZN
                   s1Kr = 0.82, # juvenile survival Kruger
                   s2Kr = 0.89, # Kruger subadult survival
                   s3Kr = 1) # Kruger adult survival


sensA <- expression(
                    # Kruger                                      # KZN
                    0,  0,  0,  0,  f1*(1-gb0),                    0,  0,  0,  0, f1*bg0,
                    s1Kr*(1-gb), 0, 0, 0, 0,                      s1Kz*bg, 0, 0, 0, 0,
                    0, s1Kr*(1-gb), 0, 0, 0,                      0, s1Kz*bg, 0, 0, 0,
                    0, 0, s2Kr*(1-gb), 0, 0,                      0, 0, s2Kz*bg, 0, 0,
                    0, 0, 0, s2Kr*(1-gb), s3Kr*(1-gb),            0, 0, 0, s2Kz*bg, s3Kz*bg,

                    0, 0, 0, 0, f1*gb0,                           0, 0, 0, 0, f1*(1-bg0),
                    s1Kr*gb, 0, 0, 0, 0,                          s1Kz*(1-bg), 0, 0, 0, 0,
                    0, s1Kr*gb, 0, 0, 0,                          0, s1Kz*(1-bg), 0, 0, 0,
                    0, 0, s2Kr*gb, 0, 0,                          0, 0, s2Kz*(1-bg), 0, 0,
                    0, 0, 0, s2Kr*gb, s3Kr*gb,                    0, 0, 0, s2Kz*(1-bg), s3Kz*(1-b
                    )

# then apply the following popbio function
llsenselas <- vitalsens(sensA,vulture.vr)
llsenselas
```

```
##       estimate   sensitivity    elasticity
## f1    0.076608   0.3926649094   2.964664e-02
## gb0   0.050000  -0.0289414414  -1.426164e-03
## bg0   0.050000   0.0014473632   7.132254e-05
## gb    0.020000  -0.9669538292  -1.905965e-02
## bg    0.020000   0.0356995188   7.036742e-04
## s1Kz  0.860000   0.0005042606   4.273983e-04
## s2Kz  0.510000   0.0004685791   2.355225e-04
## s3Kz  0.570000   0.0023708692   1.331870e-03
## s1Kr  0.820000   0.0728401008   5.886588e-02
## s2Kr  0.890000   0.0673298555   5.905775e-02
## s3Kr  1.000000   0.8629027440   8.504349e-01
```

```r
# MODELLING EXTINCTION PROBABILITIES

# Specify the number of simulations, time steps for each simulation, and the
# pseudo-extinction threshold
sims <- 500
tspan <- 100
threshold <- 20


# Define demographic parameters that do not vary over time
f1 <- 0.1824 * 0.42 # fecundity * first year survival s0
```

```r
gb0 <- 0.05 # migration rates from Kruger to KZN for ages < 1
bg0 <- 0.05 # migration rates from KZN to Kruger for ages < 1
gb <- 0.02 # migration rates from Kruger to KZN for ages > 1
bg <- 0.02 # migration rates from KZN to Kruger for ages > 1
s1Kz <- 0.86 # juvenile survival KZN
s2Kz <- 0.51 # Subadult survival KZN
s3Kz <- 0.57 # adult survival KZN
s1Kr <- 0.82 # juvenile survival Kruger

# Storage place for per time step growth rates for eventual calculation of
# the stochastic growth rate
gr <- matrix(0,sims,tspan-1)

# Storage for indicators on each simulation determining whether or not the
# population ever dropped below the pseudo-extinction threshold.
ext_ind <- matrix(0,sims,1)
extr_event <- matrix(0,sims,1)

for (j in 1:sims){
  # Define vector of initial abundance
  # juvenile < 2 years = 9%, immature, 3-5 years = 24%, adult > 5 years = 67%
  # Kruger 1200 females
  # < 2 = 108
  # 3-5 = 288 / 3 = 96
  # 5+ = 804
  # KZN 425 females
  # < 2 = 38
  # 3-5 = 102 / 3 = 34
  # 5+ = 285

  n <- c(108,96,96,96,804,38,34,34,34,285)
  nstore <- matrix(0,tspan,1) # temporary storage of time-specific abundance
  nstore[1] <- sum(n)
  for(t in 2:tspan){
    X <- rbinom(1, 1, 1/15) # probabilty that poisoning occurs, here it's once ever 10 years
    s2Kr <- 0.89 - (0.427*0.89*X) # Kruger subadult survival equals KZN under poisoning
    s3Kr <- 1 - (0.43*1*X) # Kruger adult survival equals KZN under poisoning

# The following megamatrix matrix - A - has the Kruger matrix in top left
# and KZN matrix in bottom right
# the diagonals are include the probability of emigration/immigration between sites
# that's why it's called a megamatrix
# take a look at the simpler matrices above constructed separately for each site
# to see where these values come from

    A <- matrix(c(
      # Kruger                                  # KZN
      0,  0,  0,  0,  f1*(1-gb0),               0,  0,  0,  0, f1*bg0,
      s1Kr*(1-gb), 0, 0, 0, 0,                  s1Kz*bg, 0, 0, 0, 0,
      0, s1Kr*(1-gb), 0, 0, 0,                  0, s1Kz*bg, 0, 0, 0,
      0, 0, s2Kr*(1-gb), 0, 0,                  0, 0, s2Kz*bg, 0, 0,
      0, 0, 0, s2Kr*(1-gb), s3Kr*(1-gb),        0, 0, 0, s2Kz*bg, s3Kz*bg,
```

```
       0, 0, 0, 0, f1*gb0,                              0, 0, 0, 0, f1*(1-bg0),
       s1Kr*gb, 0, 0, 0, 0,                             s1Kz*(1-bg), 0, 0, 0, 0,
       0, s1Kr*gb, 0, 0, 0,                             0, s1Kz*(1-bg), 0, 0, 0,
       0, 0, s2Kr*gb, 0, 0,                             0, 0, s2Kz*(1-bg), 0, 0,
       0, 0, 0, s2Kr*gb, s3Kr*gb,                       0, 0, 0, s2Kz*(1-bg), s3Kz*(1-bg)),

       nrow = 10, byrow = TRUE)

    nnew <- A%*%n
    nstore[t] <- sum(nnew)
    gr[j,t-1] <- sum(nnew)/sum(n)
    n <- nnew
  }
  if(min(nstore) < threshold) ext_ind[j] = 1
  if(X==1) extr_event[j]=1
}

ln_lambda_s <- mean(log(gr))        # the stochastic population growth rate
Lambda_s <- exp(ln_lambda_s)        # the stochastic population growth rate on the
nb_extr_event<-sum(extr_event)
# non-logged scale
ext_prob <- mean(ext_ind)           # the pseudo-extinction probability

ln_lambda_s
```

```
## [1] -0.0213447
```

```
Lambda_s
```

```
## [1] 0.9788815
```

```
ext_prob # the overall extinction probability
```

```
## [1] 0.046
```

```
nb_extr_event # number of extinction events over the model run
```

```
## [1] 36
```