Individual_matrices_and_combined_megamatrix_for_vulture_

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```
# MATRIX POPULATION MODEL FOR AFRICAN WHITE BACKED VULTURES
```

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

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

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

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

```
# PARAMETERS
```

```
# fecundity calculation, (Gauthier & Lebreton (2004) Population models for Greater Snow Geese)
bp <- 0.85 # 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
```

```
# KRUGER POST-BREEDING CENSUS
```

```
# survival this year is multiplied by fecundity next year because in this model
# the birds have to survive the year before they become breeders i.e. from 4 years old to
# breeding age at 5 years old - s2Kr*f1

# create the matrix for Kruger
MKrPost <- c(0,0,0,0,s2Kr*f1,s3Kr*f1,
         s0,0,0,0,0,0,
         0,s1Kr,0,0,0,0,
         0,0,s1Kr,0,0,0,
         0,0,0,s2Kr,0,0,
         0,0,0,0,s2Kr,s3Kr
)
MKrPost <- matrix ((MKrPost), ncol=6, byrow = TRUE)

# previous function is wrapped up into pop.projection
popKrugerPost<-eigen.analysis(MKrPost, zero=TRUE)
popKrugerPost$lambda1
```

```
## [1] 1.037427
```

```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)

# previous function is wrapped up into pop.projection
popKrugerPre<-eigen.analysis(MKrpre, zero=TRUE)
popKrugerPre$lambda1
```

```
## [1] 1.037427
```

```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 POST-BREEDING CENSUS
```

```r
# create the matrix for Kruger
MKZPost <- c(0,0,0,0,s2Kz*f1,s3Kz*f1,
             s0,0,0,0,0,0,
             0,s1Kz,0,0,0,0,
             0,0,s1Kz,0,0,0,
             0,0,0,s2Kz,0,0,
             0,0,0,0,s2Kz,s3Kz
)
MKZPost <- matrix ((MKZPost), ncol=6, byrow = TRUE)

# previous function is wrapped up into pop.projection
popKZPost<-eigen.analysis(MKZPost, zero=TRUE)
popKZPost$lambda1
```

```
## [1] 0.6550459
```

```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)

# previous function is wrapped up into pop.projection
popKZPre<-eigen.analysis(MKZpre, zero=TRUE)
popKZPre$lambda1
```

```
## [1] 0.6550459
```

```r
# MEGAMATRIX FOR METAPOPULATION STRUCTURE
```

```r
# Effective migration rates (dispersal * stage-specific survival)
gb <- 0.04 # Disperal from Kruger to KZN
bg <- 0.04 # Disperal from KZN to Kruger
```

```r
# resight proportions from data
# Kruger origin birds - 75 within 701 outside ~ 10% stay within the park
# KZN origin birds - 22 within 201 outside ~ 10% stay within KZN

A <- matrix(c(
  0,  0,  0,  0,  s0*f1,  0,  0,  0,  0, 0,
  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, 0, 0, 0, 0, 0, s0*f1,
  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)

A
```

```
##         [,1]   [,2]   [,3]   [,4]     [,5]   [,6]   [,7]   [,8]   [,9]
##  [1,] 0.0000 0.0000 0.0000 0.0000 0.081396 0.0000 0.0000 0.0000 0.0000
##  [2,] 0.7872 0.0000 0.0000 0.0000 0.000000 0.0344 0.0000 0.0000 0.0000
##  [3,] 0.0000 0.7872 0.0000 0.0000 0.000000 0.0000 0.0344 0.0000 0.0000
##  [4,] 0.0000 0.0000 0.8544 0.0000 0.000000 0.0000 0.0000 0.0204 0.0000
##  [5,] 0.0000 0.0000 0.0000 0.8544 0.960000 0.0000 0.0000 0.0000 0.0204
##  [6,] 0.0000 0.0000 0.0000 0.0000 0.000000 0.0000 0.0000 0.0000 0.0000
##  [7,] 0.0328 0.0000 0.0000 0.0000 0.000000 0.8256 0.0000 0.0000 0.0000
##  [8,] 0.0000 0.0328 0.0000 0.0000 0.000000 0.0000 0.8256 0.0000 0.0000
##  [9,] 0.0000 0.0000 0.0356 0.0000 0.000000 0.0000 0.0000 0.4896 0.0000
## [10,] 0.0000 0.0000 0.0000 0.0356 0.040000 0.0000 0.0000 0.0000 0.4896
##          [,10]
##  [1,] 0.000000
##  [2,] 0.000000
##  [3,] 0.000000
##  [4,] 0.000000
##  [5,] 0.022800
##  [6,] 0.081396
##  [7,] 0.000000
##  [8,] 0.000000
##  [9,] 0.000000
## [10,] 0.547200
```

```r
lambda(A)
```

```
## [1] 0.9998062
```

```r
# SENSITIVITY AND ELASTICITY ANALYSIS
```

```r
# 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

vulture.vr <- list(s0=0.42,f1=0.1938,
                   s1Kr=0.82,s2Kr=0.89,s3Kr=1,
                   s1Kz=0.86,s2Kz=0.51,s3Kz=0.57,
                   gb=0.1,bg=0.1)
```

```r
VultureA <- expression(
  0, 0, 0, 0, s0*f1, 0, 0, 0, 0, 0,
  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, 0, 0, 0, 0, 0, s0*f1,
  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))

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

```
##      estimate  sensitivity   elasticity
## s0     0.4200  0.080418065  0.035422250
## f1     0.1938  0.174280637  0.035422250
## s1Kr   0.8200  0.074978828  0.064480105
## s2Kr   0.8900  0.071323314  0.066572482
## s3Kr   1.0000  0.755165230  0.791981829
## s1Kz   0.8600  0.007056437  0.006364395
## s2Kz   0.5100  0.007987109  0.004272018
## s3Kz   0.5700  0.051702037  0.030906921
## gb     0.1000 -0.801790542 -0.084088027
## bg     0.1000  0.132113342  0.013855427
```

```r
# MEGAMATRIX FOR METAPOPULATION STRUCTURE SWITCHED
```

```r
# Effective migration rates (dispersal * stage-specific survival)
gb <- 0.1 # Disperal from Kruger to KZN
bg <- 0.1 # Disperal from KZN to Kruger

ASwtich <- matrix(c(
  0,  0,  0,  0,  s0*f1,  0,  0,  0,  0, 0,
  s1Kz*(1-bg), 0, 0, 0, 0, s1Kr*gb, 0, 0, 0, 0,
  0, s1Kz*(1-bg), 0, 0, 0, 0, s1Kr*gb, 0, 0, 0,
  0, 0, s2Kz*(1-bg), 0, 0, 0, 0, s2Kr*gb, 0, 0,
  0, 0, 0, s2Kz*(1-bg), s3Kz*(1-bg), 0, 0, 0, s2Kr*gb, s3Kr*gb,
  0, 0, 0, 0, 0, 0, 0, 0, 0, s0*f1,
  s1Kz*bg, 0, 0, 0, 0, s1Kr*(1-gb), 0, 0, 0, 0,
  0, s1Kz*bg, 0, 0, 0, 0, s1Kr*(1-gb), 0, 0, 0,
  0, 0, s2Kz*bg, 0, 0, 0, 0, s2Kr*(1-gb), 0, 0,
  0, 0, 0, s2Kz*bg, s3Kz*bg, 0, 0, 0, s2Kr*(1-gb), s3Kr*(1-gb)), nrow = 10, byrow = TRUE)

ASwtich
```

```
##        [,1]  [,2]  [,3]  [,4]     [,5]  [,6]  [,7]  [,8]  [,9]    [,10]
##  [1,] 0.000 0.000 0.000 0.000 0.081396 0.000 0.000 0.000 0.000 0.000000
##  [2,] 0.774 0.000 0.000 0.000 0.000000 0.082 0.000 0.000 0.000 0.000000
##  [3,] 0.000 0.774 0.000 0.000 0.000000 0.000 0.082 0.000 0.000 0.000000
##  [4,] 0.000 0.000 0.459 0.000 0.000000 0.000 0.000 0.089 0.000 0.000000
##  [5,] 0.000 0.000 0.000 0.459 0.513000 0.000 0.000 0.000 0.089 0.100000
##  [6,] 0.000 0.000 0.000 0.000 0.000000 0.000 0.000 0.000 0.000 0.081396
```

```
##  [7,] 0.086 0.000 0.000 0.000 0.000000 0.738 0.000 0.000 0.000 0.000000
##  [8,] 0.000 0.086 0.000 0.000 0.000000 0.000 0.738 0.000 0.000 0.000000
##  [9,] 0.000 0.000 0.051 0.000 0.000000 0.000 0.000 0.801 0.000 0.000000
## [10,] 0.000 0.000 0.000 0.051 0.057000 0.000 0.000 0.000 0.801 0.900000
```

```
lambda(ASwtich)
```

```
## [1] 0.9535133
```

```
# MEGAMATRIX TEST FOR AGE-SPECIFIC EMIGRATION/IMMIGRATION
```

```
# Effective migration rates (dispersal * stage-specific survival)
gb0 <- 0.05
bg0 <- 0.05
gb <- 0.02 # Disperal from Kruger to KZN
bg <- 0.02 # Disperal from KZN to Kruger
gbA <- 0.05
bgA <- 0.05
# resight proportions from data
# Kruger origin birds - 75 within 701 outside ~ 10% stay within the park
# KZN origin birds - 22 within 201 outside ~ 10% stay within KZN

Amig <- matrix(c(
  0,  0,  0,  0,  s0*(1-gb0)*f1,  0,  0,  0,  0, s0*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-gbA), 0, 0, 0, s2Kz*bg, s3Kz*bgA,
  0, 0, 0, 0, 0, 0, 0, 0, 0, s0*(1-bg0)*f1,
  s1Kr*gb, 0, 0, 0, s0*gb0, 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*gbA, 0, 0, 0, s2Kz*(1-bg), s3Kz*(1-bgA)), nrow = 10, byrow = TRUE)

Amig
```

```
##         [,1]   [,2]   [,3]   [,4]      [,5]   [,6]   [,7]   [,8]   [,9]
##  [1,] 0.0000 0.0000 0.0000 0.0000 0.0773262 0.0000 0.0000 0.0000 0.0000
##  [2,] 0.8036 0.0000 0.0000 0.0000 0.0000000 0.0172 0.0000 0.0000 0.0000
##  [3,] 0.0000 0.8036 0.0000 0.0000 0.0000000 0.0000 0.0172 0.0000 0.0000
##  [4,] 0.0000 0.0000 0.8722 0.0000 0.0000000 0.0000 0.0000 0.0102 0.0000
##  [5,] 0.0000 0.0000 0.0000 0.8722 0.9500000 0.0000 0.0000 0.0000 0.0102
##  [6,] 0.0000 0.0000 0.0000 0.0000 0.0000000 0.0000 0.0000 0.0000 0.0000
##  [7,] 0.0164 0.0000 0.0000 0.0000 0.0210000 0.8428 0.0000 0.0000 0.0000
##  [8,] 0.0000 0.0164 0.0000 0.0000 0.0000000 0.0000 0.8428 0.0000 0.0000
##  [9,] 0.0000 0.0000 0.0178 0.0000 0.0000000 0.0000 0.0000 0.4998 0.0000
## [10,] 0.0000 0.0000 0.0000 0.0178 0.0500000 0.0000 0.0000 0.0000 0.4998
##           [,10]
##  [1,] 0.0210000
##  [2,] 0.0000000
##  [3,] 0.0000000
##  [4,] 0.0000000
##  [5,] 0.0285000
##  [6,] 0.0773262
##  [7,] 0.0000000
##  [8,] 0.0000000
```

```
##  [9,] 0.0000000
## [10,] 0.5415000
```

```r
lambda(Amig)
```

```
## [1] 0.9947176
```