Re-analysis Angert (2016)

Mario Vallejo-Marin
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Background

This exercise consists of a reanalysis of the datasets from Angert (2006). The data is provided as part of the popbio package.

First load the library:

```
library(popbio)
```

The dataset monkeyflower contains the transition rates of 32 populations of two *Mimulus* species, measured over multiple years. For an explanation of the transition rates see Angert (2006).

Here are the first few lines of the data set:

```
#Because Rmarkdown knits from a different environment, you need so save the data set first and then rea
#save(monkeyflower,file="monkeyflower.RData")
load(file="monkeyflower.RData")
head(monkeyflower)
```

```
a11 a12 a13
                                                               a21
                                                                      a22
        species
                        site
                               year
                                                     a14
## 1 cardinalis Buck Meadows
                               2000 0.2128
                                              0 2038 9624 2.49e-05 0.0000
## 2 cardinalis Buck Meadows
                               2001 0.1840 376
                                                720 1340 2.14e-05 0.0345
                               2002 0.1840
## 3 cardinalis Buck Meadows
                                              0 144
                                                     916 3.93e-06 0.0000
## 4 cardinalis Buck Meadows pooled 0.1900 441 1262 3636 2.25e-05 0.0139
                                              0
## 5 cardinalis Rainbow Pool
                               2000 0.1858
                                                  77
                                                      668 5.76e-05 0.2606
                               2001 0.1859
## 6 cardinalis Rainbow Pool
                                              8
                                                 280 1279 2.39e-05 0.1152
##
        a23
               a24
                               a32
                                              a34
                        a31
                                      a33
                                                       a41
                                                              a42
## 1 0.0000 0.0000 3.74e-05 0.0000 0.3529 0.5000 8.31e-07 0.0000 0.0588
## 2 0.0104 0.0000 2.14e-05 0.2759 0.3229 0.2632 0.00e+00 0.1034 0.1979
## 3 0.0000 0.0000 2.23e-05 0.0303 0.3662 0.2069 0.00e+00 0.0000 0.0704
## 4 0.0043 0.0000 3.26e-05 0.1250 0.3447 0.3725 3.46e-07 0.0417 0.1191
## 5 0.0643 0.0076 1.57e-05 0.0904 0.4143 0.3106 1.16e-06 0.0000 0.0500
## 6 0.0051 0.0000 1.66e-05 0.1264 0.3299 0.3205 7.10e-07 0.0028 0.1066
##
        a44
## 1 0.2778
## 2 0.3684
## 3 0.4483
## 4 0.3431
## 5 0.4318
## 6 0.4872
```

The first three columns are species, site, and year. The data starting in the fourth column contains the transition rates.

To read the data in matrix form you need to get columns 4 to 19 for a given row. For instance, the data for the first row (*M. cardinalis*, population Buckmeadows, year 2000):

```
m1<-matrix(as.numeric(monkeyflower[1,4:19]), byrow=T, nrow=4)
m1</pre>
```

```
[,3]
                                         [,4]
##
              [,1] [,2]
## [1,] 2.128e-01
                      0 2038.0000 9624.0000
## [2,] 2.490e-05
                      0
                            0.0000
                                       0.0000
## [3,] 3.740e-05
                      0
                            0.3529
                                       0.5000
## [4,] 8.310e-07
                      0
                            0.0588
                                       0.2778
```

This produces a 4x4 matrix with 16 transition rates.

And from this you can easily conduct the population matrix analyses. For example to get lambda:

```
lambda(m1)
```

[1] 0.6997406

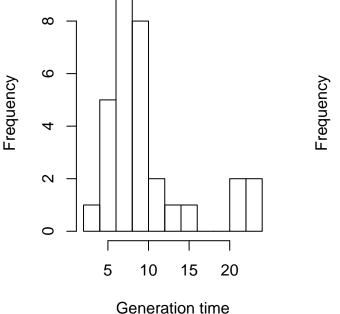
Analysis over multiple matrices

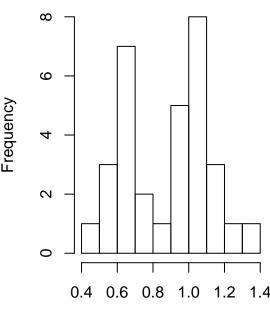
Now you can do loops to analyse the properties of the 31 matrices at once.

```
temp.res<-data.frame(lambda=rep(NA,32), gentime=rep(NA,32))
for(i in 1:32){
   mattemp<-matrix(as.numeric(monkeyflower[i,4:19]), byrow=T, nrow=4)
   temp.res[i,1]<-lambda(mattemp)
   temp.res[i,2]<- generation.time(mattemp)
}
par(mfrow=c(1,2))
hist(temp.res$gentime, breaks=10, main="Generation time", xlab="Generation time")
hist(temp.res$lambda, breaks=10, main="lambda", xlab="lambda")</pre>
```

Generation time

lambda





lambda