StructuredPoplations

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This is how you can access the data on Westslope cutthroat trout including how to access the paper

```
load("COMADRE_v.3.0.0.RData")
comadre$metadata[134,]
```

```
##
                               SpeciesAuthor
  134 Oncorhynchus_clarkii_subsp._lewisi_2
##
                           SpeciesAccepted
                                                          CommonName
## 134 Oncorhynchus clarkii subsp. lewisi Westslope cutthroat trout
##
              Genus
                        Family
                                        Order
                                                       Class
                                                                Phylum Kingdom
## 134 Oncorhynchus Salmonidae Salmoniformes Actinopterygii Chordata Animalia
         OrganismType DicotMonoc AngioGymno
##
                                                      Authors
##
  134 Actinopterygii
                             <NA>
                                        <NA> Spromberg; Birge
##
                                                     DOI.ISBN AdditionalSource
                    Journal YearPublication
##
  134 Environ Toxicol Chem
                                        2005 10.1897/04-160.1
       StudyDuration StudyStart StudyEnd ProjectionInterval NumberPopulations
##
## 134
                <NA>
                           <NA>
                                     <NA>
                                                        FRANK
##
       MatrixCriteriaSize MatrixCriteriaOntogeny MatrixCriteriaAge
## 134
                       No
                                              Yes
##
       MatrixPopulation Lat Lon Altitude Country Continent Ecoregion
## 134
                   <NA> NA NA
                                     <NA>
                                             <NA>
                                                        <NA>
##
       StudiedSex MatrixComposite MatrixTreatment MatrixCaptivity
## 134
                           Pooled
                                     Unmanipulated
##
       MatrixStartYear MatrixStartSeason MatrixStartMonth MatrixEndYear
## 134
                  <NA>
                                     <NA>
                                                                     <NA>
                                                      <NA>
##
       MatrixEndSeason MatrixEndMonth MatrixSplit MatrixFec
## 134
                                  <NA>
                                           Divided
                                                          Yes
                  <NA>
##
## 134 FRANK; Data from literature, standardized elements to allow comparisons, two species used to con
       MatrixDimension SurvivalIssue
## 134
                                 0.25
```

HW Assignment 3

- 1. I chose to study westslope cutthroat trout. I wanted to study trout species because I have experience studying trout life stages and was excited to give some of the observations I have made in the field some mathmatical context.
- 2. Does toxicity affect cutthroat trout differently according to age class?

3.

```
# get the matrix from the data from the cutthroat trout data
matrix <- comadre$mat[134][[1]]$matA

#this gives us our eigen values and vectors
eigen(comadre$mat[134][[1]]$matA)</pre>
```

```
## eigen() decomposition
## $values
## [1]
       1.0864401+0.0000000i -0.0364845+0.9762419i -0.0364845-0.9762419i
## [4] -0.8634711+0.0000000i
##
## $vectors
##
                   [,1]
                                              [,2]
                                                                        [.3]
## [1,] -0.998882798+0i -0.998601986+0.000000000i -0.998601986+0.000000000i
## [2,] -0.045970450+0i 0.001908754+0.051073876i 0.001908754-0.051073876i
## [3,] -0.010578229+0i 0.013042721-0.000976239i 0.013042721+0.000976239i
## [4,] -0.002824054+0i -0.000856759-0.003176372i -0.000856759+0.003176372i
##
                   [,4]
## [1,] -0.998179351+0i
## [2,] 0.057800393+0i
## [3,] -0.016734896+0i
## [4,] 0.004128114+0i
#get the first eigen vector
eigen(comadre$mat[134][[1]]$matA)
## eigen() decomposition
## $values
## [1]
       1.0864401+0.0000000i -0.0364845+0.9762419i -0.0364845-0.9762419i
## [4] -0.8634711+0.0000000i
##
## $vectors
##
                   [,1]
                                              [,2]
                                                                        [,3]
## [1,] -0.998882798+0i -0.998601986+0.000000000i -0.998601986+0.000000000i
## [2,] -0.045970450+0i 0.001908754+0.051073876i 0.001908754-0.051073876i
## [3,] -0.010578229+0i 0.013042721-0.000976239i 0.013042721+0.000976239i
## [4,] -0.002824054+0i -0.000856759-0.003176372i -0.000856759+0.003176372i
##
                   [,4]
## [1,] -0.998179351+0i
## [2,] 0.057800393+0i
## [3,] -0.016734896+0i
## [4,] 0.004128114+0i
eigen1 <- (eigen(comadre$mat[134][[1]]$matA))</pre>
#sum the vector 1
sum(eigen1$vector[,1])
## [1] -1.058256+0i
```

3. I used the eigenvector associated with the dominant eigen value (1.09) to calculate the stable age distribution. To do this, take the sum of the eigen vector and then create a proportion associated with each age class.

```
eigen1$vector[,1]/sum(eigen1$vector[,1])
```

[1] 0.943895656+0i 0.043439839+0i 0.009995912+0i 0.002668594+0i

This means that $\sim 94\%$ of the population is held in stage one- "YOY" young of year trout, and then the age distribution decreases as the age classes get older.

3: Calculating Elacticity

Use the popoio package in R to calculate elasticity which assess the effect of a proportional change in lambda.

```
library(popbio)
elasticity(matrix)
```

add here what elasticity means

3: Calculating Sensitivity- which refers to the rate of change of the eigen values in the context of the rest of the matrix.

sensitivity(matrix)

```
## A1 A2 A3 A4

## [1,] 0.256034 0.01178316 0.002711415 0.0007238624

## [2,] 5.563311 0.25603395 0.058915801 0.0157286624

## [3,] 24.176817 1.11266222 0.256033954 0.0683529983

## [4,] 82.023598 3.77487898 0.868634862 0.2318981382
```

This calculation reveals that changes to the number of YOY individuals exerts the largest change on the eigen value.

Notes about Git note: clone the folder git add git commit 'changes we comited' git status git remote add origin (get origin from the website) git push origin master