Simple outputs from many matrices

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This example produces some basic output such as the population growth rate (λ) and damping ratio (Caswell 2001) for a subset of species and populations given some selection criteria.

First, subset the database to the data of interest: only mean matrices for bony fish from studies of 3 years duration or longer, and with a matrix dimension of 3 or greater.

The row names from the subsetted dataframe can now be used to subset the entire comadre database using the function subsetDB which is available via GitHub (using source_url from devtools to download it).

```
library(devtools)
source_url("https://raw.githubusercontent.com/jonesor/compadreDB/master/Functions/subsetDB.R")
```

SHA-1 hash of file is 1b6085d7b556cf550c8425c76f6078a8e2f59452

```
id <- as.numeric(rownames(tempMetadata))
x<-subsetDB(comadre,id)</pre>
```

The object x is now a version of the **comadre** database object that contains only the matrices that match the search criteria.

These matrices can now be analyzed by applying functions in a loop, or by using lapply.

For example, to calculate population growth rate and damping ratio for the subset of matrices, first create an empty data.frame to accommodate the output

and then use the functions in popbio package to derive demographic output (the user may need to install the package first).

```
library(popbio)
```

> Loading required package: quadprog

```
for (i in 1:length(x$mat)){
   output$lambdas[i] <- Re(eigen(x$mat[[i]]$matA)$value)[1]
   output$damps[i] <- damping.ratio(x$mat[[i]]$matA)
}</pre>
```

To examine the output:

```
output
```

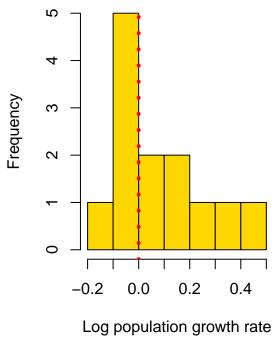
```
>
      lambdas
                 damps
> 1 1.5061504 1.303947
> 2 0.9704512 1.468910
> 3 1.0798558 1.326919
> 4 0.9529318 1.127114
> 5 1.0854466 1.146005
> 6 0.9091956 1.031997
> 7
    0.9027406 1.027850
> 8 0.9140835 1.035914
> 9 0.9999592 1.005268
> 10 1.1102061 1.310725
> 11 1.3618336 1.293028
> 12 1.2283756 1.380559
> 13 1.1321531 1.288657
```

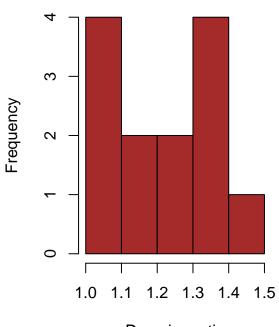
These parameters are presented in the same order as the metadata so we could also add the species name to this data.frame:

data.frame(Species = x\$metadata\$SpeciesAccepted,output)

```
Species
                                         lambdas
                                                     damps
                  Ammocrypta_pellucida 1.5061504 1.303947
> 1
                   Genypterus_blacodes 0.9704512 1.468910
> 2
> 3
                   Genypterus_blacodes 1.0798558 1.326919
> 4
                   Genypterus blacodes 0.9529318 1.127114
                   Genypterus_blacodes 1.0854466 1.146005
> 5
> 6
              Oncorhynchus_tshawytscha 0.9091956 1.031997
              Oncorhynchus_tshawytscha 0.9027406 1.027850
> 7
> 8
              Oncorhynchus_tshawytscha 0.9140835 1.035914
     Sprattus_sprattus_subsp._balticus 0.9999592 1.005268
> 9
> 10
                     Zoarces_viviparus 1.1102061 1.310725
                     Zoarces_viviparus 1.3618336 1.293028
> 11
> 12
                     Zoarces_viviparus 1.2283756 1.380559
> 13
                     Zoarces_viviparus 1.1321531 1.288657
```

Plot the population growth rates and damping ratios derived from these matrices. In this plot, the vertical, dashed red line indicates population growth rate = 1 (or log $(\lambda) = 0$)





Damping ratio