

# Simple outputs from many matrices

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This example produces some basic output such as the population growth rate ( $\lambda$ ) 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.

```
tempMetadata <- subset(comadre$metadata,  
  MatrixComposite == "Mean" &  
  Class == "Actinopterygii" &  
  StudyDuration >= 3 &  
  MatrixDimension > 3)
```

The row names from the subsetting 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)
```

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

```
output <- data.frame(lambdas = rep(NA, length(x$mat)),  
  damps = rep(NA, length(x$mat)))
```

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)  
}
```

To examine the output:

```
output
```

```

>      lambdas      damp
> 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  damp
> 1  Ammocrypta_pellucida 1.5061504 1.303947
> 2   Genypterus_blacodes 0.9704512 1.468910
> 3   Genypterus_blacodes 1.0798558 1.326919
> 4   Genypterus_blacodes 0.9529318 1.127114
> 5   Genypterus_blacodes 1.0854466 1.146005
> 6  Oncorhynchus_tshawytscha 0.9091956 1.031997
> 7  Oncorhynchus_tshawytscha 0.9027406 1.027850
> 8  Oncorhynchus_tshawytscha 0.9140835 1.035914
> 9  Sprattus_sprattus_subsp._balticus 0.9999592 1.005268
> 10   Zoarces_viviparus 1.1102061 1.310725
> 11   Zoarces_viviparus 1.3618336 1.293028
> 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  $\log(\lambda) = 0$ )

```

par(mfrow = c(1,2))
hist(log(output$lambdas),
     xlab = "Log population growth rate",
     col = "gold", main = "")
abline(v=0,col = "red", lwd = 4, lty = 3)
hist(output$damps, xlab = "Damping ratio",
     col = "brown", main = "")

```

