Animal and Plant Matrix Database

About the project

Compadre and Comadre are two open-access data bases that contain matrix population models of 695 plant and 405 animals species. The project was initiated in 1989 by Jonathan Silvertown and Miguel Franco, who started to collect plant matrices from publications. The animal part was later added by by Rob Salguero-Gomez in 2011. The project is currently hosted at the the Max Planck Institute for Demographic Research in Rostock (Germany) and supervised and updated by a team composed of three commitees (for more information, see their webpage). The data are freely availabe when properly referenced.

Database

The data bases are separated, with one containing plants (Compadre) and the other animals (Comadre). This short tutorial focuses on Comadre; but both databases are sructured very similarly. There are currently 508 studies (from 508) different animal species in Comadre, which results in a total of 1927 population matrix models. All files are part of one single R file (.Rdata), which can be easily downloaded and imported into R (R file. A much more detailed user guide is further provided on the webpage (user guide).

```
### import
load("COMADRE_v.2.0.1.RData")
##
summary(comadre)

##             Length Class      Mode
## metadata        50   data.frame list
## matrixClass   1927   -none-     list
## mat           1927   -none-     list
## version          6   -none-     list

#########
```

The comadre file consists of 4 different elements. The list 'version', as the name suggests, contains information about the current version of the file, while the lists 'mat' and 'matClass' contain the actual matrices and information about the matrices respectively (see more below).
The 'metadata' table details all the information associated with the study the data originated from. Each line in the file corresponds to a single matrix population model. A single study can have several matrix population models (for example for different seasons, and/or populations) and therefore several lines in the metadata table. The following list gives all the columns contained in 'metadata'.

```
names(comadre$metadata)

##  [1] "SpeciesAuthor"          "SpeciesAccepted"
##  [3] "CommonName"             "CoLCheckOK"
##  [5] "CoLCheckDate"           "Infraspecific"
##  [7] "SpeciesEpithetAccepted" "GenusAccepted"
##  [9] "GenusAuthor"            "Family"
## [11] "Order"                  "Class"
## [13] "Phylum"                 "Kingdom"
## [15] "OrganismType"           "Authors"
## [17] "Journal"                "YearPublication"
## [19] "DOI.ISBN"               "AdditionalSource"
## [21] "StudyDuration"          "StudyStart"
## [23] "StudyEnd"               "AnnualPeriodicity"
## [25] "NumberPopulations"      "MatrixCriteriaSize"
## [27] "MatrixCriteriaOntogeny" "MatrixCriteriaAge"
## [29] "MatrixPopulation"       "Lat"
## [31] "Lon"                    "Altitude"
## [33] "Country"                "Continent"
## [35] "Ecoregion"              "StudiedSex"
```

```
## [37] "MatrixComposite"       "MatrixTreatment"
## [39] "MatrixCaptivity"        "MatrixStartYear"
## [41] "MatrixStartSeason"      "MatrixStartMonth"
## [43] "MatrixEndYear"          "MatrixEndSeason"
## [45] "MatrixEndMonth"         "MatrixSplit"
## [47] "MatrixFec"              "Observation"
## [49] "MatrixDimension"        "SurvivalIssue"
```

The majority of the columns in the metadata table provide basic information about the study, including the study species, by whom it was conducted and published and if available further details, such as the duration of the study, the number of populations, where the data was collected, whether there were experimental manipulations and so on. A detailed list with descriptions for each column can be found in the detailed user guide.

Many of the columns are self-explanatory. The next few paragraphs focus on the columns that are are essential to understand the matrix popolution model and are therefore explained in more detail:

AnnualPeriodicity Indicates the time frame for which the seasonal or annual the MPM was constructed. One represents an iteration period of 1 year, while 2 would mean two iterations per year and 0.5 consequently an iteration every 2 years.

MatrixCriteriaSize Are the states in the matrix population model size dependent? (Yes or No)

MatrixCriteriaOntogeny Are the states in the matrix population model based on development (for example, juvenile, reproductive etc) dependent? (Yes or No)

MatrixCriteriaAge Are the states in the matrix population model based on age? (Yes or No)

StudiedSex Sex that was studied (A=All sexes analysed together, F=Females, M=Males, F/M=Males and Females separately analysed in the same model, H = hermaphrodites)

MatrixComposite Type of matrix population model (individual: single study at one population over one time period; mean: mean of population matrices across several time periods ; pooled: a model that was constructed by pooling information across popoulations or time periods; seasonal: seasonal matrix population models (less than a year)

MatrixSplit Has the matrix been divided into submatrices (survival:nU), fecundity (sexual reproduction: F, asexual reproduction: C). (Yes or No)

MatrixFec Was fecundity measured? (Yes or No)

Example

In the following one example is illustrated (line 983). The study is (among other species) about wild coyote and was conducted by [Lawler and Schumaker, 2004].

```
##      SpeciesAccepted CommonName AnnualPeriodicity NumberPopulations
## 983   Canis_latrans     Coyote                 1                 1
##      MatrixCriteriaSize MatrixCriteriaOntogeny MatrixCriteriaAge StudiedSex
## 983                  No                     No               Yes          F
##      MatrixComposite MatrixSplit MatrixFec
## 983           Pooled     Divided       Yes
```

We see, that the periodicity is 1 year and that it is an age-structured matrix population model, that describes the female part of a population. The data was pooled over several years and data about fecundity were collected and also given separately (MatrixSplit=Divided,MatrixFec=Yes).

The element matrixClass gives the different states that were used in the Matrix Population model. The model only had two stages, Juveniles and Adults (see below). The column MatrixClassOrganized details whether the states were spore-like (propagule),dormant, or active, with the latter being the case here. Spores and dormant states (seeds for example) are more commonly found in plant matrix population models, or models with microorganisms. The MatrixClassNumber simply is a numerical representation of the states in the population matrix model.

```
comadre$matrixClass[983]

## [[1]]
##      MatrixClassOrganized MatrixClassAuthor MatrixClassNumber
## 7294               active         Juveniles                 1
## 7295               active            Adults                 2
```

The following shows the matrix population model (A) for the coyote study. U represents the survival matrix and F the fecundity matrix.

```
comadre$mat[983]

## [[1]]
## [[1]]$matA
##        A1   A2
## [1,] 0.00 2.80
## [2,] 0.29 0.61
##
## [[1]]$matU
##        U1   U2
## [1,] 0.00 0.00
## [2,] 0.29 0.61
##
## [[1]]$matF
##      F1  F2
## [1,]  0 2.8
## [2,]  0 0.0
##
## [[1]]$matC
##      C1 C2
## [1,]  0  0
## [2,]  0  0
```

References

M. P. I. for Demographic Research (Germany). Comadre animal matrix database. (data downloaded on 01.03.2019, version 4.0.1), a. URL www.comadre-db.org.

M. P. I. for Demographic Research (Germany). Compadre animal matrix database, b. URL www.compadre-db.org.

J. J. Lawler and N. H. Schumaker. Evaluating habitat as a surrogate for population viability using a spatially explicit population model. *Environmental Monitoring and Assessment*, 94(1):85–100, Jun 2004. ISSN 1573-2959. doi: 10.1023/B: EMAS.0000016881.12925.b1. URL https://doi.org/10.1023/B:EMAS.0000016881.12925.b1.