

# Analysing the COMPADRE database using R

*Mario Vallejo-Marin*

*March 15 2017*

## Contents

<b>The COMPADRE database</b>	<b>1</b>
Downloading and reading the data in R . . . . .	1
Data analysis . . . . .	2

## The COMPADRE database

Is a compilation of plant population matrices. See [www.compadre-db.org](http://www.compadre-db.org). Currently it has 7,024 population matrices for thousands of species.

### Downloading and reading the data in R

You can download the data from the website. The database is in R format. Save it to your computer, within the working environment of R, so you can then load it and analyse it.

```
load(file="COMPADRE_v.4.0.1.RData")
```

This will result in a database object called `compadre`. It is a big file of about 45Mb.

The dataframe is arranged in a series of nested levels. At the highest level it has the following components:

```
summary(compadre)
```

```
##           Length Class      Mode
## metadata      47  data.frame list
## matrixClass 7024  -none-     list
## mat          7024  -none-     list
## version        6  -none-     list
```

The `metadata` section contains 47 variables. For a detailed description of the meaning of each of them see the user manual, which is available [here](#).

Accessing the elements of `compadre` can be done using the operator `$`, just as you would do to access the columns of a simple data base.

```
names(compadre$metadata)
```

```
## [1] "SpeciesAuthor"      "SpeciesAccepted"
## [3] "CommonName"         "Genus"
## [5] "Family"             "Order"
## [7] "Class"              "Phylum"
## [9] "Kingdom"            "OrganismType"
## [11] "DicotMonoc"         "AngioGymno"
## [13] "Authors"            "Journal"
## [15] "YearPublication"    "DOI.ISBN"
## [17] "AdditionalSource"    "StudyDuration"
## [19] "StudyStart"         "StudyEnd"
```

```
## [21] "AnnualPeriodicity"      "NumberPopulations"
## [23] "MatrixCriteriaSize"     "MatrixCriteriaOntogeny"
## [25] "MatrixCriteriaAge"      "MatrixPopulation"
## [27] "Lat"                    "Lon"
## [29] "Altitude"              "Country"
## [31] "Continent"             "Ecoregion"
## [33] "StudiedSex"            "MatrixComposite"
## [35] "MatrixTreatment"       "MatrixCaptivity"
## [37] "MatrixStartYear"       "MatrixStartSeason"
## [39] "MatrixStartMonth"      "MatrixEndYear"
## [41] "MatrixEndSeason"       "MatrixEndMonth"
## [43] "MatrixSplit"           "MatrixFec"
## [45] "Observation"           "MatrixDimension"
## [47] "SurvivalIssue"
```

With a bit of tweaking you can interrogate the database to obtain specific information. For example, to find out how many genera are included in the data base you can do:

```
length(levels(as.factor(compadre$metadata$Genus)))
```

```
## [1] 444
```

And you can print the first ten genera in this list:

```
levels(as.factor(compadre$metadata$Genus))[1:10]
```

```
## [1] "Abies"      "Abutilon"   "Acacia"     "Acer"
## [5] "Achillea"   "Aconitum"   "Actaea"     "Actinostemon"
## [9] "Adenocarpus" "Adenophora"
```

## Data analysis

You can analyse subsets of the data using this general approach:

```
#Subset the dataframe by Genus
mimulus.data<-subset(compadre$metadata, Genus=="Mimulus")
#Row numbers for the data containing Mimulus
keep<-as.numeric(rownames(mimulus.data))
#Subsets the matrices using the "keep" list
mat.mimulus<-compadre$mat[keep]
#This is a list of 36 matrices, which can be accessed using indices
mat.mimulus[[1]]
```

```
## $matA
##           A1           A2           A3           A4
## [1,] 1.972500e-01 938.25000000 9069.0833333 1.322798e+05
## [2,] 3.978583e-05  0.06633333  0.0244500 6.333333e-04
## [3,] 2.722000e-05  0.08722500  0.3366333 2.182167e-01
## [4,] 3.719167e-07  0.01748333  0.1384917 5.829917e-01
##
## $matU
##           U1           U2           U3           U4
## [1,] 1.972500e-01 0.00000000 0.0000000 0.0000000000
## [2,] 3.978583e-05 0.06633333 0.0244500 0.0006333333
## [3,] 2.722000e-05 0.08722500 0.3366333 0.2182166667
## [4,] 3.719167e-07 0.01748333 0.1384917 0.5829916667
```

```
##
## $matF
##      F1      F2      F3      F4
## [1,] 0 938.25 9069.083 132279.8
## [2,] 0  0.00  0.000  0.0
## [3,] 0  0.00  0.000  0.0
## [4,] 0  0.00  0.000  0.0
##
## $matC
##      C1 C2 C3 C4
## [1,] 0 0 0 0
## [2,] 0 0 0 0
## [3,] 0 0 0 0
## [4,] 0 0 0 0
```

```
#And you can subset them further:
mat.mimulus[[1]]$matC
```

```
##      C1 C2 C3 C4
## [1,] 0 0 0 0
## [2,] 0 0 0 0
## [3,] 0 0 0 0
## [4,] 0 0 0 0
```

```
sum(mat.mimulus[[1]]$matC)
```

```
## [1] 0
```

Now things more exciting, as we are ready to conduct analyses at a massive scale.

```
clonal.flag<-numeric()
```

```
#Loop to identify which matC entries are >0; i.e., have some measure of clonality
# Excludes indivisible matrices "NA"
n<-length(compadre$metadata$SpeciesAuthor)
```

```
for(i in 1:n){
  sum.matC<-sum(compadre$mat[[i]]$matC)
  # print(clonal.flag)
  if(!is.na(sum.matC) & sum.matC > 0) {
    clonal.flag<-c(clonal.flag,i)
    #print(cbind(i, clonal.flag))
  }
}
```

```
#List of species with matC > 0
compadre$metadata$SpeciesAccepted[clonal.flag][1:10]
```

```
## [1] "Murdannia nudiflora" "Murdannia nudiflora"
## [3] "Murdannia nudiflora" "Murdannia nudiflora"
## [5] "Hylocomium splendens" "Hylocomium splendens"
## [7] "Aspasia principissa" "Heteropsis flexuosa"
## [9] "Heteropsis macrophylla" "Heteropsis oblongifolia"
```

```
length(compadre$metadata$SpeciesAccepted[clonal.flag])
```

```
## [1] 816
```

```
levels(as.factor(compadre$metadata$SpeciesAccepted[clonal.flag]))[1:10]
```

```
## [1] "Aechmea magdalenae"      "Aechmea nudicaulis"
## [3] "Allium tricoccum"        "Anthericum liliago"
## [5] "Anthericum ramosum"      "Arctophila fulva"
## [7] "Arnica angustifolia"     "Asarum canadense"
## [9] "Aspasia principissa"    "Astrocaryum aculeatissimum"
```

For example, to calculate lambda:

```
#Calculate lambda for all clonal species:
```

```
require(popbio)
```

```
## Loading required package: popbio
```

```
n<-length(compadre$metadata$SpeciesAccepted[clonal.flag])
```

```
lambda.A<-rep(NA,n)
```

```
for(i in 1:n){
  tryCatch({ #Avoids error message due to missing values in x
    lambda.A[i]<-lambda(compadre$mat[[i]]$matA)
  }, error=function(e){})
}
sort(round(lambda.A,3))
```

```
## [1] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## [9] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## [17] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## [25] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.010
## [33] 0.020 0.040 0.042 0.050 0.050 0.050 0.050 0.050 0.050
## [41] 0.055 0.060 0.060 0.060 0.070 0.087 0.088 0.110
## [49] 0.117 0.211 0.220 0.228 0.230 0.246 0.250 0.266
## [57] 0.270 0.270 0.276 0.276 0.281 0.294 0.331 0.332
## [65] 0.351 0.381 0.409 0.410 0.430 0.430 0.430 0.430
## [73] 0.438 0.443 0.460 0.461 0.462 0.462 0.466 0.471
## [81] 0.493 0.507 0.510 0.513 0.528 0.537 0.553 0.556
## [89] 0.565 0.568 0.577 0.600 0.610 0.623 0.625 0.630
## [97] 0.630 0.630 0.633 0.644 0.674 0.676 0.678 0.680
## [105] 0.687 0.688 0.692 0.694 0.699 0.700 0.708 0.710
## [113] 0.713 0.713 0.714 0.714 0.714 0.714 0.714 0.714
## [121] 0.714 0.714 0.721 0.724 0.729 0.731 0.733 0.736
## [129] 0.740 0.743 0.748 0.749 0.750 0.751 0.753 0.754
## [137] 0.754 0.757 0.758 0.764 0.767 0.769 0.781 0.781
## [145] 0.782 0.784 0.786 0.787 0.787 0.787 0.798 0.802
## [153] 0.803 0.809 0.810 0.810 0.810 0.810 0.813 0.815
## [161] 0.819 0.819 0.822 0.822 0.823 0.823 0.824 0.826
## [169] 0.827 0.830 0.836 0.836 0.838 0.840 0.843 0.845
## [177] 0.847 0.848 0.849 0.852 0.853 0.856 0.858 0.859
## [185] 0.860 0.860 0.861 0.863 0.868 0.868 0.869 0.871
## [193] 0.874 0.875 0.876 0.877 0.877 0.878 0.881 0.882
## [201] 0.882 0.883 0.885 0.888 0.890 0.892 0.893 0.894
## [209] 0.895 0.896 0.897 0.901 0.902 0.902 0.906 0.906
## [217] 0.907 0.909 0.912 0.912 0.913 0.913 0.915 0.918
## [225] 0.920 0.920 0.921 0.922 0.923 0.923 0.926 0.926
## [233] 0.926 0.927 0.927 0.927 0.927 0.927 0.927 0.927
## [241] 0.927 0.927 0.927 0.927 0.927 0.927 0.927 0.927
```

## [249]	0.927	0.927	0.927	0.928	0.928	0.928	0.929	0.932
## [257]	0.933	0.933	0.933	0.934	0.934	0.934	0.934	0.934
## [265]	0.935	0.936	0.937	0.939	0.941	0.941	0.941	0.942
## [273]	0.944	0.946	0.946	0.947	0.948	0.948	0.949	0.949
## [281]	0.950	0.950	0.950	0.950	0.952	0.953	0.953	0.955
## [289]	0.955	0.956	0.957	0.958	0.959	0.960	0.960	0.960
## [297]	0.961	0.962	0.964	0.964	0.965	0.965	0.965	0.966
## [305]	0.966	0.967	0.967	0.968	0.969	0.969	0.970	0.970
## [313]	0.972	0.973	0.974	0.974	0.974	0.975	0.975	0.976
## [321]	0.976	0.976	0.977	0.977	0.978	0.978	0.979	0.980
## [329]	0.980	0.981	0.981	0.983	0.983	0.984	0.984	0.985
## [337]	0.986	0.986	0.986	0.987	0.987	0.989	0.989	0.989
## [345]	0.990	0.990	0.990	0.990	0.991	0.991	0.991	0.991
## [353]	0.992	0.994	0.994	0.994	0.995	0.996	0.998	0.998
## [361]	0.999	0.999	0.999	0.999	0.999	0.999	0.999	1.000
## [369]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
## [377]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
## [385]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
## [393]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
## [401]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
## [409]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
## [417]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
## [425]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
## [433]	1.000	1.000	1.001	1.001	1.002	1.002	1.003	1.003
## [441]	1.004	1.004	1.004	1.005	1.005	1.006	1.007	1.007
## [449]	1.007	1.008	1.009	1.009	1.009	1.010	1.010	1.010
## [457]	1.011	1.011	1.011	1.011	1.014	1.014	1.014	1.016
## [465]	1.017	1.018	1.019	1.019	1.019	1.020	1.021	1.021
## [473]	1.024	1.024	1.025	1.025	1.025	1.026	1.026	1.027
## [481]	1.029	1.029	1.030	1.030	1.031	1.032	1.032	1.033
## [489]	1.033	1.034	1.034	1.034	1.035	1.036	1.036	1.036
## [497]	1.037	1.037	1.038	1.038	1.038	1.038	1.039	1.040
## [505]	1.040	1.040	1.043	1.043	1.043	1.043	1.043	1.043
## [513]	1.044	1.044	1.044	1.045	1.045	1.045	1.046	1.048
## [521]	1.049	1.049	1.049	1.050	1.051	1.051	1.052	1.053
## [529]	1.053	1.054	1.056	1.057	1.060	1.062	1.064	1.064
## [537]	1.065	1.066	1.066	1.066	1.067	1.068	1.068	1.069
## [545]	1.072	1.073	1.075	1.076	1.076	1.078	1.078	1.078
## [553]	1.078	1.080	1.081	1.085	1.086	1.087	1.088	1.090
## [561]	1.091	1.091	1.092	1.093	1.094	1.096	1.096	1.096
## [569]	1.097	1.099	1.100	1.101	1.101	1.102	1.104	1.104
## [577]	1.105	1.105	1.109	1.114	1.114	1.116	1.117	1.118
## [585]	1.120	1.121	1.121	1.122	1.124	1.125	1.126	1.127
## [593]	1.130	1.130	1.132	1.133	1.133	1.134	1.136	1.138
## [601]	1.141	1.144	1.149	1.149	1.150	1.153	1.154	1.155
## [609]	1.156	1.156	1.159	1.160	1.163	1.163	1.164	1.167
## [617]	1.167	1.169	1.169	1.171	1.172	1.173	1.173	1.175
## [625]	1.181	1.181	1.181	1.184	1.184	1.189	1.191	1.192
## [633]	1.194	1.194	1.195	1.199	1.199	1.201	1.215	1.217
## [641]	1.219	1.224	1.225	1.231	1.231	1.232	1.232	1.237
## [649]	1.238	1.243	1.247	1.249	1.252	1.254	1.256	1.258
## [657]	1.259	1.262	1.263	1.270	1.278	1.282	1.284	1.284
## [665]	1.299	1.303	1.305	1.306	1.310	1.310	1.318	1.324
## [673]	1.334	1.339	1.340	1.354	1.357	1.359	1.365	1.366

```
## [681]  1.372  1.375  1.375  1.375  1.376  1.377  1.381  1.388
## [689]  1.394  1.400  1.404  1.408  1.409  1.410  1.412  1.415
## [697]  1.418  1.425  1.439  1.451  1.471  1.478  1.478  1.480
## [705]  1.489  1.496  1.540  1.553  1.567  1.576  1.588  1.620
## [713]  1.673  1.679  1.683  1.683  1.685  1.686  1.689  1.703
## [721]  1.737  1.761  1.774  1.793  1.804  1.810  1.813  1.823
## [729]  1.832  1.860  1.867  1.906  1.907  1.925  1.976  2.003
## [737]  2.036  2.054  2.085  2.111  2.116  2.116  2.154  2.168
## [745]  2.225  2.227  2.264  2.289  2.293  2.300  2.380  2.494
## [753]  2.558  2.564  2.614  2.658  2.679  2.702  2.723  2.723
## [761]  2.739  2.744  2.810  2.946  2.963  3.058  3.097  3.124
## [769]  3.124  3.161  3.175  3.199  3.220  3.275  3.278  3.293
## [777]  3.509  3.592  3.613  3.631  3.731  3.829  4.028  4.134
## [785]  4.134  4.134  4.134  4.137  4.309  4.581  5.162  5.341
## [793]  5.399  5.748  5.755  5.789  6.329  6.537  7.088  7.682
## [801]  7.774  7.900  8.119 10.112 10.262 16.451 17.242 39.363
## [809] 43.321 46.854 48.744 53.362 238.061 272.359 320.544
```

```
hist(lambda.A, breaks="fd", xlim=c(0,7), col="black") #Omits from the plot all values of lambda>7
```

**Histogram of lambda.A**

