

# Running the CoevoMutAntag simulations

*Lucas Arantes Camacho*

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## Introduction

This is a guide to show step-by-step how to run the coevolution simulations in mutualistic networks with exploitation interactions inserted. You will see that the process use different functions from the *R/functions* folder depending on what we wanna do in our scripts (which are saved in the *R/scripts* folder). Also, you will see that the scripts base structure have a organization pattern which helps in the understanding of the code steps in the specific function that it's being realized.

## Basic structure

We start setting our work directory that must contain the *.txt* file with the empirical matrices that you interested in work with. Also, we gonna load some packages and functions that we gonna need in our script. Remember of install the required packages before runing the script.

```
# loading packages and functions
setwd("~/Dropbox/Master/Code/coevo_mut_antag/R/scripts/")

library(ggplot2)
library(reshape2)
library(cowplot)

source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/Antagonize.R")
source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/Counting.R")
source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/FindInteractors.R")
source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/SpDegree.R")
source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/CoevoMutAntNet.R")
```

Ok, we have our packages and functions. Now we can think about the matrix we wanna work with. In this example I will construct a fully connected bipartite adjacency matrix. If you wanna run the scripts with a empirical data matrix just read the matrix with *read.table* function and remember of use the *Square.Matrix* (provided in the *R/functions* folder) if you have a retangular matrix.

Let's first define our antprob value ( $p$ ) which is the probability of the elements from our mutualistic matrix  $M$  pass from mutualism to exploitation. Also, let's construct our  $M$  matrix defining the number of species (animals + plants) that we wanna in our matrix. It's important to note that we are not interested in intraespecific interactions so diagonal of  $M$  is zeroed.

```
# initial parameters
antprob = 0.8 # current probability value
n_sp = 10 # defining number of species
M = matrix(1, ncol = n_sp, nrow = n_sp) # building matrix M
diag(M) = 0 # no intraespecific interactions
```

We already have our adjacency matrix  $M$  of positive effects. Now let's apply our first function in the  $M$  matrix: Antagonize. This function creates the  $V$  matrix and transform positive in negative effects follow the antprob value. The functions return the  $M$  and  $V$  matrices as a list which is used to define  $M$  and  $V$  to the next step.

```
# Antagonize M (transform positive links in negative)
antagonize = Antagonize(M, antprob)
M = antagonize[[1]]
V = antagonize[[2]]
```

We have the two layers of our initial matrix, the positive effects layer matrix  $M$  and negative effects layer matrix  $V$ . With those matrices in hand, we can apply some functions to get some informations about the numbers of different outcomes interactions in the community and how much each species are interaction with mutualists or exploiters. Let's apply three functions: Counting, FindInteractors and SpDegree. The Counting functions first:

```
c = Counting(M, V)
c

## [[1]]
## [1] 0
##
## [[2]]
## [1] 39
##
## [[3]]
## [1] 6
```

The Counting function provides the counting of the number of interaction in our adjacency matrix after the Antagonize process. You see a list with three values: [1] number of double negative effects which are not the focus of this work and never reproduced by the Antagonize function, [2] number of exploitation interactions and [3] number of mutualism interactions. Useful to do some consistency tests about the frequency of interaction in the network. Next function, the FindInteractors:

```
f = FindInteractors(M, V)
f

## [[1]]
## integer(0)
##
```

```
## [[2]]
## [1] 1 2 3 4 5 6 7 8 9 10
##
## [[3]]
## [1] 1 3 4 5 6 7 9 10
```

The FindInteractors function provides a list with the identity of species that has mutualism and/or exploitation interactions in the community. Due to the way Antagonize works, a single species could be in the exploiters group [[2]] and mutualism group [[3]] at the same time. Usefull when we wanna separate species in groups depending on the interaction they have. Finally, the last function before we run the coevolution process, the SpDegree:

```
sp = SpDegree(M, V)
sp
```

```
##      AA AM MM
## 1    0  7  2
## 2    0  9  0
## 3    0  7  2
## 4    0  8  1
## 5    0  7  2
## 6    0  8  1
## 7    0  8  1
## 8    0  9  0
## 9    0  8  1
## 10   0  7  2
```

The SpDegree function just count the interactions of each species separating by type. With that we could know how much each species have of double negative (AA, but not considered in this paper), AM as exploitation and MM as mutualisms. Usefull to idenfify assimetrys of interactions between species.

Ok, until now we just explore our matrices of interaction. Let's work with coevolution know. First, let's define our coevolution model parameters

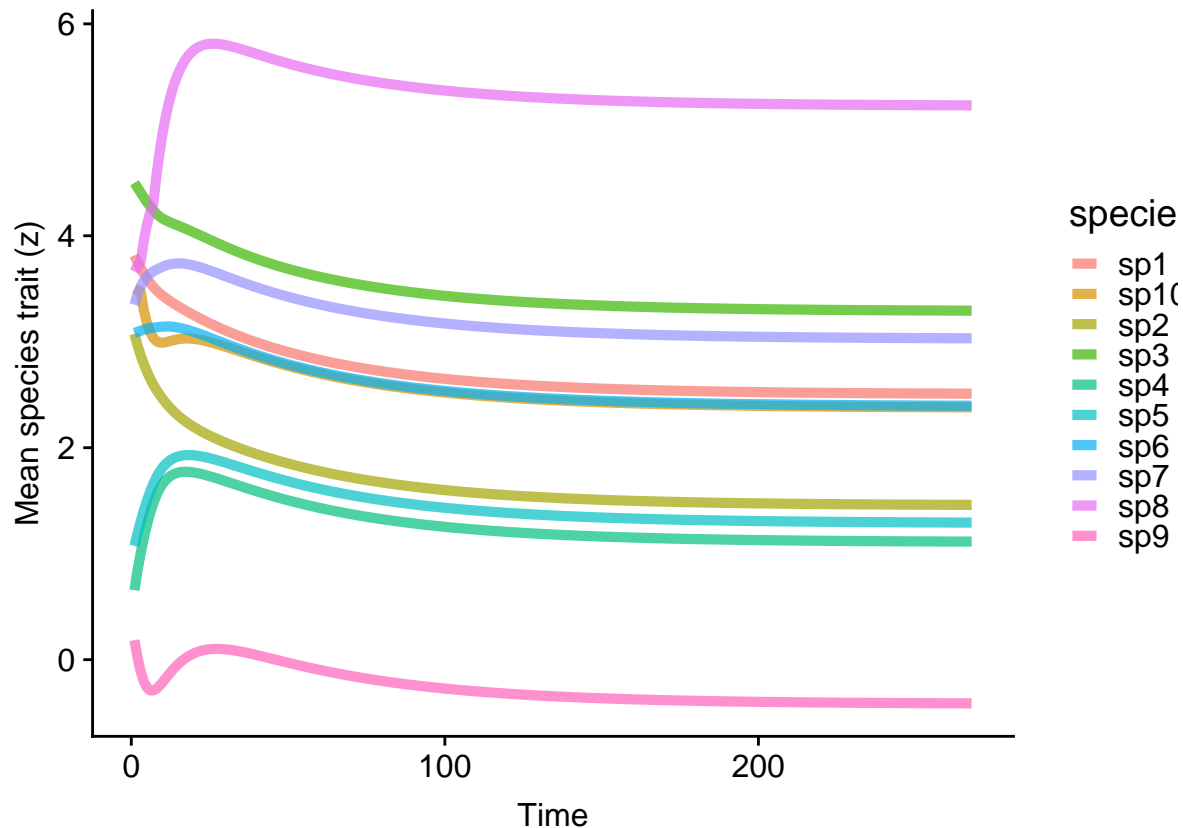
```
# coevolutionary model parameters
phi = 0.2
alpha = 0.2
theta = runif(n_sp, 0, 5)
init = runif(n_sp, 0, 5)
p = 0.1
epsilon = 3
eq_dif = 0.0001
t_max = 1000
```

After that we gonna use the last (and maybe most important) function that we load in the beggining of this tutorial: the CoevoMutAntNet which runs the coevolution process in the community. You can understand the functioning of this function in the file Guide\_CoevoMutAntag

from my GitHub account.

```
# running coevolution simulation
z_mat = CoevoMutAntNet(n_sp, M, V, phi, alpha, theta, init, p, epsilon,
                      eq_dif, t_max)
```

The CoevoMutAntNet function provides an final matrix here called `z_mat` which has the species in the collums and the timesteps in the rows which each element of this matrix shows the trait values of species. With this matrix we can plot the species traits in time using the `reshape2`, `ggplot2` and `cowplot` packages to help us. This is the end of the script.



## Full code

Heres is the full code that we detailed in the section above. That's the script-base of all other scripts that we have in the *R/scripts* folder, this one in particular called `Basic_Traits.R`. See the code and comments organization and how the functions are called with new *M* and *V* matrices created from functions like `Antagonize`.

```
# Basic script to test the R base-functions to simulate the coevolutionary process
# of networks with positive and negative interactions outcomes.
# This script returns a simple graph with species traits changing in time.

# loading packages and functions
setwd("~/Dropbox/Master/Code/coevo_mut_antag/R/scripts/")
```

```

library(ggplot2)
library(reshape2)
library(cowplot)

source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/Antagonize.R")
source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/Counting.R")
source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/FindInteractors.R")
source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/SpDegree.R")
source("~/Dropbox/Master/Code/coevo_mut_antag/R/functions/CoevoMutAntNet.R")

# initial parameters
antprob = 0.8 # current probability value
n_sp = 10 # defining number of species
M = matrix(1, ncol = n_sp, nrow = n_sp) # building matrix M
diag(M) = 0 # no intraespecific interactions

# Antagonize M (transform positive links in negative)
antagonize = Antagonize(M, antprob)
M = antagonize[[1]]
V = antagonize[[2]]

# Count the number of mutualism and exploitation in network
c = Counting(M, V)
c

# Which species are having the mutualism and exploitation?
f = FindInteractors
f

# Degree of each species separated by the interaction outcome
sp = SpDegree(M, V)
sp

# coevolutionary model parameters
phi = 0.2
alpha = 0.2
theta = runif(n_sp, 0, 5)
init = runif(n_sp, 0, 5)
p = 0.1
epsilon = 3
eq_dif = 0.0001
t_max = 1000

# running coevolution simulation

```

```

z_mat = CoevoMutAntNet(n_sp, M, V, phi, alpha, theta, init, p, epsilon,
                      eq_dif, t_max)

# building data frame to plot the results
traits = as.data.frame(traits)
n_sp = ncol(traits)
traits_vec = c(as.matrix(traits))
traits_df = data.frame(species = rep(paste("sp", 1:n_sp, sep = ""),
                                     each = nrow(traits)),
                      time = rep(1:nrow(traits), times = n_sp),
                      trait = traits_vec)

# plotting traits through time
plotar = ggplot(traits_df, aes(x = time, y = trait, color = species)) +
  geom_path(size = 1.8, alpha = 0.7) +
  xlab("Time") +
  ylab("Mean species trait (z)") +
  theme(axis.text.x = element_text(size = 12),
        axis.text.y = element_text(size = 12),
        axis.title = element_text(size = 12),
        legend.key.size = unit(0.4, "cm"),
        legend.text = element_text(size = 12))

```

## Final considerations

You will see that the scripts used in this paper are just variations of this script-base structure that I show in this small tutorial. For example you could use the CentralAntagonize instead of Antagonize to transform only the central mutualistic species in exploiters or use some of the ConDep functions to considerer the temporal variation of species interactions and their influence on coevolution.

Finally, if you have some doubts or suggestions please let me know in [lucas.camacho@usp.br](mailto:lucas.camacho@usp.br).

Good bye.