

demoniche

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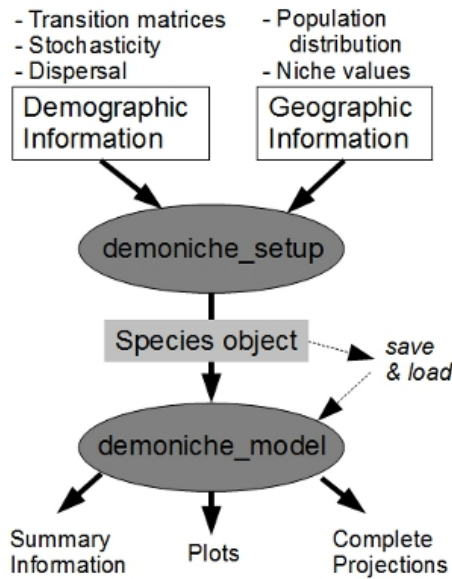


Figure 1: Simplified schema of the demoniche framework. First the user enters demographic and geographic information into the setup function. The model function runs the demographic modelling on the species object.

1 Introduction

demoniche is a freely available R-package to simulate stochastic population growth for various subpopulations of a species. Demographic models projects population sizes with various transition matrices that represent demographic impacts on species growth. The Demographic modelling is linked to a time series of geographically distributed 'Niche values' that also affect species growth. The demoniche model offers flexible options for stochasticity, density dependence and dispersal. With the demoniche package it is possible to investigate population sizes, extinction probabilities and range shift of a species influenced by scenarios of environmental and human impacts.

The **demoniche** package is offered without any guarantees, and we encourage users to examine the code to learn what is modelled, and to adapt it to their own needs. The annotated code can be found when browsing the Subversion repository on R-forge (under SCM)

The main steps to running a model are as follows:

- Load or write the information (demographical, geographical) of the species that is being modelled
- Create a species object with **demoniche_setup** function, which contains all the information about the species
- Run the **demoniche_model** function on the species object
- Analyse the results

2 How to use demoniche

First install R. We also recommend that users are familiar with the R environment. This can be gained from, for example www.cran.r-project.org, where the program can be downloaded too.

2.1 Install the package

To install the *demoniche* package please type `install.packages("demoniche", repos="http://R-Forge.R-project.org")` in R. Or go to the webpage <http://demoniche.r-forge.r-project.org/> and follow the directions. The package and manual are often updated, so please download an updated package often.

The *demoniche* package depends on functions and data from three other packages; *popbio*, *lattice* and *sp* that are available from CRAN. They should install automatically, please do it manually if not.

Set the working directory, and then load the package. This makes the two main functions *demoniche_model* and *demoniche_setup* available (Figure 1). The *demoniche_model* function runs two internal functions, *demoniche_population* that carries out demographic modelling in each population and year, and *demoniche_dispersal* that calculates the dispersal if selected.

```
> library(demoniche)
```

The code used in this manual is also provided in the *demoniche_manual.R* script in the `/doc` folder where the package is saved, normally this is at `C:\Program Files\R\R-2.13.0\library` in Windows, or a similar location.

2.2 Loading data supplied with package

We load the example data file supplied in the package. The object is called *Hmontana* and contains demographic and geographic data about Mountain Goldenheater *Hudsonia montana* (Gross et al. 1998). We can inspect the object with `str()`. We find that *Hmontana* is a list with 26 items. We can examine separate items of the list using `$`. This object contains all the information needed about the species to carry out modelling.

```
> data(Hmontana)
```

```
> str(Hmontana)
```

List of 27

```
$ Orig_Populations      : 'data.frame':      34 obs. of  4 variables:
..$ PatchID            : int [1:34] 8000 8001 8002 8003 8004 8005 8006 8007 8008 8009 ...
..$ XCOORD             : int [1:34] 2 3 6 7 9 11 12 17 18 19 ...
..$ YCOORD             : int [1:34] 29 29 29 29 29 29 29 29 29 29 ...
..$ area_population: int [1:34] 2 2 2 2 2 2 2 2 2 2 ...
$ Niche_ID              : 'data.frame':      900 obs. of  4 variables:
..$ Niche_ID           : int [1:900] 5000 5001 5002 5003 5004 5005 5006 5007 5008 5009 ...
..$ X                  : int [1:900] 1 2 3 4 5 6 7 8 9 10 ...
..$ Y                  : int [1:900] 1 1 1 1 1 1 1 1 1 1 ...
..$ PopulationID: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
$ Niche_values          : 'data.frame':      900 obs. of  9 variables:
..$ period2000: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
..$ period2010: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
..$ period2020: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
..$ period2030: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
..$ period2040: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
..$ period2050: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
..$ period2060: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
```

```

..$ period2070: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
..$ period2080: num [1:900] 0 0 0 0 0 0 0 0 0 0 ...
$ years_projections      : chr [1:9] "period2000" "period2010" "period2020" "period2030" ...
$ matrices               : num [1:36, 1:5] 0.4995 0.0004 0 0 0 ...
..- attr(*, "dimnames")=List of 2
.. ..$ : NULL
.. ..$ : chr [1:5] "Reference_matrix" "Mx1" "Mx2" "Mx3" ...
$ matrices_var           : num [1:36, 1] 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 ...
..- attr(*, "dimnames")=List of 2
.. ..$ : NULL
.. ..$ : chr "sd"
$ prob_scenario          : num [1:2] 0.5 0.5
$ noise                  : num 0.95
$ stages                 : chr [1:6] "seed" "seedlings" "tiny" "small" ...
$ proportion_initial     : num [1:6] 0.98181 0.000691 0.006908 0.003684 0.005756 ...
$ density_individuals    : num [1:34] 20000 20000 20000 20000 20000 20000 20000 20000 20000 20000 ...
$ fraction_SDD           : num 0.05
$ dispersal_probabilities : num [1:900, 1:900] 0 0 0 0 0 0 0 0 0 0 ...
..- attr(*, "dimnames")=List of 2
.. ..$ : chr [1:900] "5000" "5001" "5002" "5003" ...
.. ..$ : chr [1:900] "5000" "5001" "5002" "5003" ...
$ dist_latlong           : num [1:900, 1:900] 0 1 2 3 4 5 6 7 8 9 ...
..- attr(*, "dimnames")=List of 2
.. ..$ : chr [1:900] "5000" "5001" "5002" "5003" ...
.. ..$ : chr [1:900] "5000" "5001" "5002" "5003" ...
$ neigh_index            : num [1:2] 1 1.4
$ fraction_LDD           : num 0.05
$ no_yrs                 : num 10
$ K                       : num 10000
$ Kweight                : num [1:6] 0 1.5 1 1 1 1
$ populationmax_all      : num [1:900, 1:9] 10000 10000 10000 10000 10000 10000 10000 10000 10000 ...
$ n0_all                 : num [1:900, 1:6] 0 0 0 0 0 0 0 0 0 0 ...
$ list_names_matrices    :List of 5
..$ : chr "Reference_matrix"
..$ : chr "Mx1"
..$ : chr "Mx2"
..$ : chr "Mx3"
..$ : chr "Mx4"
$ sumweight              : num [1:6] 0 1 1 1 1 1
$ transition_affected_env : int [1:24] 1 2 9 13 14 15 16 19 20 21 ...
$ transition_affected_niche : num [1:2] 1 3
$ transition_affected_demogr: int [1:24] 1 2 9 13 14 15 16 19 20 21 ...
$ env_stochas_type       : chr "normal"
NULL

> Hmontana$env_stochas_type

[1] "normal"

```

2.3 Modelling

We use the modelling function `demoniche_model(modelname, Niche, Dispersal, repetitions, foldername)` to carry out the demographic modelling, and specifying the `Hmontana` list of species information as the species object we want to use. As arguments to the function the user also needs

to specify if you want to run simulations with the effects of the Niche values (TRUE or FALSE) and if you want to allow long-distance dispersal (TRUE or FALSE). You also need to specify how many repetitions you want to carry out (for stochastic simulations the number should be over 1000), and a name for the folder where the simulations will be stored. But all these simulations are carried out with the same species information.

The `demoniche_model` function runs two internal functions, `demoniche_population` that carries out demographic modelling, and `demoniche_dispersal` which calculates the dispersal if selected.

When we run the `demoniche_model` function messages are printed on the screen, to let us know how the simulations are going.

```
> noCC_nodispersal <- demoniche_model(modelname = "Hmontana",
+   Niche = FALSE, Dispersal = FALSE, repetitions = 2,
+   foldername = "noCC_nodispersal")
```

```
[1] Starting projections for repetition: 1
[1] Projecting for scenario/matrix: Reference_matrix
[1] Projecting for scenario/matrix: Mx1
[1] Projecting for scenario/matrix: Mx2
[1] Projecting for scenario/matrix: Mx3
[1] Projecting for scenario/matrix: Mx4
[1] Starting projections for repetition: 2
[1] Projecting for scenario/matrix: Reference_matrix
[1] Projecting for scenario/matrix: Mx1
[1] Projecting for scenario/matrix: Mx2
[1] Projecting for scenario/matrix: Mx3
[1] Projecting for scenario/matrix: Mx4
[1] Calculating summary values
[1] All repetitions completed!
```

To change any of the parameters, we simply change the arguments in the function, and the foldername, to change where the objects are saved. Here we have chosen to include effects of Niche values but no dispersal.

```
> CC_nodispersal <- demoniche_model(modelname = "Hmontana",
+   Niche = TRUE, Dispersal = FALSE, repetitions = 2, foldername = "CC_nodispersal")
```

```
[1] Starting projections for repetition: 1
[1] Projecting for scenario/matrix: Reference_matrix
[1] Projecting for scenario/matrix: Mx1
[1] Projecting for scenario/matrix: Mx2
[1] Projecting for scenario/matrix: Mx3
[1] Projecting for scenario/matrix: Mx4
[1] Starting projections for repetition: 2
[1] Projecting for scenario/matrix: Reference_matrix
[1] Projecting for scenario/matrix: Mx1
[1] Projecting for scenario/matrix: Mx2
[1] Projecting for scenario/matrix: Mx3
[1] Projecting for scenario/matrix: Mx4
[1] Calculating summary values
[1] All repetitions completed!
```

2.4 Analyse data

From running the `demoniche_model` function we get these outputs:

- Summary statistics from all the repetitions in the workspace (as value of function)
- Plots of EMA, population sizes and patch occupancy
- Population simulation results and EMAs saved in a csv file and as R objects (.rda)
- Population data, Eigen analysis, EMAs, saved in folder as R objects

First, the output from the `demoniche_model` function itself is an array containing the population sizes at each time step (mean, standard deviation of mean population sizes, minimum and maximum), calculated from all repetitions. If you only have one transition matrix, and run models without stochasticity, the mean the standard deviation will be zero, regardless of numbers of repetitions. The third dimension of the array are the results for the different treatment matrices.

Complete yearly population stage distributions from each repetition and each population are saved in the folder with the specified name. These data can be visually or statistically analysed, or exported to other formats for further analysis of transient dynamics. The function also creates line graphs of the mean population results for each year, EMA of each transition matrix treatment scenario for each time period, and maps of the occupancy throughout the modelled area, at each time step (Fig. 2)

```
> dim(noCC_nodispersal)

[1] 90  4  5

> dimnames(noCC_nodispersal)

[[1]]
[1] "year1" "year2" "year3" "year4" "year5" "year6" "year7"
[8] "year8" "year9" "year10" "year11" "year12" "year13" "year14"
[15] "year15" "year16" "year17" "year18" "year19" "year20" "year21"
[22] "year22" "year23" "year24" "year25" "year26" "year27" "year28"
[29] "year29" "year30" "year31" "year32" "year33" "year34" "year35"
[36] "year36" "year37" "year38" "year39" "year40" "year41" "year42"
[43] "year43" "year44" "year45" "year46" "year47" "year48" "year49"
[50] "year50" "year51" "year52" "year53" "year54" "year55" "year56"
[57] "year57" "year58" "year59" "year60" "year61" "year62" "year63"
[64] "year64" "year65" "year66" "year67" "year68" "year69" "year70"
[71] "year71" "year72" "year73" "year74" "year75" "year76" "year77"
[78] "year78" "year79" "year80" "year81" "year82" "year83" "year84"
[85] "year85" "year86" "year87" "year88" "year89" "year90"

[[2]]
[1] "Meanpop" "SD" "Max" "Min"

[[3]]
[1] "Reference_matrix" "Mx1" "Mx2"
[4] "Mx3" "Mx4"
```

We can also look at parts of the object itself, here the mean populations from simulations with the treatment matrix Mx4:

```
> noCC_nodispersal[, "Meanpop", "Mx4"]

  year1  year2  year3  year4  year5  year6  year7  year8  year9
23676.0 22650.5 21873.5 21353.5 20848.0 20368.0 20102.5 19808.0 19709.0
  year10 year11 year12 year13 year14 year15 year16 year17 year18
19533.0 19278.5 19158.0 18944.5 18793.0 18630.0 18469.0 18299.0 18117.0
```

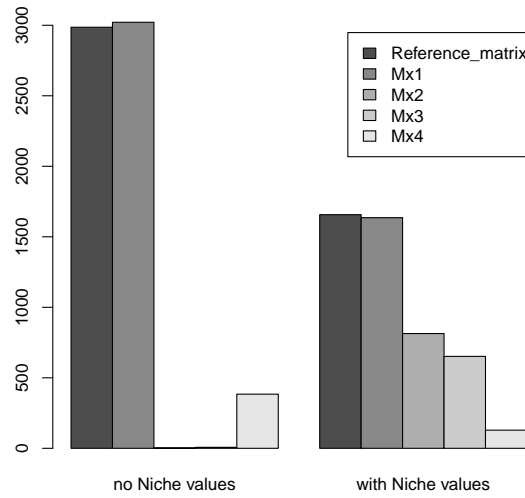


Figure 2: Population size (number of individuals) for simulations under each treatment matrix scenario of human land use, in the last year of simulation (year 90). With climate change there was a lower predicted population size

```

year19 year20 year21 year22 year23 year24 year25 year26 year27
17945.5 17777.5 17618.0 17488.0 17330.5 17115.0 16959.0 16829.5 16661.5
year28 year29 year30 year31 year32 year33 year34 year35 year36
16547.0 16424.5 16335.0 16164.0 16052.0 15969.0 15816.5 15677.5 15554.0
year37 year38 year39 year40 year41 year42 year43 year44 year45
15417.5 15259.5 15149.0 15036.5 14899.5 14795.5 14650.0 14538.5 14409.5
year46 year47 year48 year49 year50 year51 year52 year53 year54
14299.0 14135.0 14004.0 13847.5 13696.0 13568.0 13436.5 13315.0 13190.5
year55 year56 year57 year58 year59 year60 year61 year62 year63
13067.5 12918.5 12772.5 12585.0 12445.0 12368.5 12259.0 12127.0 12006.5
year64 year65 year66 year67 year68 year69 year70 year71 year72
11900.0 11791.0 11680.5 11538.0 11372.5 11245.5 11122.0 11029.5 10897.5
year73 year74 year75 year76 year77 year78 year79 year80 year81
10800.0 10697.0 10608.5 10525.0 10415.0 10298.0 10200.0 10108.5 9999.0
year82 year83 year84 year85 year86 year87 year88 year89 year90
9883.5 9740.0 9611.0 9497.0 9371.0 9278.0 9191.5 9065.0 8919.5

```

The values obtained in other runs will be different as their population growth is stochastic.

We can plot the population sizes. Figure 2 is produced by the following code:

```

> barplot(cbind(noCC_nodispersal[90, 2, ], CC_nodispersal[90,
+   2, ]), beside = TRUE, legend.text = Hmontana$list_names_matrices,
+   names.arg = c("no Niche values", "with Niche values"))

```

Apart from the summary object, the results from each simulation are saved in the folder with the specified name, in the working directory. If any of the files are open while we run new simulations, they will not be updated (i.e. automatically overwrites files, but cannot do it if files are open). We can look at what results are called:

```
> list.files(path = "noCC_nodispersal")

[1] "EMA.rda"
[2] "EMA_Mx1.jpeg"
[3] "EMA_Mx2.jpeg"
[4] "EMA_Mx3.jpeg"
[5] "EMA_Mx4.jpeg"
[6] "EMA_Reference_matrix.jpeg"
[7] "EMAs.jpeg"
[8] "Projection_rep10_Mx1.rda"
[9] "Projection_rep10_Mx2.rda"
[10] "Projection_rep10_Mx3.rda"
[11] "Projection_rep10_Mx4.rda"
[12] "Projection_rep10_Reference_matrix.rda"
[13] "Projection_rep1_Mx1.rda"
[14] "Projection_rep1_Mx2.rda"
[15] "Projection_rep1_Mx3.rda"
[16] "Projection_rep1_Mx4.rda"
[17] "Projection_rep1_Reference_matrix.rda"
[18] "Projection_rep2_Mx1.rda"
[19] "Projection_rep2_Mx2.rda"
[20] "Projection_rep2_Mx3.rda"
[21] "Projection_rep2_Mx4.rda"
[22] "Projection_rep2_Reference_matrix.rda"
[23] "Projection_rep3_Mx1.rda"
[24] "Projection_rep3_Mx2.rda"
[25] "Projection_rep3_Mx3.rda"
[26] "Projection_rep3_Mx4.rda"
[27] "Projection_rep3_Reference_matrix.rda"
[28] "Projection_rep4_Mx1.rda"
[29] "Projection_rep4_Mx2.rda"
[30] "Projection_rep4_Mx3.rda"
[31] "Projection_rep4_Mx4.rda"
[32] "Projection_rep4_Reference_matrix.rda"
[33] "Projection_rep5_Mx1.rda"
[34] "Projection_rep5_Mx2.rda"
[35] "Projection_rep5_Mx3.rda"
[36] "Projection_rep5_Mx4.rda"
[37] "Projection_rep5_Reference_matrix.rda"
[38] "Projection_rep6_Mx1.rda"
[39] "Projection_rep6_Mx2.rda"
[40] "Projection_rep6_Mx3.rda"
[41] "Projection_rep6_Mx4.rda"
[42] "Projection_rep6_Reference_matrix.rda"
[43] "Projection_rep7_Mx1.rda"
[44] "Projection_rep7_Mx2.rda"
[45] "Projection_rep7_Mx3.rda"
[46] "Projection_rep7_Mx4.rda"
[47] "Projection_rep7_Reference_matrix.rda"
[48] "Projection_rep8_Mx1.rda"
```



```

[49] "Projection_rep8_Mx2.rda"
[50] "Projection_rep8_Mx3.rda"
[51] "Projection_rep8_Mx4.rda"
[52] "Projection_rep8_Reference_matrix.rda"
[53] "Projection_rep9_Mx1.rda"
[54] "Projection_rep9_Mx2.rda"
[55] "Projection_rep9_Mx3.rda"
[56] "Projection_rep9_Mx4.rda"
[57] "Projection_rep9_Reference_matrix.rda"
[58] "Simulation_results.jpeg"
[59] "eigen_results.rda"
[60] "map_Mx1.jpeg"
[61] "map_Mx2.jpeg"
[62] "map_Mx3.jpeg"
[63] "map_Mx4.jpeg"
[64] "map_Reference_matrix.jpeg"
[65] "metapop_results.rda"
[66] "population_results.rda"
[67] "population_sizes.rda"
[68] "simulation_results.csv"
[69] "simulation_results.rda"

```

In the folder there are various .jpgs that show the Mean population sizes (with ± 1 standard deviation on each side in the same color if there are more than one repetition), EMA through time for all transition matrices, and the patch occupancy at each time period, for the last repetition. These are intended for a quick visualization of results. The original data can be accessed and plotted as the user wants.

Other results are saved in .csv which can be opened in for example excel, such as the `population_results.csv`. The rows are the information for each matrix. The columns contain information about the projects: initial total population area, initial population, percentage of populations that went extinct during the simulations, the growth rate (λ , the first eigenvalue) of the treatment matrix (not the reference matrix, function from `popbio` package), the stochastic λ from the two matrices (50.000 time intervals, function from `popbio` package).

Other data, such as the complete occupancy for each population and each repetition, for all stages, are saved in other formats. The .rda format can be loaded with the command `load()` into R. This data can then be used for plotting, further analyzed, etc.

The user can also load the object `eigen_results_yourmatrixname.rda` for each transition matrix. It is a list with an entry for each matrix, which is made up of the results from the function `eigen.analysis` from the `popbio` package. The list contains the eigenvalue of the matrix (λ), the stable stage distribution, the sensitivities and elasticities, the reproductive value of each life stage, and the damping ratio. For explanation of these values please see `popbio` package helpfiles, Morris and Doak, 2002 and other publications listed below.

```
> load("noCC_nodispersal/eigen_results.rda")
```

```
[1] "eigen_results"
```

```
> str(eigen_results)
```

```
List of 5
```

```
$ Reference_matrix:List of 7
```

```
..$ lambda1 : num 0.959
```

```
..$ stable.stage : num [1:6] 0.98142 0.00075 0.00398 0.00342 0.00476 ...
```

```
..$ sensitivities: num [1:6, 1:6] 0.0113 12.9282 0 0 0 ...
```

```
..$ elasticities : num [1:6, 1:6] 0.00587 0.00539 0 0 0 ...
```

```

..$ repro.value : num [1:6] 1 1148 2305 4340 5552 ...
..$ damping.ratio: num 1.4
..$ LTRE : num [1:6, 1:6] 0 0 0 0 0 0 0 0 0 0 ...
$ Mx1 :List of 7
..$ lambda1 : num 0.959
..$ stable.stage : num [1:6] 0.974 0.0008 0.0075 0.00653 0.00811 ...
..$ sensitivities: num [1:6, 1:6] 0.00964 11.07891 0 0 0 ...
..$ elasticities : num [1:6, 1:6] 0.00502 0.00462 0 0 0 ...
..$ repro.value : num [1:6] 1 1150 2311 4287 4661 ...
..$ damping.ratio: num 1.44
..$ LTRE : num [1:6, 1:6] 0 0 0 0 0 0 0 0 0 0 ...
$ Mx2 :List of 7
..$ lambda1 : num 1.01
..$ stable.stage : num [1:6] 0.987575 0.000812 0.001046 0.000606 0.000291 ...
..$ sensitivities: num [1:6, 1:6] 0.00926 11.8108 0 0 0 ...
..$ elasticities : num [1:6, 1:6] 0.00458 0.00468 0 0 0 ...
..$ repro.value : num [1:6] 1 1276 2699 4696 7653 ...
..$ damping.ratio: num 1.29
..$ LTRE : num [1:6, 1:6] 0 0 0 0 0 0 0 0 0 0 ...
$ Mx3 :List of 7
..$ lambda1 : num 0.845
..$ stable.stage : num [1:6] 0.979559 0.000598 0.006777 0.005622 0.004388 ...
..$ sensitivities: num [1:6, 1:6] 0.00389 4.48501 0 0 0 ...
..$ elasticities : num [1:6, 1:6] 0.0023 0.00159 0 0 0 ...
..$ repro.value : num [1:6] 1 1153 2144 7201 22964 ...
..$ damping.ratio: num 1.26
..$ LTRE : num [1:6, 1:6] 0 -0.000826 0 0 0 ...
$ Mx4 :List of 7
..$ lambda1 : num 1.02
..$ stable.stage : num [1:6] 0.986585 0.000589 0.00127 0.000474 0.002607 ...
..$ sensitivities: num [1:6, 1:6] 0.0152 26.2875 0 0 0 ...
..$ elasticities : num [1:6, 1:6] 0.00746 0.00774 0 0 0 ...
..$ repro.value : num [1:6] 1 1729 3522 4523 4990 ...
..$ damping.ratio: num 1.36
..$ LTRE : num [1:6, 1:6] 0 -0.00176 0 0 0 ...
NULL

```

We can use the `popbio` package function `image2` to plot the Sensitivity matrix (Figure 3). We can see that the stage with the highest sensitivity is the stage from seed to seedling (12.928).

```

$mar
[1] 1 3 3 1

$xp
[1] TRUE

NULL

```

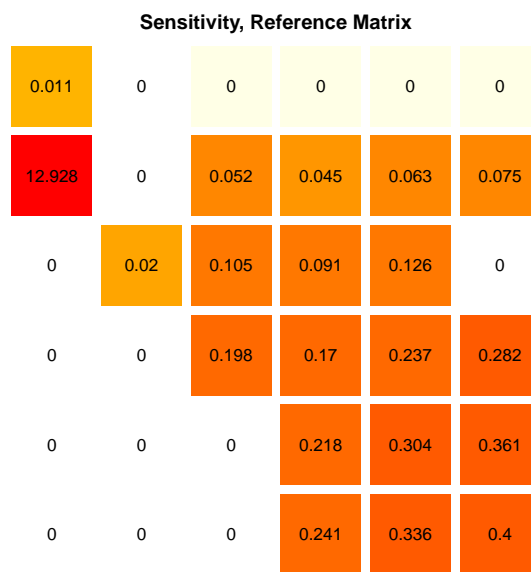


Figure 3: Sensitivities of the Reference Matrix for Mountain Goldenheather *Hudsonia montana*.

3 Setting up our own data

The `demoniche` model, and demographic modelling in general is 'data-hungry' and requires both detailed geographic and demographic information for the modelled species. For further discussion about how to obtain data, please see Morris and Doak (2002). Overview of required information:

Geographic information, [3.1](#)

- [3.1.1](#) Information about occupied populations, with at least two sub-populations. Each patch must have coordinates, a (numeric) identifier, and a size (size can be the same for all patches if the model is grid-based).
- [3.1.2](#) A grid of present and future niche suitability values (Niche values), from 0-1 or 0-1000. They can be outputs from niche modelling (Species Distribution Modelling), scenarios derived from General Circulation Models (GCM), predictions of land use-changes, habitat cover types, topology, etc. They can also be any other values thought to influence the species growth (they can also be zeros if the surrounding environment is completely unsuitable for the species). If no Nichevalues are made, a background grid is automatically created.

Demographic information, [3.2](#)

- [3.2.1](#) Age(Leslie)- or stage(Lefkovitch)-based transition matrix. Various treatment or catastrophe matrices that represent a certain environmental effect (or threat). At each year in the simulation, either the mean matrix will be chosen, or the treatment matrix, with a user-defined probability, [3.2.12](#).
- [3.2.2](#) Name of each life stage
- [3.2.3](#) Weight of stages
- [3.2.4](#), [3.2.5](#) and [3.2.6](#) Which stages in the transition matrix which are affected by Niche values, and environmental and demographic stochasticity.
- [3.2.7](#) Type of distribution of the environmental stochasticity
- [3.2.8](#) Coefficients of variation in vital rates. Optional coefficient of variation matrix for each value in the transition matrix.
- [3.2.9](#) The initial proportion of individuals in each stage.
- [3.2.10](#) Initial population density.
- [3.2.11](#) Type of carrying capacity (K) to implement density dependent growth. The maximum population size for each patch, or a multiple above which the population cannot grow. The K can be set to vary both spatially and temporally.
- [3.2.13](#) Noise Intensity in matrix selection.
- [3.2.14](#) and [3.2.15](#) The fraction that seeds that undergo short and long distance dispersal.
- [3.2.16](#) Dispersal kernel

We can examine the arguments that are required for the setup function and their defaults.

```
> args(demoniche_setup)
```

```
function (modelname, Populations, stages, Nichemap = FALSE, matrices,
  matrices_var, prob_scenario = c(0.5, 0.5), proportion_initial,
  density_individuals, transition_affected_niche = FALSE, transition_affected_env = FALSE,
  transition_affected_demogr = FALSE, env_stochas_type = "normal",
  noise = 1, fraction_SDD = FALSE, fraction_LDD = FALSE, dispersal_constants = FALSE,
  no_yrs, Ktype = "celing", K = NULL, Kweight = FALSE, sumweight = FALSE)
NULL
```

As an example of how we would load and model with our own data, we here re-create our example file `Hmontana` (Gross et al. 1998). We show how we could load our own information about a species, step by step. When we run `demoniche_setup` function on this information, we create the object `Hmontana`. This example can be run directly from the R-script `demoniche_manual.R` which is located in the `/doc` folder of the package folder. The package is usually saved in the R library folder, normally this is at `C:\Program Files\R\R-2.13.0\library` in Windows, or a similar location.

The information that we need to enter into the model can either be written into the workspace, or read from for example `.csv` files. They can either be defined as objects, or defined directly in the `demoniche_setup(...)` function. These objects can have any name, and in this example we have named them with the suffix `_mine` for clarity. Then, when running the setup function we specify which object corresponds to which argument in the function. For example, instead of `no_yrs_mine <- 10` and then defining the object in the setup function: `demoniche_setup(... no_years = no_yrs_mine)` we can simply write the value `demoniche_setup(... no_years = 10)`. This is easier when values are short.

Each argument needs either an already defined object or a value, except those that already have a default.

3.1 Geographic information

3.1.1 Original population distribution

This should be one file with ID of patches, coordinates of original locations, area of the population (in same unit as density data). If all populations have the same size (grid-based) the area will be the same for all populations. The data should be in lat/long format.

```
> Populations_mine <- read.table(file = "Hudsonia_Populations_grids.csv",
+   sep = ",", header = TRUE)
> head(Populations_mine)
```

| | patchID | X | Y | area |
|---|---------|----|----|------|
| 1 | 8000 | 2 | 29 | 2 |
| 2 | 8001 | 3 | 29 | 2 |
| 3 | 8002 | 6 | 29 | 2 |
| 4 | 8003 | 7 | 29 | 2 |
| 5 | 8004 | 9 | 29 | 2 |
| 6 | 8005 | 11 | 29 | 2 |

3.1.2 Niche data

This should be a regular grid with the niche values (habitat suitability values), within the same geographical areas as the locations of the populations. The first column should be IDs, the second and third should be grid coordinates. The following columns should be the different time periods that we wish to model. If there is no `Nichemap` supplied, this object should be a character vector of what our time periods should be called (i.e. `Nichemap <- "2050"`). Then a background grid is created, with the resolution of the smallest distance between populations.

It is the niche data map resolution that determines the scale of the population sizes. Each population that falls within a grid of the niche data is spatially joined together to make one population (and their carrying capacities are summed). So using a niche map with a high resolution ensures that populations are kept separately, that each original population is maintained within its own grid cell, and also that the maps are larger and use more memory. For memory maximization, all plots which will have a Niche value of zero at all time periods will be removed from the modellizations, as they are unsuitable for the species.

In this example we are using predicted probabilities of presence under climate change (from a GLM).

```
> Nichemap_mine <- read.table(file = "Hudsonia_SDMmodelling.csv",
+   sep = ",", header = TRUE)
> tail(Nichemap_mine)
```

| | gridID | X | Y | period2000 | period2010 | period2020 | period2030 | period2040 |
|-----|--------|----|----|------------|------------|------------|------------|------------|
| 895 | 5894 | 25 | 30 | 0.9 | 0.87 | 0 | 0.73 | 0.67 |
| 896 | 5895 | 26 | 30 | 0.9 | 0.87 | 0 | 0.73 | 0.67 |
| 897 | 5896 | 27 | 30 | 0.9 | 0.87 | 0 | 0.73 | 0.67 |
| 898 | 5897 | 28 | 30 | 0.9 | 0.87 | 0 | 0.73 | 0.67 |
| 899 | 5898 | 29 | 30 | 0.9 | 0.87 | 0 | 0.73 | 0.67 |
| 900 | 5899 | 30 | 30 | 0.9 | 0.87 | 0 | 0.73 | 0.67 |

| | period2050 | period2060 | period2070 | period2080 |
|-----|------------|------------|------------|------------|
| 895 | 0 | 0 | 0 | 0 |
| 896 | 0 | 0 | 0 | 0 |
| 897 | 0 | 0 | 0 | 0 |
| 898 | 0 | 0 | 0 | 0 |
| 899 | 0 | 0 | 0 | 0 |
| 900 | 0 | 0 | 0 | 0 |

With the `lattice` package we can plot the Niche values and see how the most suitable areas move towards the south, Figure 3.1.2.

```
> niche_formulas <- as.formula(paste(paste(colnames(Nichemap_mine)[-c(1:3)],
+   collapse = "+"), "X+Y", sep = "~"))

period2000 + period2010 + period2020 + period2030 + period2040 +
  period2050 + period2060 + period2070 + period2080 ~ X + Y

> print(levelplot(niche_formulas, Nichemap_mine, col.regions = rev(heat.colors(100)),
+   main = "Niche Values"))
```

Length in years of each time period (each of the columns with niche values in the Nichemap is a time period).

```
> no_yrs_mine <- 10

[1] 10
```

3.2 Demographic information

3.2.1 Transition matrices

A matrix/data frame of transtion matrices for different scenarios, one column per matrix. The dimension should be a multiple of the number of stages. The first matrix should be the 'reference' matrix. The model can also run with a single matrix, in which case the mean population will be the same as the minimum and maximum population numbers, and the standard deviation NA (deterministic modelling).

Here we use data from the `popbio` package. The transition probabilities (matrix elements, a_{ij}) were originally in a square matrix format, so we unlist each matrix so that each matrix is now one column in the matrix object.

```
> library(popbio)
> data(hudvrs)
> data(hudsonia)
> matrices_mine <- cbind(meanmatrix = as.vector(hudmxdef(hudvrs$mean)),
+   sapply(hudsonia, unlist))
> head(matrices_mine)
```

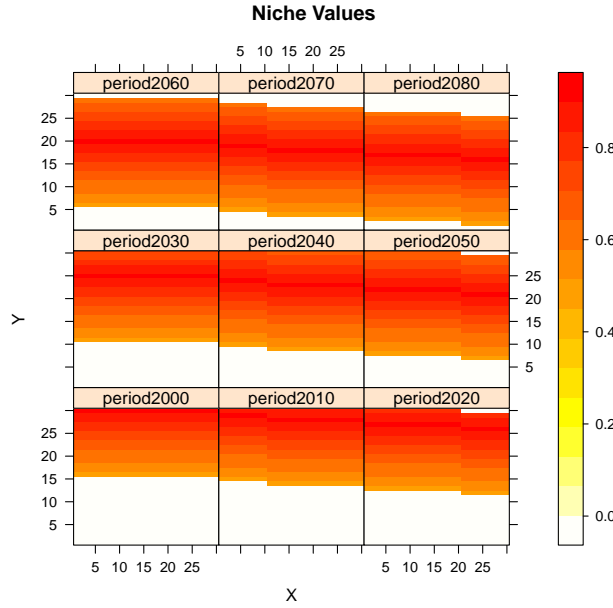


Figure 4: Niche values at each modelled time period.

```

      meanmatrix   A85   A86   A87   A88
[1,]      0.4995 0.4995 0.4995 0.4995 0.4995
[2,]      0.0004 0.0004 0.0004 0.0003 0.0003
[3,]      0.0000 0.0000 0.0000 0.0000 0.0000
[4,]      0.0000 0.0000 0.0000 0.0000 0.0000
[5,]      0.0000 0.0000 0.0000 0.0000 0.0000
[6,]      0.0000 0.0000 0.0000 0.0000 0.0000

```

```

> colnames(matrices_mine) <- c("Reference_matrix", "Mx1",
+   "Mx2", "Mx3", "Mx4")

```

We see that the `matrices` object is a matrix with each original transition matrix as a column and the names of the matrices as the column names (that do not agree with the original matrix names in this case).

The order of the transition probabilities is important. Make sure that running the function `matrix()` function with the option `byrow = FALSE` on one of the matrix columns reproduces the correct matrix. This depends on the original order of the matrix elements, if the matrix was constructed by row or by column. Below we see that the seed (fertility) stage is on the top row, which is correct. When later we select which transition probabilities stochasticity should effect, it is the row numbers in the matrix object that we use as a reference. For example, if we set effects on matrix entry 1, is refers to top left matrix element ([1,1]) of the matrix.

```

> matrix(matrices_mine[, "Reference_matrix"], ncol = 6, byrow = FALSE)

```

```

      [,1] [,2] [,3] [,4] [,5] [,6]
[1,] 0.4995 0.0000 4.5782000 12.1425000 22.31670000 50.18950000
[2,] 0.0004 0.0000 0.0033000 0.0088000 0.01620000 0.03640000
[3,] 0.0000 0.4773 0.5988709 0.2025511 0.07961523 0.00000000
[4,] 0.0000 0.0000 0.1891171 0.4726192 0.10947094 0.06865331
[5,] 0.0000 0.0000 0.0000000 0.2662100 0.55730661 0.17653707
[6,] 0.0000 0.0000 0.0000000 0.0231487 0.24879760 0.73557114

```

3.2.2 Stages

In this case, the column names of the original matrix are used to make the `stages` object which has the names of each life stage.

```
> stages_mine <- colnames(hudsonia$A85)
[1] "seed"      "seedlings" "tiny"      "small"     "medium"
[6] "large"
```

3.2.3 Weight of stages

We can specify which life stages should be counted when calculating population sizes, and to which stages that the density dependent growth should be applied to. In this example, we do not count the seed stage when calculating population sizes, and the seeds are not subject to density dependent growth. It can also be "all_stages" if all stages should be included.

```
> sumweight_mine <- c(0, 1, 1, 1, 1, 1)
[1] 0 1 1 1 1 1
```

3.2.4 Stages affected by Niche values

Here we specify which transition probabilities (matrix elements, a_{ij}) should be affected by the Niche values. We can specify the character string "all" which means that all non-zero stages are affected. Alternatively, we enter the matrix stages as a vector of numbers which corresponds to the correct matrix element. In this case, we set Niche values to affect rows 1 and 3 of the `matrices` object. We know that the first and third row in our `matrices` object refer to the probability of a seed surviving in the seed-bank and the probability of a seed becoming a seedling. Below we set which probabilities should be affected, and see what probabilities in the reference matrix they refer too.

```
> transition_affected_niche_mine <- c(1, 3)
[1] 1 3
> matrices_mine[transition_affected_niche_mine, 1]
[1] 0.4995 0.0000
```

3.2.5 Stages affected by environmental stochasticity

Here we specify which transition probabilities (matrix elements, a_{ij}) should be affected by and environmental and demographic stochasticity. To use no stochasticity and carry out deterministic modelling, we set this to `FALSE` (default). This vector refers to the affected transition stages in the same way as the Niche values, 3.2.4.

Possible arguments: "all" (all nonzero transition probabilities) or a vector of affected stages.

```
> transition_affected_env_mine <- "all"
[1] "all"
```

3.2.6 Stages affected by demographic stochasticity

Possible arguments: either "all" (all nonzero transition probabilities) *Demographic stochasticity is currently unimplemented.* or a vector of affected stages.

```
> transition_affected_demogr_mine <- "all"
[1] "all"
```


3.2.7 Type of environmental stochasticity

Do you want the environmental stochasticity to be normal or lognormal? Indicate "normal" or "lognormal" here. The default is a "normal" distribution.

```
> env_stochas_type_mine <- "normal"

[1] "normal"
```

3.2.8 Coefficients of variation in vital rates

Coefficients of variation in vital rates which are used to set how variable the environmental and demographic stochasticity should be. In this case they are set as 0.01 for all matrix elements.

```
> matrices_var_mine <- matrix(0.01, ncol = 1, nrow = nrow(matrices_mine),
+   dimnames = list(NULL, "sd"))
```

3.2.9 Initial proportion

This is the initial proportion of individuals in all stages, and should be a vector of the same length as the number of stages, and should add to 1.

```
> proportion_initial_mine <- c(0.9818098089, 0.0006907668,
+   0.0069076675, 0.0036840893, 0.0057563896, 0.0011512779)

[1] 0.9818098089 0.0006907668 0.0069076675 0.0036840893 0.0057563896
[6] 0.0011512779
```

3.2.10 Population density

Density of individuals (all stages, including seeds) in each grid cell. This number is automatically multiplied by the column named 'area Populations_mine, and should be in the same units as the area in the Populations object. This can be a single value, which is then used for all populations, or a vector if densities in each population are known. Multiply by niche values to get like ramases. This density value only affects the initial abundances, and not future projections.

```
> density_individuals_mine <- 20000

[1] 20000
```

3.2.11 Density dependence

Density dependent growth. When populations are over this value they will reach carrying capacity, and will be reduced to the value of K. This can take place by a ceiling ("ceiling") or Ricker ("ricker") function. If it is NULL, there is no carrying capacity limit in the simulations. The demoniche model also provides the alternative of defining a carrying capacity for each population, in this case the K should be a vector of values with the same length as the number of populations. It can also be a K for each timeperiod, and it should then be a vector with the same length as the number of time periods (the Niche values at each time period). It can also vary for each population and each timeperiod, and should be a matrix in this case. The carrying capacity of newly colonized cells will be set to the mean carrying capacity supplied.

The Kweight defines which population stages should be affected by the density dependence, and should be a vector with the same number of values as the number of life stages. When calculating density dependent growth, the vector is multiplied by the population size when the population size is computed. A value of "1" means that it is counted as is, and a value above, means that it is counted proportionately more. If we want a stage to be ignored when determining density dependence, we make it a zero. In this case, we want mostly juveniles to be counted, but not

seeds. The default is FALSE (same as a vector of ones). Changing the Kweight means that populations could grow above or below the actual K set.

The values of carrying capacity could be defined by various means, for example from multiplying the population density by the Nichevalues, but this has to be done separately.

```
> K_mine <- 10000
[1] 10000
> Kweight_mine <- c(0, 1.5, 1, 1, 1, 1)
[1] 0.0 1.5 1.0 1.0 1.0 1.0
```

3.2.12 Scenario probabilities

With which probability should the scenario matrices should be drawn? Should be a vector of two numbers, and the default is equal probability.

```
> prob_scenario_mine <- c(0.5, 0.5)
[1] 0.5 0.5
```

3.2.13 Noise

An option of specifying the intensity of temporal autocorrelation (noise) in the matrix selections also exists, so that the probability of choosing the same matrix in subsequent years is decreased or increased. Is the change in probability that the same matrix as the last iteration will be chosen the next time period. A noise value of 1 is completely random (default). $0 < \text{noise} < 2$.

```
> noise_mine <- 0.95
[1] 0.95
```

3.2.14 Short distance dispersal

Dispersal between populations can be either short (with dispersal to the eight contiguous cells) or long-distance dispersal. Fraction of seeds that disperse short distance, beyond patch borders. Dispersal takes place to the 8 contiguous cells. The seeds that disperse to these cells will be subjected to the same matrix multiplication as all cells. If this is zero, no SDD is modelled.

```
> fraction_SDD_mine <- 0.05
[1] 0.05
```

3.2.15 Long distance dispersal

The long-distance dispersal is modelled by an exponential dispersal kernel with user-defined constants according to the formula $P = a * \exp(D(c/b))$, with D = distance in kilometers between populations. These constants describe the shape of the species dispersal probability curve, and define a maximum distance beyond which dispersal is impossible. Long- and short-distance dispersal can be applied separately or together; alternatively, simulations without dispersal can be run.

The direction of seeds is determined by the distances between populations. If this is zero, no LDD is modelled.

```
> fraction_LDD_mine <- 0.05
[1] 0.05
```

3.2.16 Dispersal kernel

Constants for LDD dispersal kernel as a vector in the format: `c(a, b, c, Distmax)` If the distance between populations is larger than `Distmax` (in kilometers, there will be no dispersal between patches.

```
> dispersal_constants_mine <- c(0.7, 0.7, 0.1, 200)
```

```
[1] 0.7 0.7 0.1 200.0
```

3.3 Run setup function

Now we have defined all the information we need to run the setup function, and we can examine what objects we have in the work space. First we remove objects created earlier.

```
> rm(CC_nodispersal, eigen_results, Hmontana, hudsonia, hudvrs,  
+     niche_formulas, noCC_nodispersal)
```

```
NULL
```

```
> ls()
```

```
[1] "K_mine"                  "Kweight_mine"  
[3] "Nichemap_mine"          "Populations_mine"  
[5] "density_individuals_mine" "dispersal_constants_mine"  
[7] "env_stochas_type_mine"   "fraction_LDD_mine"  
[9] "fraction_SDD_mine"       "matrices_mine"  
[11] "matrices_var_mine"      "no_yrs_mine"  
[13] "noise_mine"             "prob_scenario_mine"  
[15] "proportion_initial_mine" "stages_mine"  
[17] "sumweight_mine"         "transition_affected_demogr_mine"  
[19] "transition_affected_env_mine" "transition_affected_niche_mine"
```

We specify these objects to each argument in the `demoniche_setup()` function and create the species object. Below is the complete function, with all the arguments specified. The setup function generates one species object with all the necessary information for the modeling in the workspace. It also checks the consistency of data, and prints any error messages. The order of the arguments does not matter, as long as all are present. The species object is also saved in the working directory, as an R-object (`.rda`) which can be loaded at a later time, or shared.

```
> demoniche_setup(modelname = "Hmontana", Populations = Populations_mine,  
+   Nichemap = Nichemap_mine, matrices = matrices_mine,  
+   matrices_var = matrices_var_mine, noise = noise_mine,  
+   prob_scenario = prob_scenario_mine, stages = stages_mine,  
+   proportion_initial = proportion_initial_mine, density_individuals = density_individuals_mine,  
+   fraction_LDD = 0.05, fraction_SDD = fraction_SDD_mine,  
+   dispersal_constants = dispersal_constants_mine, transition_affected_niche = transition_affected_niche_mine,  
+   transition_affected_demogr = transition_affected_demogr_mine,  
+   transition_affected_env = transition_affected_env_mine,  
+   env_stochas_type = env_stochas_type_mine, no_yrs = no_yrs_mine,  
+   K = K_mine, Kweight = Kweight_mine, sumweight = sumweight_mine)
```

We have now re-created the species object which is called the `'modelname'` argument that we specified. As above, this can be used in the `demoniche_model` function (section 2.3).

Note that we defined the fraction of seeds dispersing long distances directly in the function, instead of `fraction_LDD_mine <- 0.05` and then defining the object in the setup function: `demoniche_setup(..., fraction_LDD = fraction_LDD_mine)`, we simply wrote the value directly: `demoniche_setup(..., fraction_LDD = 0.05)`. Either way works.

4 Modifying demoniche functions

We encourage users to inspect the code in the `demoniche` functions, to find out how the algorithm is set up. By typing in only the function names in R (i.e. `demoniche_setup` directly into the console, without parentheses) the algorithm is printed.

If the user wishes to change how a function is carried out, this is possible and encouraged. Briefly, one copies the code to a new R-script, makes the desired changes to the function definition, and then reads the new function into the workspace. Then the modified function can be used as the original package function.

For example, say we wish to change the short-distance dispersal function. Currently propagules can spread to the 8 neighboring grid cells, as the function now is defined (the neighborhood index in the species object). In this case, whenever two patches are 1.0 or 1.4 degrees apart, we know that they are contiguous or diagonal from each other and propagules flow between them.

```
> Hmontana$neigh_index  
[1] 1.0 1.4
```

The neighborhood index is defined in the `demoniche_setup` function (around line 100). First a distance matrix between all locations in the Niche values file is calculated, then the second and third largest values are saved in the species object. The behaviour of this code can be examined with the original coordinates from the Niche values.

```
dist_latlong <- round(as.matrix(dist(Niche_ID[,2:3])), 1)  
neigh_index <- sort(unique(as.numeric(dist_latlong)))[2:3]
```

We wish to modify this, so that migrating propagules only can spread to the 4 neighboring cells, directly contiguous cells. We would have to change the function so that only the first value is saved in the neighborhood index, i.e. only 1 in this case, in the `demoniche_setup` function.

To make our own function, we first type: `demoniche_setup` into the console. The current function definition is returned to us, starting with `> demoniche_setup function(modelname, Populations,, etc.` We copy everything to a new R script, taking care to copy the last `}` which ends the function. We change the top of the function so that it becomes a standard function definition: `demoniche_setup_fourneighbors <- function(modelname, Populations, etc.` Here we can also change the actual name of the function, to distinguish it from the original function: maybe `demoniche_setup_fourneighbors`. We then change the lines in the function that we wish to modify: `neigh_index <- sort(unique(as.numeric(dist_latlong)))[2]` to only save the second number. If we run this entire function we have defined a new function called `demoniche_setup_fourneighbors` (check it!).

It is sometimes easier to save an R-script with only the function, like for example `fcf_fourneighbors.R`. Then the command `source("fcf_fourneighbors.R")` can be used which reads the function into the working space (just like when loading a package).

To run our modified function, we do the same thing as when running the original setup function but with the new function name: `demoniche_setup_fourneighbors(modelname = "Hmontana", Populations = Populations_mine,, etc.` This will create a species object in which the `Hmontana$neigh_index` only has one number. When we run the model function on this object, dispersal will only take modelled to the four contiguous cells.

5 Other resources

Related models: Vortex (Lacy et al. 1993), ULM (Legendre and Clobert 1995) RamasGIS/Metapop (Akaçkaya and Root 2005), Patch (Schumaker 1998, Schumaker et al. 2004), TreeMig (Lischke et al. 2006), Prunus (Sebert-Cuvillier et al. 2009), BioMove (Midgely et al. 2010).

Related R-packages: `popbio`, `Rramas`, `demography`.

Recommended packages: `sp` to load shapefiles, `BIOMOD` and `dismo` to carry out Species Distribution Modelling, `SDMTools` to calculate fragmentation indices.

6 Acknowledgements

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