

demoniche

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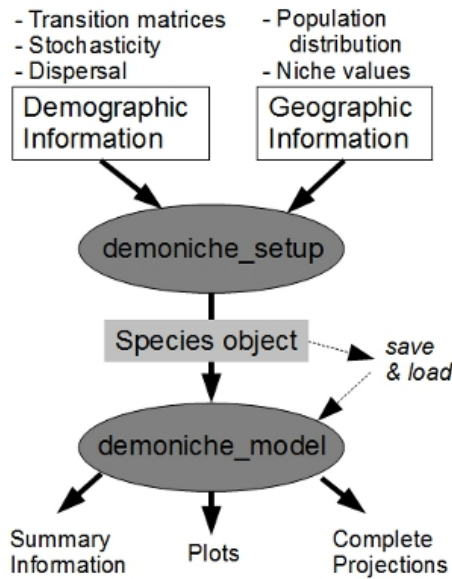


Figure 1: Simplified schema of the demoniche framework. First the user enters demographic and geographic information into the setup function. The model function runs the demographic modelling on the species object.

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 under the influence of scenarios of environmental and human impacts.

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

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 up-dated 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 26

```
$ 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 ...
$ fraction_SDD          : num 0.5
$ dispersal_probabilities : num [1:900, 1:900] 0.0 8.7e-08 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
$ 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_LDD           : num 0.05
$ no_yrs                 : num 10
$ K                       : num 100
$ populationmax_all      : num [1:900] 4e+06 4e+06 4e+06 4e+06 4e+06 4e+06 4e+06 4e+06 4e+06 4e+06 ...
$ 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
- Plots of population sizes and patch occupancy
- Simulation results in csv file
- Population data saved in folder, as R object
- Eigen analysis saved in folder, as R object

First, the output from the `demoniche_model` function itself is an array containing the population sizes at each time step (mean, Expected Minimum Abundance (EMA), and standard deviation of mean population sizes), calculated from all repetitions. The third dimension of the array is 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 EMA of each transition matrix treatment scenario, and maps of the occupancy throughout the modelled area, at each time step (Fig. 2)

```
> dim(noCC_nodispersal)

[1] 90  3  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" "EMA" "SD"

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

We can also look at parts of the object itself, here the Expected Minimum Abundance from simulations with the treatment matrix Mx4:

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

  year1  year2  year3  year4  year5  year6  year7  year8  year9
29031  29380  29635  29940  32413  31404  34182  36448  36581
year10 year11 year12 year13 year14 year15 year16 year17 year18
 38517  39959  39872  43902  45452  48148  50724  51630  54914
year19 year20 year21 year22 year23 year24 year25 year26 year27
 56632  60007  58040  65760  64491  72659  75391  78328  83192
year28 year29 year30 year31 year32 year33 year34 year35 year36
 85856  85873  94927 102670  97232 103841 111753 111806 129121
year37 year38 year39 year40 year41 year42 year43 year44 year45
139360 139991 141995 147541 152549 160312 165075 174352 175521
year46 year47 year48 year49 year50 year51 year52 year53 year54
192081 201066 210115 208043 220997 235806 256456 259129 290808
```

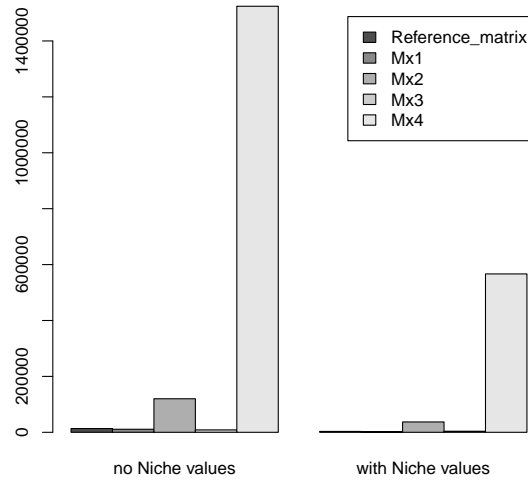


Figure 2: Population size (number of individuals) for simulations under each treatment matrix scenario of human land use, in the last year of simulation (year 90). With climate change there was a lower predicted population size

```

year55 year56 year57 year58 year59 year60 year61 year62 year63
298944 304274 311246 381566 359299 380796 409143 426651 417323
year64 year65 year66 year67 year68 year69 year70 year71 year72
453021 435163 469342 472214 537996 545534 589797 612076 670540
year73 year74 year75 year76 year77 year78 year79 year80 year81
693574 711539 768411 766189 874297 916745 881385 910911 997116
year82 year83 year84 year85 year86 year87 year88 year89 year90
1034620 1053008 1107235 1176145 1119363 1272121 1320712 1454659 1524193

```

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. We can look at what they are called:

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

[1] "eigen_results.rda"
[2] "EMA_Mx1.jpeg"
[3] "EMA_Mx2.jpeg"
[4] "EMA_Mx3.jpeg"
[5] "EMA_Mx4.jpeg"
[6] "EMA_Reference_matrix.jpeg"
[7] "map_Mx1.jpeg"
[8] "map_Mx2.jpeg"
[9] "map_Mx3.jpeg"
[10] "map_Mx4.jpeg"
[11] "map_Reference_matrix.jpeg"
[12] "metapop_results.rda"
[13] "population_sizes.rda"
[14] "Projection_rep1_Mx1.rda"
[15] "Projection_rep1_Mx2.rda"
[16] "Projection_rep1_Mx3.rda"
[17] "Projection_rep1_Mx4.rda"
[18] "Projection_rep1_Reference_matrix.rda"
[19] "Projection_rep2_Mx1.rda"
[20] "Projection_rep2_Mx2.rda"
[21] "Projection_rep2_Mx3.rda"
[22] "Projection_rep2_Mx4.rda"
[23] "Projection_rep2_Reference_matrix.rda"
[24] "simulation_results.csv"
[25] "simulation_results.rda"
```

In the folder there are various .jpgs that show the EMA through time for all repetitions, 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 `simulation_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). *Some of these results might not be working correctly.*

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 0 0 0 0 0 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 0 0 0 0 0 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

$xpd
[1] TRUE

NULL

```



Figure 3: Sensitivities of the Reference Matrix for Mountain Goldenheater *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 future conditions (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 Niche values 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' 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.
- 3.2.2 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 environmental stochasticity
- 3.2.8 Variances in vital rates. Optional variance matrix for each value in the transition matrix.
- 3.2.9 The initial proportion of individuals in each stage.
- 3.2.10 Population density
- 3.2.11 Density dependence. The maximum population size for each patch, or a multiple above which the population cannot grow. The multiple can either be a value for each patch or one value for all patches.
- 3.2.12 Scenario probabilities
- 3.2.13 Noise
- 3.2.14 and 3.2.15 The fraction that seeds that undergo short and long distance dispersal.
- 3.2.16 Dispersal kernel

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 also be read directly from the R-script **demoniche_manual.R** which is located in the 'doc' folder in the package.

The information 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_years_mine)`, we can simply write the value `demoniche_setup(... no_years = 10)`. This is easier for short values.

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 (must be numeric), 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 can be a regular grid comprising the locations of the populations. In this case we are using predicted probabilities of presence under climate change (from a GLM for example). If not supplied, a background grid is created.

```
> 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.

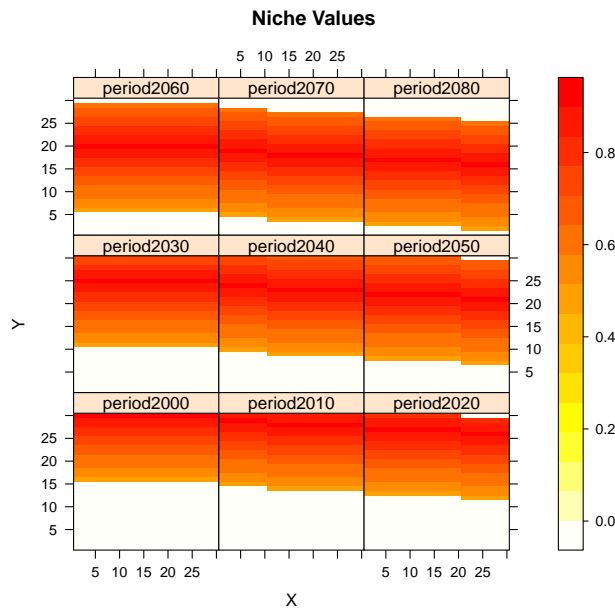


Figure 4: Niche values at each modelled time period.

```
> 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.

> 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.

Load required data from the popbio package. The life stage (or transition probabilities, a_{ij}) were originally in a square matrix format, so we unlist each matrix so that each matrix is now one column.

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

```

      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 transtion 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 life stages 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 it was by row or by column. Below we see that the seed (fertility) stage is on the top row, which is correct. When later we set which life stages a certain stochasticity should effect, it is these row numbers that we refer to. For example, if we set effects on matrix entry 1, is the 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 `stage` 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 dependence should be applied to. In this case, 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 matrix element (life stage) 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. There is no default.

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

3.2.5 Stages affected by environmental stochasticity

Here we specify which matrix element (life stage) should be affected by and environmental and demographic stochasticity. To use no stochasticity, we set this to `FALSE`. This uses the same method as the Niche values, 3.2.4.

Possible arguments: either `FALSE` (no), "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 `FALSE` (no), "all" (all nonzero transition probabilities) 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 Variances in vital rates

Variances 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 patches. This should be in the same units as area sizes as in `Populations_mine` (which can sometimes be lat/long)

```
> density_individuals_mine <- 20000
```

```
[1] 20000
```

3.2.11 Density dependence

Density dependent growth. When populations are over this (a multiple) above compared to the population with the largest original population they will reach K carrying capacity, and will be reduced to K. If it is NULL, there is no density dependence effects in the model. 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.

```
> K_mine <- 100
```

```
[1] 100
```

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 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.

```
> ls()
```

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

Recommended packages: `sp` to load shapefiles, `BIOMOD` and `dismo` to carry out Species Distribution Modelling

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