

Range Expansion Simulation

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1 Introduction

Modelling approaches for estimating species ability to track environmental change over large scales may rely on different assumptions regarding the role of dispersal (Barbet-Massin et al. 2012; Engler et al. 2012; Bateman et al. 2013; Zhou and Kot, 2013): i) The species cannot disperse, thus considering null dispersal ability (which would, in most cases, underestimate the potential future area); ii) Infinite dispersal ability, which means that the species will be able to cope with the shifts of its ecological niche by fully occupying all newly available areas (in most cases, maybe with the exception of highly mobile species, this is an unrealistic assumption which will produce optimistic results); iii) A mean dispersal distance per decade (p.ex.) is defined, considering the ability of the species to disperse (this approach can be a bit arbitrary, if not carefully considered); iv) a dispersal kernel is developed based on a set of species traits (this is a more realistic approach which represents a good compromise between the full dispersal and no-dispersal approaches). It is known however that the species ability to disperse depends not only on its own traits but also on the landscape configuration and composition (Nathan et al. 2012). This package allows a simplified approach to derive a dispersal model from the simulation of range expansion in landscapes with different characteristics, using the function 'range.expansion'. Similar approaches require parameters about the demographic rates of the species, or other data that, in most cases, are difficult to obtain. This approach might be considered simpler, once it requires data that can be obtained from capture-recapture, telemetry or bibliography (such as dispersal ability) and the information on basic landscape structure, which can be obtained using GIS. Furthermore, the function 'range_raster' allows the projection of the produced dispersal model into the geographical space.

2 Work-flow

2.1 Parametrization

This is crucial, and can be achieved using the function `parameter.estimate`. A vignette is available, detailing the process, which must be carefully implemented,

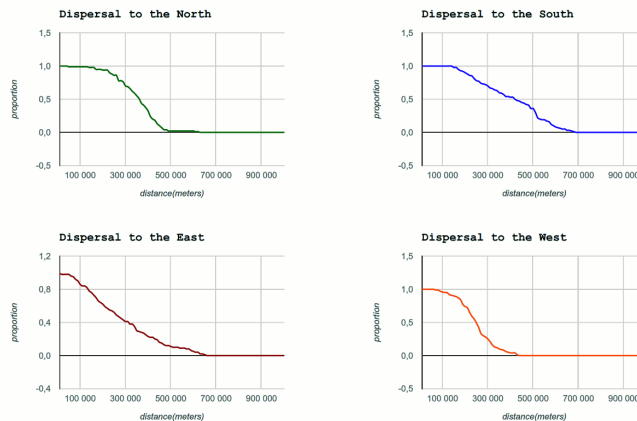
as this is the process that allows the characterization of the study species and its relation with the landscape.

2.2 Simulation of range expansion

This is done using the function `range.expansion`, which will simulate the range expansion into new, empty, landscape mosaics a given (user defined) number of times (defined by parameter `'iter'`). This simulation will be carried out for a given time period (defined by the parameter `'tsteps'`). The output of this function is a list of four data frames with the result of the occupation of sequences of landscapes in the four cardinal directions.

```
> library(MetaLandSim)
> #Load starting landscape (the simulation will assume that
> #all subsequent landscapes are built with the same parameter
> #combination).
>
> data(rland)
> #Create range expansion model. Here run only with two repetitions
> #(iter=2).
> #Ideally it should be run with more repetitions to provide more
> #robust results.
>
> data(param1)
> rg_exp1 <- range_expansion(rl=rland, percI=50, param=param1,b=1,
+ tsteps=100, iter=2)
```

The previous range expansion simulation produces a graphic output similar to the following (which opens in a html page):



Range expansion in the four cardinal directions, considering that 50% of the patches are occupied in the first landscape mosaic.
R version 3.0.1 (2013-05-16) • [google/vis/0.4.7](#) • [MetaLandSim-0.1.0](#) • [Google Terms of Use](#) • [Data Policy](#)

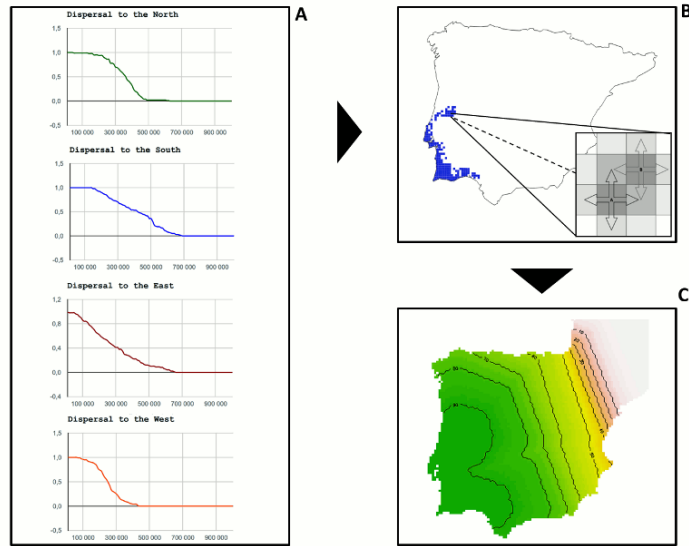
This represents the probability of occupation (in the four cardinal directions) of the landscape at a given distance from the closer current species occurrence. It is the dispersal model (DM) produced by MetaLandSim. Also, as an output of this simulation, the time steps at which each distance is reached is also estimated.

2.3 Conversion of the output to a spatial model

The dispersal simulation generated for each time step in the previous section should be converted into a model of species occurrence based only in the dispersal. This is done using the function `range.to.raster`. The output will be a raster file with the dispersal-only occupancy model after a given time period. This dispersal model can be, subsequently, combined with the output of an ecological niche model. This will allow the projection of potential occupancy considering three important factors: the species ecological niche, the species dispersal ability and the landscape characteristics. After MetaLandSim version 0.5.2, a new raster is produced representing the temporal factor. This raster depicts the average time step in which each distance is reached by the simulated range expansion. Furthermore, both these raster maps are saved in the working directory.

```
> data(rg_exp)
> presences <- paste(system.file(package="MetaLandSim"),
+ "/examples/presences.asc", sep="")
> landmask <- paste(system.file(package="MetaLandSim"),
+ "/examples/landmask.asc", sep="")
> library(rgrass7)
> #First, start GRASS from R:
> initGRASS(gisBase = "grass folder", home = tempdir(),
+ gisDbase = "mapset location", override = TRUE)
> #Create raster, using the sample dataset
> #rg_exp (generated with 100 repetitions)
>
> data("rg_exp")
> range_raster(presences.map = presences, re.out=rg_exp,
+ mask.map=landmask, plot.directions=FALSE)
```

By combining the expansion model with the current species occurrences (B) provides a future occurrence model based only on dispersal ability and landscape configuration, such as:



The four sub-models (A), considering each of the cardinal directions, are combined in a final dispersal model (C). The user should run several scenarios to evaluate the species expansion with a diversity of landscapes (or even species, depending on research question). This DM can then be combined with the output of an Ecological Niche Model projected into the future using any common GIS software or R GIS-related packages.

3 Note

The output of these functions is dependent upon species dispersal ability and current distribution. The mask should be chosen carefully, considering biological realism.

4 References

1. Barbet-Massin, M., Thuiller, W., and Jiguet, F. (2012). The fate of European breeding birds under climate, land-use and dispersal scenarios. *Global Change Biology*, 18(3), 881-890.
2. Bateman, B. L., Murphy, H. T., Reside, A. E., Mokany, K., and VanDerWal, J. (2013). Appropriateness of full-, partial-and no-dispersal scenarios in climate change impact modelling. *Diversity and Distributions*, 19(10), 1224-1234.
3. Engler, R., Hordijk, W., and Guisan, A. (2012). The MIGCLIM R package - seamless integration of dispersal constraints into projections of species

distribution models. *Ecography*, 35(10), 872-878.

4. Nathan R, Klein E, Robledo-Arnuncio JJ and Revilla E (2012). Dispersal Kernels: review. In Colbert J, Baguette M, Benton TG and Bullock JM (Eds.). *Dispersal Ecology and Evolution*. Oxford University Press. Oxford. pp: 187-210.
5. Zhou, Y., and Kot, M. (2013). Life on the Move: Modeling the effects of Climate-Driven Range Shifts with Integro-difference Equations. In: Lewis MA, Maini PK and Petroski S. (Eds.). *Dispersal, Individual Movement and Spatial Ecology. A Mathematical Perspective. Lecture Notes in Mathematics 2071*. Springer-Verlag. Berlin. pp: 263-292.