Package 'kissmig'

October 13, 2022

Type Package

Title a Keep It Simple Species Migration Model

Version 1.0-4

Date 2022-06-01

Depends raster, methods, R (>= 3.5.0)

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Description Simulating species migration and range dynamics under stable or changing environmental conditions based on a simple, raster-based, stochastic migration model. Providing accessibility from an origin or previous distribution for niche-based species distribution models. Nobis & Normand (2014) <doi:10.1111/ecog.00930>.

License GPL (>= 3)

URL https://purl.oclc.org/wsl/kissmig

Encoding UTF-8

Imports Rcpp

LinkingTo Rcpp

RoxygenNote 7.2.0

NeedsCompilation yes

Repository CRAN

Date/Publication 2022-06-01 14:20:01 UTC

R topics documented:

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kissmig	*Run a simple species migration model*

Description

`kissmig` runs a simple, raster-based, stochastic migration model to simulate species migration and range shifts. It uses a geographic area of origin along with suitability maps to iteratively run a simple 3x3 cell algorithm. Specifically, it allows for generating accessibility maps for easy integration of limited migration in species distribution models (doi:10.1111/ecog.00930Nobis and Normand 2014).

Usage

```
kissmig(O, S=NULL, it, type='FOC', signed=FALSE, pext=1.0, pcor=0.2, seed=NULL)
```

Arguments

O	a single RasterLayer of the geographic origin
S	a Raster* object of suitability, i.e., a RasterLayer, RasterStack, or RasterBrick
it	number of iteration steps
type	type of result: final distribution ('DIS'), iteration step of first occurrence ('FOC'), iteration step of last occurrence ('LOC'), or number of iteration steps with occurrence ('NOC')
signed	if TRUE, the sign indicates whether the cells was colonized (positive) or uncolonized (negative) after the last iteration step
pext	propability [0,1] a colonized cell becomes uncolonized between iteration steps, i.e., the species gets locally extinct
pcor	propability [0,1] corner cells are considered in the 3x3 cell neighborhood
seed	integer used to set the seed of the random number generator

Details

Starting from origin "O" `kissmig` simulates migration for "it" iteration steps in a heterogeneous environment characterised by the suitability layer(s) "S". The colonized cells of the origin "O" have value 1, uncolonized cells value 0. In case "S" consists of several suitability layers to cover environmental change, "it" is applied to each layer. Suitability ranges between 0 (unsuitable) and 1 (suitability maximum). `kissmig` uses a 3x3 algorithm for species spread/migration. All cells get exstinct before an iteration step with probability "pext", and for a recolonization or new colonization event corner cells within the 3x3 neighborhood are considers with probability "pcor" ("pcor"=0.2 produces more realistic circular spread patterns - see Nobis & Normand 2014). For runtime optimization, signed results are generate for "signed"=TRUE, i.e, in addtion to the result type 'FOC, 'LCO', or 'NOC', the sign indicates the final distribution ('DIS') with positive values beeing colonized and negative values beeing previously colonized but uncolonized after the last iteration step. To get reproducible results, the seed of the R random number generator can be set using the "seed" parameter.

References

- doi:10.1111/ecog.00930Nobis MP and Normand S (2014) KISSMig - a simple model for R to account for limited migration in analyses of species distributions. *Ecography* 37: 1282-1287.

- KISSMig homepage https://purl.oclc.org/wsl/kissmig

See Also

kissmigAccess, kissmigOrigin

Examples

```
library(kissmig)

s <- kissmigDummyS(mean=12,sd=3, download=TRUE)   # a suitability map
o <- kissmigOrigin(s, 8, 44.5, 0.5)               # geographic origin
l <- s>=0                                         # land mask
plot(s, asp=1.0, main='suitability + origin (in black)')
plot(o, col=c(NA,"black"), legend=FALSE, add=TRUE) # add origin


# run kissmig with different type of output

k <- kissmig(o, s, it=150, type='DIS')
plot(k*l, asp=1.0, main='final distribution')
plot(o, col=c(NA,"black"), legend=FALSE, add=TRUE) # add origin

k <- kissmig(o, s, it=150, type='FOC')
plot(k*l, asp=1.0, main='first iteration step of occurrence')
plot(o, col=c(NA,"black"), legend=FALSE, add=TRUE) # add origin

a <- kissmigAccess(k)
plot(a*l, asp=1.0, main='accessibility based on "FOC", absolute values')
plot(o, col=c(NA,"black"), legend=FALSE, add=TRUE) # add origin

a <- kissmigAccess(k, rel=TRUE)
plot(a*l, asp=1.0, main='accessibility based on "FOC", relative values')
plot(o, col=c(NA,"black"), legend=FALSE, add=TRUE) # add origin

k <- kissmig(o, s, it=150, type='LOC')
plot(k*l, asp=1.0, main='last iteration step of occurrence')
plot(o, col=c(NA,"black"), legend=FALSE, add=TRUE) # add origin

k <- kissmig(o, s, it=150, type='NOC')
plot(k*l, asp=1.0, main='number of iteration steps with occurrences')
plot(o, col=c(NA,"black"), legend=FALSE, add=TRUE) # add origin
```

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kissmigAccess	*Get accessiblity map from kissmig output*

Description

kissmigAccess calculates a accessibility map from a kissmig output of first occurrence (type='FOC'). These maps allows the integration of limited migration in species distribution models and macroecological analyses.

Usage

```
kissmigAccess(grd, rel=FALSE)
```

Arguments

grd	a single RasterLayer of first occurrence generated by kissmig
rel	if TRUE, kissmigAccess returns relative values with maximum 1, otherwise absolute interger values

Details

kissmig maps of first occurrences show values of the first iteration step a raster cell was colonized. Early colonized cells have low values, late colonized cells high values. These values are the opposite of accessibility, which is high for early colonized, and low for late colonized cells. kissmigAccess simply calculates for each cell the accessibility as the difference between the cell value and max(grd)+1. Cells which have never been colonized remain unchanged (value 0).

See Also

kissmig

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kissmigDummyS	*Get suitability maps of Europe*

Description

kissmigDummyS is a support function to generate suitability maps of Europe for example code.

Usage

```
kissmigDummyS(mean, sd, download=FALSE)
```

Arguments

mean	temperature mean (degree celsius) of the suitability distribution
sd	temperature standard deviation (degree celsius) of the suitability distribution
download	if TRUE, required climate data are downloaded from www.worldclim.org

Details

`kissmigDummyS` returns a suitability map of Europe based on mean annual temperature. It uses data of worldclim and calculates suitability as a normal distribution defined by `mean` and `sd` of mean annual temperature. The density function is linarely rescaled to a maximum of 1, the maximum suitability used in `kissmig`. Set `download=TRUE` to download the required climate data when running the function the first time.

References

https://www.worldclim.org/

See Also

kissmig

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kissmigOrigin	*Define a geographic origin*

Description

`kissmigOrigin` is a support function to define the geographic origin for a `kissmig` call.

Usage

```
kissmigOrigin(grd, x, y, size)
```

Arguments

grd	a single RasterLayer as reference layer
x	lower left x-coordinate of geographic origin
y	lower left y-coordinate of geographic origin
size	size of the quadratic origin

Details

`kissmigOrigin` returns a rasterLayer characterized by the reference `grd`. Cell values are set to zero, except for cells of the origin defined by `extent(x, x+size, y, y+size)` which are set to one.

See Also

kissmig

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