Package ‘kissmig’

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Type Package

Title a Keep It Simple Species Migration Model

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Description Simulating species migration and range dynamics under stable or changing environmental conditions based on a simple, raster-based, deterministic or stochastic migration model. Kissmig runs on binary or quantitative suitability maps, which are pre-calculated with niche-based habitat suitability models (also called ecological niche models (ENMs) or species distribution models (SDMs)). Nobis & Normand (2014), <doi:10.1111/ecog.00930>.

License GPL (>= 3)

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

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LinkingTo Rcpp

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Contents

`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 (Nobis and Normand 2014, <doi:10.1111/ecog.00930>).

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

- Nobis 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. <doi:10.1111/ecog.00930>
- KISSMig homepage <`https://purl.oclc.org/wsl/kissmig`>

See Also

`kissmigAccess`, `kissmigOrigin`

Examples

```
library(kissmig)

# create a suitability map and geographic origin

s <- kissmigDummyS(mean=12, sd=3)
o <- kissmigOrigin(s, x=8, y=44.5, size=0.5)
l <- s>=0 # land mask used for plotting kissmig results below
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='FOC')
plot(k*l, asp=1.0, main='First iteration step of occurrence (type="FOC")')
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='DIS')
plot(k*l, asp=1.0, main='Final distribution (type="DIS")')
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 (type="LOC")')
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 (type="NOC")')
plot(o, col=c(NA,"black"), legend=FALSE, add=TRUE) # add origin
```

`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`

`kissmigDummyS` *Get a simple suitability map*

Description

`kissmigDummyS` is a support function to generate simple suitability maps based on mean annual air temperature for example code.

Usage

```
kissmigDummyS(mean, sd)
```

Arguments

`mean`	temperature mean (degree celsius) of the suitability distribution
`sd`	temperature standard deviation (degree celsius) of the suitability distribution

Details

`kissmigDummyS` returns a suitability map for a given extent 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 linearly rescaled to a maximum of 1, the maximum suitability used in `kissmig`.

References

`https://www.worldclim.org/`

See Also

`kissmig`

`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`

`wcl_bio1_europe` *Map of annual mean temperature covering Europe*

Description

Map of the bioclimatic variable BIO1 (annual mean temperature in °C) covering Europe.

Usage

```
wcl_bio1_europe
```

Format

A `RasterLayer` object.

Details

The map is based on WorldClim version 2.1 climate data for 1970-2000 and has a spatial resolution of five minutes.

Source

<https://geodata.ucdavis.edu/climate/worldclim/2_1/base/wc2.1_5m_bio.zip>

References

`https://www.worldclim.org`

Index