Package ‘kissmig’

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Type Package

Title a Keep It Simple Species Migration Model

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Depends R (>= 3.5.0), Rcpp, terra

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>.

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

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Author Michael P. Nobis [cre, aut] (ORCID: <`https://orcid.org/0000-0003-3285-1590`>),
Signe Normand [ctb] (ORCID: <`https://orcid.org/0000-0002-8782-4154`>),
Dominik F. Landolt [ctb]

Maintainer Michael P. Nobis <`michael.nobis@wsl.ch`>

Repository CRAN

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Contents

`kissmig` *Run a simple dynamic species distribution model*

Description

`kissmig` runs a simple, raster-based, stochastic model to simulate species distribution dynamics driven by environmental suitability and the migration ability of the species.

Usage

```
kissmig(
  O,
  S = NULL,
  it,
  type = "FOC",
  signed = FALSE,
  pext = 1,
  pcor = 0.2,
  seed = NULL,
  n_threads = 1,
  n_random = 1e+05
)
```

Arguments

`O`	SpatRaster with a single layer of the initial species distribution as the geographic origin.
`S`	SpatRaster with a single or multiple suitability layers. For the default setting `NULL` the suitability of all cells is set to 1.0 (maximum).
`it`	integer of the number of iteration steps representing the species' migration ability and applied to each suitability layer of S.
`type`	string defining the type of resulting map. Default setting is `"FOC"`. • `"DIS"` final species distribution after the last iteration step • `"FOC"` number of the iteration step of the first occurrence • `"LOC"` number of the iteration step of the last occurrence • `"NOC"` number of the iteration steps with occurrence
`signed`	bool. If `TRUE`, the sign indicates whether the cells was colonized (positive) or uncolonized (negative) after the last iteration step. Used in combination with `"FOC"`, `"LOC"`, or `"NOC"`. Default setting is `FALSE`.

`pext`	probability [0,1] that a colonized cell becomes uncolonized between iteration steps, i.e., without recolonization the species gets locally extinct. Default setting is `1.0`.
`pcor`	probability [0,1] that corner cells are considered in the 3x3 cell neighborhood. Default setting is `0.2`.
`seed`	integer used to set the seed of the random number generator. Default setting is `NULL`.
`n_threads`	integer of the number of threads for parallel computing. Default setting is `1` (i.e., no parallel computing).
`n_random`	integer defining the amount of random numbers for the simulation. Default setting is `100000`.

Details

Starting from an initial species distribution `O` as the geographic origin, `kissmig` simulates species distributions in an environment characterized by a single or multiple (time series) suitability layers `S`. The simulation uses a simple 3x3 cell algorithm, applied `it` iteration steps. Colonized cells have value `1`, uncolonized cells value `0`, and environmental suitability values vary binary or continuously between `0` (unsuitable) and `1` (suitability maximum). In case `S` consists of multiple suitability layers, `it` is applied to each layer.

Between iteration steps, colonized cells become extinct with the probability `pext`, and for a recolonization or new colonization event corner cells within the 3x3 neighborhood are considered with probability `pcor` (`pcor=0.2` produces more realistic circular spread patterns in homogeneous environments - see Nobis and Normand 2014, doi:10.1111/ecog.00930). If required, the random numbers are reused as a ring, and small values of `n_random` may produce regular structures in spread pattern.

To get reproducible results, the seed of the R random number generator can be set using the `seed` parameter. In addition, for reproducibility the value of `n_random` needs to stay the same between simulations. Changing one of these parameters will generate stochastically different results - even with binary suitability due to the probability `pcor` of the corner events.

Signed results with `signed=TRUE` can be generated to get in addition to the result type `"FOC"`, `"LCO"`, or `"NOC"` with the same call the final distribution (`"DIS"`) with positive values being colonized and negative values being previously colonized but uncolonized after the last iteration step.

Runtime optimization by parallel computing can be initialized by increasing `n_threads`. Depending on the hardware used, it is advantageous to set `n_threads` significantly higher than the number of available CPU cores. To figure out optimal settings compare execution time with `n_threads` set to 2^x (e.g. 4, 8, 16, 32, ...). The implementation uses the OpenMP specification for parallel programming, `https://www.openmp.org/`.

References

- Nobis, M.P. 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

```
# generate some SpatRaster data to run kissmig

s <- kissmigDummyS(mean = 12, sd = 3) # a simple climate suitability map
o <- kissmigOrigin(s, 8.0, 44.5, 0.5) # geographic origin
l <- s >= 0 # land mask used for visualization
plot(s, asp = 1.0, main = "Climate suitability & origin (in red)")
plot(o, col = c(rgb(0,0,0,0), "red"), legend = FALSE, add = TRUE) # add origin

# run kissmig with different types of output

sb <- s>0.5 # binary suitability for an arbitrary threshold of 0.5
k1 <- kissmig(o, sb, it = 150, type = "DIS")
plot(k1*l, asp = 1.0, main = "Final distribution (DIS) using binary suitability")
plot(o, col = c(rgb(0,0,0,0), "red"), legend = FALSE, add = TRUE) # add origin

k2 <- kissmig(o, s, it = 150, type = "DIS")
plot(k2*l, asp = 1.0, main = "Final distribution (DIS) using quantitative suitability")
plot(o, col = c(rgb(0,0,0,0), "red"), legend = FALSE, add = TRUE) # add origin

k3 <- kissmig(o, s, it = 150, type = "FOC")
plot(k3*l, asp = 1.0, main = "First iteration step of occurrence (FOC)",
     col = c("lightgrey", map.pal("viridis", n = max(values(k3))+1)))
plot(o, col = c(rgb(0,0,0,0), "red"), legend = FALSE, add = TRUE) # add origin

a <- kissmigAccess(k3, rel = TRUE)
plot(a*l, asp = 1.0, main = "Accessibility based on 'FOC', relative values",
     col = c("lightgrey", map.pal("viridis", n = max(values(k3))+1)))
plot(o, col = c(rgb(0,0,0,0), "red"), legend = FALSE, add = TRUE) # add origin

k4 <- kissmig(o, s, it = 150, type = "NOC")
plot(k4*l, asp = 1.0, main = "Number of iteration steps with occurrences (NOC)",
     col = c("lightgrey", map.pal("viridis", n = max(values(k4))+1)))
plot(o, col = c(rgb(0,0,0,0), "red"), legend = FALSE, add = TRUE) # add origin
```

`kissmigAccess` *Get accessiblity map from kissmig output*

Description

`kissmigAccess` calculates an 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`	SpatRaster with one layer as first occurrence generated by kissmig.
`rel`	bool. If `TRUE`, kissmigAccess returns relative values with maximum `1`, otherwise absolute integer values. Defaults to `FALSE`.

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 climate suitability maps for example code.

Usage

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

Arguments

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

Details

`kissmigDummyS` returns a SpatRaster of a simple climate suitability map for 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 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 a rectangular origin for a `kissmig` call.

Usage

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

Arguments

`grd`	SpatRaster with one layer as reference.
`x`	integer as lower left x-coordinate of geographic origin.
`y`	integer as lower left y-coordinate of geographic origin.
`size`	number as size of the quadratic origin.

Details

`kissmigOrigin` returns a SpatRaster with one layer characterized by the reference `grd`. Cell values are set to `0`, except for cells of the origin defined by `ext(x, x+size, y, y+size)` which are set to `1`.

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 `PackedSpatRaster` object generated by `terra::wrap()`; use 'terra::rast()' to unpack and load it as `SpatRaster`.

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