Package 'dynamAedes'

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Title A Unified Mechanistic Model for the Population Dynamics of
Invasive Aedes Mosquitoes

Depends R (>= 3.6.0), raster

Imports drc, fields, foreach, insol, slam, doParallel, sp

BugReports <https://github.com/mattmar/dynamAedes>

Description Generalised model for population dynamics of invasive Aedes mosquitoes. Rationale and model structure are described here: <doi:10.1016/j.ecoinf.2020.101180> and <doi:10.1101/2021.12.21.473628> .

VignetteBuilder knitr

Encoding UTF-8

Language en-GB

License GPL (>= 2)

RoxygenNote 7.2.1

Suggests parallel, rmarkdown, knitr, eesim, geosphere, ggplot2, gstat, rgeos, spatstat, tidyverse

Config/testthat/edition 3

URL <https://mattmar.github.io/dynamAedes/>

NeedsCompilation no

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R topics documented:

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adci   *Summaries of mosquito abundance.*

Description

Summaries of mosquito abundance at each life stage for each day.

Usage

```
adci(
  input_sim = NA,
  stage = 1,
  n.clusters = 1,
  eval_date = 0,
  breaks = c(0.25, 0.5, 0.75)
)
```

Arguments

input_sim	matrix. dynamAedes.m compressed output matrix.
stage	positive integer. 0 (all), 1 (egg), 2 (juvenile), 3 (adult), 4 (diapausing egg).
n.clusters	positive integer. Define the number of parallel processes.
eval_date	positive integer. Define the day of successful introduction evaluation, referring to the column number of the temperature matrix used to inform the model.
breaks	numeric vector. Quantile breaks, default the first, the second and the third quantile: c(0.25,0.5,0.75).

Value

Returns a table with the summary of mosquito abundance per life stage (or substage if compressed.output=FALSE in dynamAedes.m function) for each day.

Author(s)

Matteo Marcantonio <marcantoniomatteo@gmail.com>, Daniele Da Re <daniele.dare@uclouvain.be>

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adci_sp   *Summaries of mosquito abundance (spatial)*

Description

Summaries of mosquito abundance at each life stage for each day.

Usage

```
adci_sp(
  input_sim = NULL,
  coords = NULL,
  eval_date = NULL,
  stage = 1,
  breaks = c(0.25, 0.5, 0.75)
)
```

Arguments

input_sim	matrix. dynamAedes.m compressed output matrix
coords	matrix. A matrix reporting the spatial coordinates of the temperature observations.
eval_date	positive integer. Define the day of successful introduction evaluation, referring to the column number of the temperature matrix used to inform the model.
stage	positive integer. 0 (all), 1 (egg), 2 (juvenile), 3 (adult), 4 (diapausing egg).
breaks	numeric vector. Quantile breaks, default the first, the second and the third quantile: c(0.25,0.5,0.75).

Value

Returns a raster with the summary of mosquito abundance at each life stage for each day.

Author(s)

Matteo Marcantonio <marcantoniomatteo@gmail.com>, Daniele Da Re <daniele.dare@uclouvain.be>

---

dici   *Estimate of of mosquito dispersal*

Description

Estimates of dispersal (in km^2) for the simulated mosquito population when `scale = "lc"`.

Usage

```
dici(
  input_sim = NULL,
  coords = NULL,
  eval_date = NULL,
  breaks = c(0.25, 0.5, 0.75),
  space = FALSE
)
```

Arguments

input_sim	matrix. `dynamAedes.m` compressed output matrix (`compressed=TRUE`).
coords	matrix. A matrix reporting the spatial coordinates of the temperature observations.
eval_date	numeric. Define the day of evaluation; it refers to the column number of the input temperature matrix.
breaks	numeric vector. Quantile breaks, default interquartile range: `c(0.25,0.5,0.75)`.
space	See below for more details.

Value

if space=FALSE then it returns a dataframe with quantiles of the distribution of dispersal distances; if space=TRUE (experimental) then it returns the invaded cells on the last day of model simulations for each of the iterations.

Author(s)

Matteo Marcantonio <marcantoniomatteo@gmail.com>, Daniele Da Re <daniele.dare@uclouvain.be>

---

dynamAedes.m   *Life cycle simulation of* Aedes *mosquitoes*

Description

Function to simulate population dynamics of *Aedes* mosquitoes

Usage

```
dynamAedes.m(
  species = "aegypti",
  intro.eggs = 0,
  intro.deggs = 0,
  intro.adults = 0,
  intro.juveniles = 0,
  scale = "ws",
  intro.cells = NULL,
  jhwv = 2,
  temps.matrix = NULL,
  startd = 1,
  endd = NA,
  cells.coords = NULL,
  coords.proj4 = NA,
  lat = NA,
  long = NA,
  road.dist.matrix = NULL,
  avgpdisp = NA,
  iter = 1,
  n.clusters = 1,
  cluster.type = "PSOCK",
  sparse.output = FALSE,
  compressed.output = TRUE,
  suffix = NA,
  cellsize = 250,
  maxadisp = 600,
  dispbins = 10,
  verbose = FALSE,
  seeding = FALSE
)
```

Arguments

species	character. Select what species to model: "aegypti", "albopictus", "japonicus", "koreicus". Default species = "aegypti".
intro.eggs	positive integer. number of introduced eggs, default intro.eggs = 0.
intro.deggs	positive integer. number of introduced diapause eggs, default intro.deggs = 100.

intro.adults	positive integer. number of introduced adults, default intro.adults = 0.
intro.juveniles	
	positive integer. number of introduced juveniles, default intro.juveniles = 0.
scale	character. Define the model spatial scale: punctual/weather station "ws", local "lc", or regional "rg". Active and passive dispersal is enabled only for scale = "lc". Default scale = "ws".
intro.cells	positive integer. One or more cells (id) where to introduce the population at local ("lc") scale. If intro.cells=NULL, then a random cell is used for introduction; If intro.cells is a vector of cell ids then a cell is drawn at random from the vector (with repetition) for introduction in each model iteration.
jhwv	positive integer. Juvenile-habitat water volume, define the volume (L) of water habitat presents in each spatial unit (parametrised with data retrieved from doi:10.1111/13652664.12620). Default lhwv = 1.
temps.matrix	matrix. A matrix of daily (average) temperatures (in degrees **Celsius degree x 1000**) used to fit the life cycle rates. This matrix must be organised with the daily temperature observations as columns and the geographic position of the i-grid cell as rows. **Importantly**, the first column must match startd date.
startd	Character date (ISO format "%Y-%m-%d"). Date of start of simulations.
endd	Character date (ISO format "%Y-%m-%d"). Date of end of simulation. It can be NA; then it will be derived using the number of columns in temps.matrix.
cells.coords	matrix. A matrix reporting the spatial coordinates of the temperature observations.
coords.proj4	string. Proj4 string of cell coordinates used for the calculation of photoperiod.
lat	numeric. Latitude value of the area of interested used to derive the photoperiod (and thus the diapause eggs allocation function).
long	numeric. Longitude value of the area of interested used to derive the photoperiod (and thus the diapause eggs allocation function)
road.dist.matrix	
	matrix. when scale = "lc", defines the matrix containing the distances (in meters) between grid cells intersecting the road network for the mosquito passive dispersal process.
avgpdisp	optional. when scale = "lc", define the average car trip distance for the mosquito passive dispersal process. The value can be set by the users (positive numeric), or the estimates made by Pasaoglu et al. 2012) for the following European countries: France "fra", Germany "deu", Italy "ita", Poland "pol", Spain "esp" and the United Kingdom "uk". The average passive dispersal distance must be smaller than the maximum distance in **road.dist.matrix**.
iter	positive integer. Define the number of model iterations.
n.clusters	positive integer. Defines the number of parallel processes.
cluster.type	character. Defines the type of cluster, default "PSOCK".
sparse.output	logical. The output matrix is optimised for sparse-matrix algebra (e.g. zeros are indexed).

compressed.output	
	logical. Default TRUE, if FALSE provide abundance for each model's subcompartiment; if FALSE abundances are summed per compartment.
suffix	character. Model output suffix for output RDS.
cellsize	(positive integer. When `scale = "lc"`, defines the minimal distance for the active dispersal kernel and should match the spatial resolution of temps.matrix to avoid inconsistencies. Default cellsize = 250
maxadisp	positive integer. When `scale = "lc"`, defines the maximum daily dispersal, default maxadisp = 600.
dispbins	positive integer. When scale = "lc", defines the resolution of the dispersal kernel, default dispbins = 10.
verbose	logical. if TRUE then an overview of population dynamics is printed in the console.
seeding	logical, default FALSE, if seeding=TRUE a fixed seed is applied for result reproducibility.

Value

Matrix or a list of matrices containing, for each iteration, the number of individuals in each life stage per day (and for each grid cell of the study area if scale="lc" or "rg"). If the argument compressed.output=FALSE (default TRUE), the model returns the daily number of individuals in each life stage sub-compartment.

Author(s)

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See Also

Beta regression functions were taken from the R package aomisc, which may be available at <https://github.com/OnofriAndreaPG/aomisc>.

Examples

```
## Run dynmAedes at local scale for 5 days
# Make a toy temperature time series
## Not run:
w <- matrix(seq(20,25,length.out=5),ncol=5)*1000
# Run the model
dynamAedes.m(
species="koreicus",
scale="ws",
intro.eggs=10,
ihwv=2,
temps.matrix=w,
startd=2,
endd=5,
lat=42,
long=8,
```

```
n.clusters=1,
iter=1,
compressed.output=TRUE)

## End(Not run)
```

---

icci   *Number of invaded cells*

Description

Compute a summary of the number of invaded cells over model iterations

Usage

```
icci(input_sim = NA, eval_date = 0, breaks = c(0.25, 0.5, 0.75))
```

Arguments

input_sim	matrix. dynamAedes.m compressed output matrix (compressed=TRUE).
eval_date	numeric. Define the day of evaluation; it refers to the column number of the input temperature matrix.
breaks	numeric vector. Quantile breaks, default interquartile range: c(0.25,0.5,0.75).

Value

icci returns quantiles of the distribution of the invaded cell number for the specified. The output should be interpreted according to model spatial scale (i.e. scale='rg' or scale='lc' give different interpretation).

Author(s)

Matteo Marcantonio <marcantoniomatteo@gmail.com>, Daniele Da Re <daniele.dare@uclouvain.be>

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psi   *Proportion of successful introductions*

Description

Compute the proportion of "successful" introductions.

Usage

```
psi(input_sim = NULL, eval_date = NULL)
```

Arguments

input_sim	matrix. dynamAedes.m compressed output matrix (compressed=TRUE).
eval_date	positive integer. define the day(s) to calculate the proportion of successful introductions which should match the column number of the temperature matrix used to inform the model.

Value

psi returns the proportion of model iterations that resulted in a viable mosquito population (defined as: iterations with at least one individual alive in any life stage) at a given date.

Author(s)

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psi_sp	*Probability of successful introduction (spatial)*

Description

Compute the proportion of successful introductions per each cell of the grid.

Usage

```
psi_sp(input_sim = NULL, coords = NULL, eval_date = NULL, n.clusters = 1)
```

Arguments

input_sim	matrix. dynamAedes.m compressed output matrix (compressed=TRUE).
coords	matrix. A matrix reporting the spatial coordinates of temperature observations.
eval_date	positive integer. Define the day(s) to calculate the proportion of successful introductions which should match the column number of the temperature matrix used to inform the model.
n.clusters	positive integer. Define the number of parallel processes.

Value

psi_sp returns a raster with the proportion of model iterations that resulted in a viable mosquito population at a given date for a given life stage in each cell of the grid.

Author(s)

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