Package ‘dynamAedes’

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

Depends R (>= 4.0.0)

Imports abind, doParallel, drc, foreach, geosphere, methods, parallel, terra

BugReports `https://github.com/mattmar/dynamAedes`

Description Generalised model for population dynamics of invasive Aedes mosquitoes. Rationale and model structure are described here: Da Re et al. (2021) <doi:10.1016/j.ecoinf.2020.101180> and Da Re et al. (2022) <doi:10.1101/2021.12.21.473

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Suggests rmarkdown, knitr, eesim, gstat, stats, ggplot2, dplyr, lubridate, stringr

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URL `https://mattmar.github.io/dynamAedes/`

NeedsCompilation no

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R topics documented:

`adci` *Summaries of mosquito abundance*

Description

Summaries of mosquito abundance at each life stage and sub-stage for each day.

Usage

```
adci(
  input_sim = NULL,
  stage = NULL,
  sub_stage = NULL,
  breaks = c(0.25, 0.5, 0.75),
  eval_date = NULL,
  n.clusters = 1,
  type = "N"
)
```

Arguments

`input_sim`	matrix. `dynamAedes` compressed or uncompressed output matrix.
`stage`	character. "Eggs", "Juveniles", "Adults", or "DiapauseEggs" or any shorter attempt longer than 3 letters.
`sub_stage`	character. For uncompressed outputs only, defines the substage of interest. Please see cheat-sheet table.
`breaks`	numeric vector. Quantile breaks, default the first, the second and the third quartile: `c(0.25,0.5,0.75)`.
`eval_date`	positive integer. Define the day to evaluate from the first day of introduction. Note that this can be particularly demanding in the case of spatial outputs.

`n.clusters`	integer. Number of parallel processes.
`type`	character. The type of output. Set "O" to force overall time-only summary over spatial. Default is "N" (normal).

Value

Returns a data frame or 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 <`dare.daniele@gmail.com`>

`AedeslifeHistoryList` *Reference list for* **Aedes** *stages and substages*

Description

Reference files to match simulation output matrices with **Aedes** stages and substages as modelled in dynamAedes. The list contains:

Usage

```
data(AedeslifeHistoryList)
```

Format

A list of two matrices

Details

- speciesheet: description of each substage for each species
- codesheet: reference coding to match substages to simulation output

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

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)`.
`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 = NULL,
  intro.eggs = 0,
  intro.deggs = 0,
  intro.adults = 0,
  intro.juveniles = 0,
  scale = NULL,
  intro.cells = NULL,
  jhwv = NULL,
  temps.matrix = NULL,
  startd = 1,
  endd = NA,
  cells.coords = NULL,
  coords.proj4 = NA,
  lat = NA,
  long = NA,
  road.dist.matrix = NULL,
  avgpdisp = NA,
  pDispersal = TRUE,
  iter = 1,
  n.clusters = 1,
  cluster.type = "PSOCK",
  compressed.output = TRUE,
  suffix = NA,
  cellsize = 250,
  maxadisp = 600,
  dispbins = 10,
  verbose = 0,
  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. colnames(road.dist.matrix) must correspond to the same cell in temps.matrix (may be an issue if the coordinates used for creating road.dist.matrix have been subset to match road segments).
`avgpdisp`	optional. when `scale = "lc"`, define the average car trip distance (in meters) 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**.
`pDispersal`	boolean. if TRUE (default) then the model considers passive dispersal.
`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".
`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 active dispersal, default maxadisp = 600.

`dispbins`	positive integer. When scale = "lc", defines the resolution of the active dispersal kernel, default dispbins = 10.
`verbose`	integer. if 1 then an overview of population dynamics is printed in the console, if 2 more information on population dynamics are printed out. Default is 0 (silent).
`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)

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

See Also

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

Examples

```
## Run dynamAedes at local scale for 5 days
# Make a toy temperature time series
w <- matrix(seq(20,25,length.out=5),ncol=5)*1000
# Run the model
simout <- dynamAedes.m(
species="koreicus",
scale="ws",
intro.eggs=10,
jhwv=2,
temps.matrix=w,
startd="2021-06-21",
endd="2021-06-25",
lat=42,
long=8,
n.clusters=1,
iter=1,
compressed.output=TRUE,
verbose=FALSE)
```

`dynamAedesClass-class` *S4 class representing the output of dynamAedes.m*

Description

S4 class representing the output of dynamAedes.m

Slots

`species` Character. The simulated species.

`scale` Character. The scale of the simulation.

`start_date` Character. The introduction date.

`end_date` Character. The end date of the simulation.

`n_iterations` Numeric. The number of iterations.

`stage_intro` Character. The introduced mosquito stage.

`n_intro` Numeric. The number of propagules introduced.

`coordinates` Matrix. The coordinates of each cell.

`compressed_output` Logical. If output is at stage or substage level.

`jhwv` Numeric. The volume of water in the system.

`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 = NULL, 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`>

`max,dynamAedesClass-method`

Max method for dynamAedesClass Provides the max number of days with at least one propagule in the system (any stage) along iterations.

Description

Max method for dynamAedesClass Provides the max number of days with at least one propagule in the system (any stage) along iterations.

Usage

```
## S4 method for signature 'dynamAedesClass'
max(x, na.rm = FALSE)
```

Arguments

`x`	An object of class `dynamAedesClass`.
`na.rm`	logic.

Value

An integer.

Examples

```
## Not run:
max(sim)

## End(Not run)
```

`min,dynamAedesClass-method`

Min method for dynamAedesClass Provides the min number of days with at least one propagule in the system (any stage) along iterations.

Description

Min method for dynamAedesClass Provides the min number of days with at least one propagule in the system (any stage) along iterations.

Usage

```
## S4 method for signature 'dynamAedesClass'
min(x, na.rm = FALSE)
```

Arguments

`x`	An object of class `dynamAedesClass`.
`na.rm`	logic.

Value

An integer.

Examples

```
## Not run:
min(sim)

## End(Not run)
```

`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)

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

`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, eval_date = NULL, n.clusters = 1)
```

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.
`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)

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

`spreader` *Temporal downscaling of entomological surveillance observations*

Description

Temporal downscaling of entomological surveillance observations

Usage

```
spreader(
  mydf = NULL,
  date.field = NULL,
  value.field = NULL,
  counter.field = NULL,
  seed = 123
)
```

Arguments

`mydf`	A data.frame.
`date.field`	character, name of field containing dates.
`value.field`	integer, name of field containing the number of individuals sampled.
`counter.field`	integer, name of the field containing the number of days/weeks between each sampling. This is optional, if NULL then the function will compute the value assuming the trap was active during the whole period between two consecutive samplings.
`seed`	integer, define the seed for the binomial draws, default `seed = 123`.

Value

Returns a data.frame with the "adjusted value", i.e. the observation spread over the period of activity of the trap

Author(s)

Daniele Da Re <`dare.daniele@gmail.com`>, Giovanni Marini <`dare.daniele@gmail.com`>

`summary,dynamAedesClass-method`

Summary method for dynamAedesClass Provides a summary of simulations based on the dynamAedesClass.

Description

Summary method for dynamAedesClass Provides a summary of simulations based on the dynamAedesClass.

Usage

```
## S4 method for signature 'dynamAedesClass'
summary(object)
```

Arguments

`object`	An object of class `dynamAedesClass`.

Value

A character vector with the summary details of the simulation.

Examples

```
## Not run:
summary(sim)

## End(Not run)
```

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