Package 'miaSim'

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`.applyInterType` *Generate pairs of interactions according to interaction types*

Description

A helper function to be used in combination with .getInteractions()

Usage

```
.applyInterType(I, pair, interType)
```

Arguments

I	Matrix: defining the interaction between each pair of species
pair	Numeric: a vector with a length of 2, indicating the 2 focusing species in the process of applying the interaction types
interType	Character: one of 'mutualism', 'commensalism', 'parasitism', 'amensalism', or 'competition'. Defining the interaction type

Value

A matrix of interaction types with one pair changed

.estimateAFromSimulations

Get the interspecies interaction matrix A using leave-one-out method

---

Description

generate matrix A from the comparisons between simulations with one absent species and a simulation with complete species (leave-one-out)

Usage

```
.estimateAFromSimulations(
  simulations,
  simulations2,
  n_instances = 1,
  t_end = NULL,
  scale_off_diagonal = 0.1,
  diagonal = -0.5,
  connectance = 0.2
)
```

Arguments

simulations	A list of simulation(s) with complete species
simulations2	A list of simulation(s), each with one absent species
n_instances	Integer: number of instances to generate (default: n_instances = 1)
t_end	Numeric: end time of the simulation. If not identical with t_end in params_list, then it will overwrite t_end in each simulation (default: t_end = 1000)
scale_off_diagonal	Numeric: scale of the off-diagonal elements compared to the diagonal. Same to the parameter in function randomA. (default: scale_off_diagonal = 0.1)
diagonal	Values defining the strength of self-interactions. Input can be a number (will be applied to all species) or a vector of length n_species. Positive self-interaction values lead to exponential growth. Same to the parameter in function randomA. (default: diagonal = -0.5)

connectance	Numeric frequency of inter-species interactions. i.e. proportion of non-zero off-diagonal terms. Should be in the interval 0 <= connectance <= 1. Same to the parameter in function randomA. (default: connectance = 0.2)

Value

a matrix A with dimensions (n_species x n_species) where n_species equals to the number of elements in simulations2

.getInteractions *Generate interactions according to five types of interactions and their weights*

Description

Generate interactions according to five types of interactions and their weights

Usage

```
.getInteractions(n_species, weights, connectance)
```

Arguments

n_species	Integer: defining the dimension of matrix of interaction
weights	Numeric: defining the weights of mutualism, commensalism, parasitism, amensalism, and competition in all interspecies interactions.
connectance	Numeric: defining the density of the interaction network. Ranging from 0 to 1

Value

A matrix of interactions with all interactions changed according to the weights and connectance.

.isPosInt *Check whether a number is a positive integer*

Description

Check whether a number is a positive integer

Usage

```
.isPosInt(x, tol = .Machine$double.eps^0.5)
```

Arguments

x	Numeric number to test
tol	Numeric tolerance of detection

Value

A logical value: whether the number is a positive integer.

.replaceByZero *Replace one element with zero in a list*

Description

If the list contains m elements, then lengths of each element must be m, too. This function is intended to generate a list of x0 (the initial community) with one missing species, to prepare the parameter simulations_compare in `estimateAFromSimulations`.

Usage

```
.replaceByZero(input_list)
```

Arguments

input_list	A list containing m elements, and lengths of each element must be m, too.

Value

A list of same dimension as input_list, but with 0 at specific positions in the elements of the list.

.simulationTimes *Generate simulation times and the indices of time points to return in simulation functions.*

Description

Generate simulation times and the indices of time points to return in simulation functions.

Usage

```
.simulationTimes(t_start = 0, t_end = 1000, t_step = 0.1, t_store = 1000)
```

Arguments

t_start	Numeric scalar. Indicates the initial time of the simulation. (Default: 0)
t_end	Numeric scalar. Indicates the final time of the simulation (Default: 1000)
t_step	Numeric scalar. Indicates the interval between simulation steps (Default: 0.1)
t_store	Integer scalar. Indicates the number of evenly distributed time points to keep (Default: 100)

Value

lists containing simulation times (t_sys) and the indices to keep.

Examples

```
Time <- .simulationTimes(
    t_start = 0, t_end = 100, t_step = 0.5,
    t_store = 100
)
DefaultTime <- .simulationTimes(t_end = 1000)
```

---

powerlawA *Interaction matrix with Power-Law network adjacency matrix*

Description

N is the an Interspecific Interaction matrix with values drawn from a normal distribution H the interaction strength heterogeneity drawn from a power-law distribution with the parameter alpha, and G the adjacency matrix of with out-degree that reflects the heterogeneity of the powerlaw. A scaling factor s may be used to constrain the values of the interaction matrix to be within a desired range. Diagonal elements of A are defined by the parameter d.

Usage

```
powerlawA(n_species, alpha = 3, stdev = 1, s = 0.1, d = -1, symmetric = FALSE)
```

Arguments

n_species	Integer scalar. Indicates the number of species.
alpha	Numeric scalar. Specifies the power-law distribution. Should be > 1. Larger values will give lower interaction strength heterogeneity, whereas values closer to 1 give strong heterogeneity in interaction strengths between the species. In other words, values of alpha close to 1 will give Strongly Interacting Species (SIS). (Default: 3.0)
stdev	Numeric scalar. Specifies the standard deviation of the normal distribution with mean 0 from which the elements of the nominal interspecific interaction matrix N are drawn. (Default: 1)

s	Numeric scalar. Specifies the scaling with which the final global interaction matrix A is multiplied. (Default: 0.1)
d	Numeric scalar. Diagonal values, indicating self-interactions (use negative values for stability). (Default: 1.0)
symmetric	Logical scalar. Whether a symmetric interaction matrix is returned. (Default: FALSE)

Value

The interaction matrix A with dimensions (n_species x n_species)

References

Gibson TE, Bashan A, Cao HT, Weiss ST, Liu YY (2016) On the Origins and Control of Community Types in the Human Microbiome. PLOS Computational Biology 12(2): e1004688. https://doi.org/10.1371/journal.pcbi.1004

Examples

```
# Low interaction heterogeneity
A_low <- powerlawA(n_species = 10, alpha = 3)
# Strong interaction heterogeneity
A_strong <- powerlawA(n_species = 10, alpha = 1.01)
```

---

randomA *Generate random interaction matrix for GLV model*

Description

Generates a random interaction matrix for Generalized Lotka-Volterra (GLV) model.

Usage

```
randomA(
  n_species,
  names_species = NULL,
  diagonal = -0.5,
  connectance = 0.2,
  scale_off_diagonal = 0.1,
  mutualism = 1,
  commensalism = 1,
  parasitism = 1,
  amensalism = 1,
  competition = 1,
  interactions = NULL,
  symmetric = FALSE,
  list_A = NULL
)
```

Arguments

n_species	Integer: number of species
names_species	Character: names of species. If NULL, paste0("sp", seq_len(n_species)) is used. (default: names_species = NULL)
diagonal	Numeric vector. Defines the strength of self-interactions. Input can be a number (will be applied to all species) or a vector of length n_species. Positive self-interaction values lead to exponential growth. (Default: -0.5)
connectance	Numeric scalar. Specifies the frequency of inter-species interactions. i.e. proportion of non-zero off-diagonal terms. Between 0 and 1. (Default: 0.2)
scale_off_diagonal	Numeric scalar. Indicates the scale of the off-diagonal elements compared to the diagonal. (Default: 0.1)
mutualism	Numerical scalar. Specifies the relative proportion of interactions terms consistent with mutualism (positive <-> positive). (Default: 1)
commensalism	Numeric scalar. Indicates the relative proportion of interactions terms consistent with commensalism (positive <-> neutral). (Default: 1)
parasitism	Numeric scalar. Indicates the relative proportion of interactions terms consistent with parasitism (positive <-> negative). (Default: 1)
amensalism	Numeric scalar. Indicates the relative proportion of interactions terms consistent with amensalism (neutral <-> negative). (Default: 1)
competition	Numeric scalar. Indicates the relative proportion of interactions terms consistent with competition (negative <-> negative). (Default: 1)
interactions	Numeric scalar. Indicates the values of the n_species^2 pairwise interaction strengths. Diagonal terms will be replaced by the 'diagonal' parameter. If NULL, interactions are drawn from runif(n_species^2, min=0, max=abs(diagonal)). Negative values are first converted to positive then the signs are defined by the relative weights of the biological interactions (i.e. mutualism, commensalism, parasitism, amensalism, competition). (Default: NULL)
symmetric	Logical scalar. whether the strength of mutualistic and competitive interactions are symmetric. This is implemented by overwrite a half of the matrix, so the proportions of interactions might deviate from expectations. (Default: FALSE)
list_A	List. A list of matrices generated by randomA. Used to support different groups of interactions. If NULL (by default), no group is considered. Otherwise the given list of matrices will overwrite values around the diagonal. (Default: NULL)

Value

randomA returns a matrix A with dimensions (n_species x n_species)

Examples

```
dense_A <- randomA(
    n_species = 10,
    scale_off_diagonal = 1,
```

```
    diagonal = -1.0,
    connectance = 0.9
)

sparse_A <- randomA(
    n_species = 10,
    diagonal = -1.0,
    connectance = 0.09
)

user_interactions <- rbeta(n = 10^2, .5, .5)
user_A <- randomA(n_species = 10, interactions = user_interactions)

competitive_A <- randomA(
    n_species = 10,
    mutualism = 0,
    commensalism = 0,
    parasitism = 0,
    amensalism = 0,
    competition = 1,
    connectance = 1,
    scale_off_diagonal = 1
)

parasitism_A <- randomA(
    n_species = 10,
    mutualism = 0,
    commensalism = 0,
    parasitism = 1,
    amensalism = 0,
    competition = 0,
    connectance = 1,
    scale_off_diagonal = 1,
    symmetric = TRUE
)

list_A <- list(dense_A, sparse_A, competitive_A, parasitism_A)
groupA <- randomA(n_species = 40, list_A = list_A)
```

---

randomE *Generate random efficiency matrix*

Description

Generate random efficiency matrix for consumer resource model from Dirichlet distribution, where positive efficiencies indicate the consumption of resources, whilst negatives indicate that the species would produce the resource.

Usage

```
randomE(
  n_species,
  n_resources,
  names_species = NULL,
  names_resources = NULL,
  mean_consumption = n_resources/4,
  mean_production = n_resources/6,
  maintenance = 0.5,
  trophic_levels = NULL,
  trophic_preferences = NULL,
  exact = FALSE
)
```

Arguments

n_species	Integer: number of species
n_resources	Integer: number of resources
names_species	Character: names of species. If NULL, paste0("sp", seq_len(n_species)) is used. (default: names_species = NULL)
names_resources	Character: names of resources. If NULL, paste0("res", seq_len(n_resources)) is used.
mean_consumption	Numeric scalar. Specifies the mean number of resources consumed by each species drawn from a poisson distribution (Default: n_resources/4)
mean_production	Numeric scalar. Specifies the mean number of resources produced by each species drawn from a poisson distribution (Default: n_resources/6)
maintenance	Numeric scalar. Specifies the proportion of resources that cannot be converted into products between 0~1 the proportion of resources used to maintain the living of microorganisms. 0 means all the resources will be used for the reproduction of microorganisms, and 1 means all the resources would be used to maintain the living of organisms and no resources would be left for their growth(reproduction). (Default: 0.5)
trophic_levels	Integer scalar. Indicates the number of species in microbial trophic levels. If NULL, by default, microbial trophic levels would not be considered. (Default: NULL)
trophic_preferences	List. Indicates the preferred resources and productions of each trophic level. Positive values indicate the consumption of resources, whilst negatives indicate that the species would produce the resource. (Default: NULL)
exact	Logical scalar. Whether to set the number of consumption/production to be exact as mean_consumption/mean_production or to set them using a Poisson distribution. (Default: FALSE) If length(trophic_preferences) is smaller than length(trophic_levels), then NULL values would be appended to lower

trophic levels. If NULL, by default, the consumption preference will be defined randomly. (Default: `trophic_preferences = NULL`)

Value

`randomE` returns a matrix E with dimensions (n_species x n_resources), and each row represents a species.

Examples

```
# example with minimum parameters
ExampleEfficiencyMatrix <- randomE(n_species = 5, n_resources = 12)

# examples with specific parameters
ExampleEfficiencyMatrix <- randomE(
    n_species = 3, n_resources = 6,
    names_species = letters[1:3],
    names_resources = paste0("res", LETTERS[1:6]),
    mean_consumption = 3, mean_production = 1
)
ExampleEfficiencyMatrix <- randomE(
    n_species = 3, n_resources = 6,
    maintenance = 0.4
)
ExampleEfficiencyMatrix <- randomE(
    n_species = 3, n_resources = 6,
    mean_consumption = 3, mean_production = 1, maintenance = 0.4
)

# examples with microbial trophic levels
ExampleEfficiencyMatrix <- randomE(
    n_species = 10, n_resources = 15,
    trophic_levels = c(6, 3, 1),
    trophic_preferences = list(
        c(rep(1, 5), rep(-1, 5), rep(0, 5)),
        c(rep(0, 5), rep(1, 5), rep(-1, 5)),
        c(rep(0, 10), rep(1, 5))
    )
)
ExampleEfficiencyMatrix <- randomE(
    n_species = 10, n_resources = 15,
    trophic_levels = c(6, 3, 1),
    trophic_preferences = list(c(rep(1, 5), rep(-1, 5), rep(0, 5)), NULL, NULL)
)
ExampleEfficiencyMatrix <- randomE(
    n_species = 10, n_resources = 15,
    trophic_levels = c(6, 3, 1)
)
```

rdirichlet *Generate dirichlet random deviates*

Description

Generate dirichlet random deviates

Usage

```
rdirichlet(n, alpha)
```

Arguments

n	Number of random vectors to generate.
alpha	Vector containing shape parameters.

Value

a vector containing the Dirichlet density

Examples

```
dirichletExample <- rdirichlet(1, c(1, 2, 3))
```

simulateConsumerResource *Consumer-resource model simulation*

Description

Simulates time series with the consumer-resource model.

Usage

```
simulateConsumerResource(
  n_species,
  n_resources,
  names_species = NULL,
  names_resources = NULL,
  E = NULL,
  x0 = NULL,
  resources = NULL,
  resources_dilution = NULL,
  growth_rates = NULL,
  monod_constant = NULL,
```

```
  sigma_drift = 0.001,
  sigma_epoch = 0.1,
  sigma_external = 0.3,
  sigma_migration = 0.01,
  epoch_p = 0.001,
  t_external_events = NULL,
  t_external_durations = NULL,
  stochastic = FALSE,
  migration_p = 0.01,
  metacommunity_probability = NULL,
  error_variance = 0,
  norm = FALSE,
  t_end = 1000,
  trophic_priority = NULL,
  inflow_rate = 0,
  outflow_rate = 0,
  volume = 1000,
  ...
)
```

Arguments

n_species	Integer: number of species
n_resources	Integer: number of resources
names_species	Character: names of species. If NULL, paste0("sp", seq_len(n_species)) is used. (default: names_species = NULL)
names_resources	Character: names of resources. If NULL, paste0("res", seq_len(n_resources)) is used.
E	Matrix. Defines the efficiency of resource-to-biomass conversion (positive values) and the relative conversion of metabolic by-products (negative values). If NULL, randomE(n_species, n_resources) is used. (Default: NULL)
x0	Numeric scalar. Specifies the initial abundances of simulated species. If NULL, runif(n = n_species, min = 0.1, max = 10) is used. (Default: NULL)
resources	Numeric scalar. Specifies the initial concentrations of resources. If NULL, runif(n = n_resources, min = 1, max = 100) is used. (Default: NULL)
resources_dilution	Numeric scalar. Specifies the concentrations of resources in the continuous inflow (applicable when inflow_rate > 0). If NULL, resources is used. (Default: NULL)
growth_rates	Numeric vector. Specifies the maximum growth rates(mu) of species. If NULL, rep(1, n_species) is used. (Default: NULL)
monod_constant	Matrix. Specifies the constant of additive monod growth of n_species consuming n_resources. If NULL, matrix(rgamma(n = n_species*n_resources, shape = 50*max(resources), rate = 1), nrow = n_species) is used. (Default: NULL)

sigma_drift Numeric: standard deviation of a normally distributed noise applied in each time step (t_step) (default: sigma_drift = 0.001)

sigma_epoch Numeric: standard deviation of a normally distributed noise applied to random periods of the community composition with frequency defined by the epoch_p parameter (default: sigma_epoch = 0.1)

sigma_external Numeric: standard deviation of a normally distributed noise applied to user-defined external events/disturbances (default: sigma_external = 0.3)

sigma_migration
Numeric: standard deviation of a normally distributed variable that defines the intensity of migration at each time step (t_step) (default: sigma_migration = 0.01)

epoch_p Numeric: the probability/frequency of random periodic changes introduced to the community composition (default: epoch_p = 0.001)

t_external_events
Numeric: the starting time points of defined external events that introduce random changes to the community composition (default: t_external_events = NULL)

t_external_durations
Numeric: respective duration of the external events that are defined in the 't_external_events' (times) and sigma_external (std). (default: t_external_durations = NULL)

stochastic Logical: whether to introduce noise in the simulation. If False, sigma_drift, sigma_epoch, and sigma_external are ignored. (default: stochastic = FALSE)

migration_p Numeric: the probability/frequency of migration from a metacommunity. (default: migration_p = 0.01)

metacommunity_probability
Numeric: Normalized probability distribution of the likelihood that species from the metacommunity can enter the community during the simulation. If NULL, rdirichlet(1, alpha = rep(1,n_species)) is used. (default: metacommunity_probability = NULL)

error_variance Numeric: the variance of measurement error. By default it equals to 0, indicating that the result won't contain any measurement error. This value should be non-negative. (default: error_variance = 0)

norm Logical: whether the time series should be returned with the abundances as proportions (norm = TRUE) or the raw counts (default: norm = FALSE) (default: norm = FALSE)

t_end Numeric: the end time of the simulationTimes, defining the modeled time length of the community. (default: t_end = 1000)

trophic_priority
Matrix. Defines the orders of resources to be consumed by each species. If NULL, by default, this feature won't be turned on, and species will consume all resources simultaneously to grow. The dimension should be identical to matrix E. (Default: NULL)

inflow_rate outflow_rate Numeric scalar. The inflow of a culture process. By default, inflow_rate and is 0, indicating a batch culture process. When larger than 0, we can simulate a continuous culture(e.g. chemostat).

outflow_rate	Numeric scalar. outflow rate of a culture process By default, outflow_rate is 0, indicating a batch culture process. When larger than 0, we can simulate a continuous culture(e.g. chemostat).
volume	Numeric scalar. Indicates the volume of the continuous cultivation. This parameter is important for simulations where inflow_rate or outflow_rate are not 0. (Default: 1000)
...	additional parameters, see utils to know more.

Value

an TreeSummarizedExperiment class object

Examples

```
n_species <- 2
n_resources <- 4
tse <- simulateConsumerResource(
    n_species = n_species,
    n_resources = n_resources
)

## Not run:
# example with user-defined values (names_species, names_resources, E, x0,
# resources, growth_rates, error_variance, t_end, t_step)

ExampleE <- randomE(
    n_species = n_species, n_resources = n_resources,
    mean_consumption = 3, mean_production = 1, maintenance = 0.4
)
ExampleResources <- rep(100, n_resources)
tse1 <- simulateConsumerResource(
    n_species = n_species,
    n_resources = n_resources, names_species = letters[seq_len(n_species)],
    names_resources = paste0("res", LETTERS[seq_len(n_resources)]), E = ExampleE,
    x0 = rep(0.001, n_species), resources = ExampleResources,
    growth_rates = runif(n_species),
    error_variance = 0.01,
    t_end = 5000,
    t_step = 1
)

# example with trophic levels
n_species <- 10
n_resources <- 15
ExampleEfficiencyMatrix <- randomE(
    n_species = 10, n_resources = 15,
    trophic_levels = c(6, 3, 1),
    trophic_preferences = list(
        c(rep(1, 5), rep(-1, 5), rep(0, 5)),
        c(rep(0, 5), rep(1, 5), rep(-1, 5)),
        c(rep(0, 10), rep(1, 5))
    )
```

```
)

ExampleResources <- c(rep(500, 5), rep(200, 5), rep(50, 5))
tse2 <- simulateConsumerResource(
    n_species = n_species,
    n_resources = n_resources,
    names_species = letters[1:n_species],
    names_resources = paste0(
        "res", LETTERS[1:n_resources]
    ),
    E = ExampleEfficiencyMatrix,
    x0 = rep(0.001, n_species),
    resources = ExampleResources,
    growth_rates = rep(1, n_species),
    # error_variance = 0.001,
    t_end = 5000, t_step = 1
)

# example with trophic priority
n_species <- 4
n_resources <- 6
ExampleE <- randomE(
    n_species = n_species,
    n_resources = n_resources,
    mean_consumption = n_resources,
    mean_production = 0
)
ExampleTrophicPriority <- t(apply(
    matrix(sample(n_species * n_resources),
        nrow = n_species
    ),
    1, order
))
# make sure that for non-consumables resources for each species,
# the priority is 0 (smaller than any given priority)
ExampleTrophicPriority <- (ExampleE > 0) * ExampleTrophicPriority
tse3 <- simulateConsumerResource(
    n_species = n_species,
    n_resources = n_resources,
    E = ExampleE,
    trophic_priority = ExampleTrophicPriority,
    t_end = 2000
)

## End(Not run)
```

---

simulateEventTimes *Generate a vector of event times*

Description

Generate a vector of event times

Usage

```
simulateEventTimes(t_events = NULL, t_duration = NULL, t_end = 1000, ...)
```

Arguments

t_events	Numeric vector; starting time of the events
t_duration	Numeric vector; duration of the events
t_end	Numeric: end time of the simulation
...	: additional parameters to pass to simulationTimes, including t_start, t_step, and t_store.

Value

A vector of time points in the simulation

Examples

```
tEvent <- simulateEventTimes(
    t_events = c(10, 50, 100),
    t_duration = c(1, 2, 3),
    t_end = 100,
    t_store = 100,
    t_step = 1
)
```

---

simulateGLV *Generalized Lotka-Volterra (gLV) simulation*

Description

Simulates time series with the generalized Lotka-Volterra model.

Usage

```
simulateGLV(
  n_species,
  names_species = NULL,
  A = NULL,
  x0 = NULL,
  growth_rates = NULL,
  sigma_drift = 0.001,
  sigma_epoch = 0.1,
  sigma_external = 0.3,
```

```
  sigma_migration = 0.01,
  epoch_p = 0.001,
  t_external_events = NULL,
  t_external_durations = NULL,
  stochastic = TRUE,
  migration_p = 0.01,
  metacommunity_probability = NULL,
  error_variance = 0,
  norm = FALSE,
  t_end = 1000,
  ...
)
```

Arguments

n_species	Integer: number of species
names_species	Character: names of species. If NULL, paste0("sp", seq_len(n_species)) is used. (default: names_species = NULL)
A	Matrix. Interaction matrix defining the positive and negative interactions between n_species. If NULL, randomA(n_species) is used. (Default: NULL)
x0	Numeric scalar. Indicates the initial abundances of simulated species. If NULL, runif(n = n_species, min = 0, max = 1) is used. (Default: NULL)
growth_rates	Numeric scalar. Indicates the growth rates of simulated species. If NULL, runif(n = n_species, min = 0, max = 1) is used. (Default: NULL)
sigma_drift	Numeric: standard deviation of a normally distributed noise applied in each time step (t_step) (default: sigma_drift = 0.001)
sigma_epoch	Numeric: standard deviation of a normally distributed noise applied to random periods of the community composition with frequency defined by the epoch_p parameter (default: sigma_epoch = 0.1)
sigma_external	Numeric: standard deviation of a normally distributed noise applied to user-defined external events/disturbances (default: sigma_external = 0.3)
sigma_migration	Numeric: standard deviation of a normally distributed variable that defines the intensity of migration at each time step (t_step) (default: sigma_migration = 0.01)
epoch_p	Numeric: the probability/frequency of random periodic changes introduced to the community composition (default: epoch_p = 0.001)
t_external_events	Numeric: the starting time points of defined external events that introduce random changes to the community composition (default: t_external_events = NULL)
t_external_durations	Numeric: respective duration of the external events that are defined in the 't_external_events' (times) and sigma_external (std). (default: t_external_durations = NULL)
stochastic	Logical: whether to introduce noise in the simulation. If False, sigma_drift, sigma_epoch, and sigma_external are ignored. (default: stochastic = FALSE)

migration_p — Numeric: the probability/frequency of migration from a metacommunity. (default: migration_p = 0.01)

metacommunity_probability — Numeric: Normalized probability distribution of the likelihood that species from the metacommunity can enter the community during the simulation. If NULL, rdirichlet(1, alpha = rep(1,n_species)) is used. (default: metacommunity_probability = NULL)

error_variance — Numeric: the variance of measurement error. By default it equals to 0, indicating that the result won't contain any measurement error. This value should be non-negative. (default: error_variance = 0)

norm — Logical: whether the time series should be returned with the abundances as proportions (norm = TRUE) or the raw counts (default: norm = FALSE) (default: norm = FALSE)

t_end — Numeric: the end time of the simulationTimes, defining the modeled time length of the community. (default: t_end = 1000)

... — additional parameters, see utils to know more.

Details

Simulates a community time series using the generalized Lotka-Volterra model, defined as dx/dt = x(b+Ax), where x is the vector of species abundances, diag(x) is a diagonal matrix with the diagonal values set to x. A is the interaction matrix and b is the vector of growth rates.

Value

simulateGLV returns a TreeSummarizedExperiment class object

Examples

```
# generate a random interaction matrix
ExampleA <- randomA(n_species = 4, diagonal = -1)

# run the model with default values (only stochastic migration considered)
tse <- simulateGLV(n_species = 4, A = ExampleA)

# run the model with two external disturbances at time points 240 and 480
# with durations equal to 1 (10 time steps when t_step by default is 0.1).
ExampleGLV <- simulateGLV(
    n_species = 4, A = ExampleA,
    t_external_events = c(0, 240, 480), t_external_durations = c(0, 1, 1)
)

# run the model with no perturbation nor migration
set.seed(42)
tse1 <- simulateGLV(
    n_species = 4, A = ExampleA, stochastic = FALSE,
    sigma_migration = 0
)
```

```
# run the model with no perturbation nor migration but with measurement error
set.seed(42)
tse2 <- simulateGLV(
    n_species = 4, A = ExampleA, stochastic = FALSE,
    error_variance = 0.001, sigma_migration = 0
)
```

---

simulateHubbell *Hubbell's neutral model simulation*

Description

Neutral species abundances simulation according to the Hubbell model.

Usage

```
simulateHubbell(
  n_species,
  M,
  carrying_capacity = 1000,
  k_events = 10,
  migration_p = 0.02,
  t_skip = 0,
  t_end,
  norm = FALSE
)
```

Arguments

n_species	Integer scalar. Specifies the amount of different species initially in the local community.
M	Integer scalar. Specifies the amount of different species in the metacommunity, including those of the local community
carrying_capacity	Integer scalar. Indicates the fixed amount of individuals in the local community. (Default: 1000)
k_events	Inteer scalar. Indicates the fixed amount of deaths of local community individuals in each generation (Default: 10)
migration_p	Numeric scalar. The immigration rate; specifies the probability that a death in the local community is replaced by a migrant of the metacommunity rather than by the birth of a local community member (Default: 0.02)
t_skip	Integer scalar. Indicates the number of generations that should not be included in the outputted species abundance matrix. (Default: 0)
t_end	Integer scalar. Indicates the number of simulations to be simulated
norm	Logical scalar. Whether the time series should be returned with the abundances as proportions (norm = TRUE) or the raw counts. (Default: FALSE)

Value

simulateHubbell returns a TreeSummarizedExperiment class object

References

Rosindell, James et al. "The unified neutral theory of biodiversity and biogeography at age ten." Trends in ecology & evolution vol. 26,7 (2011).

Examples

```
tse <- simulateHubbell(
    n_species = 8, M = 10, carrying_capacity = 1000, k_events = 50,
    migration_p = 0.02, t_end = 100
)
```

---

simulateHubbellRates *Hubbell's neutral model simulation applied to time series*

Description

Neutral species abundances simulation according to the Hubbell model. This model shows that losses in society can be replaced either by the birth of individuals or by immigration depending on their probabilities. The specific time between the events of birth or migration is calculated and time effect is considered to determine the next event.

Usage

```
simulateHubbellRates(
  n_species = NULL,
  x0 = NULL,
  names_species = NULL,
  migration_p = 0.01,
  metacommunity_probability = NULL,
  k_events = 1,
  growth_rates = NULL,
  error_variance = 0,
  norm = FALSE,
  t_end = 1000,
  ...
)
```

Arguments

n_species	Integer: number of species
x0	Numeric scalar. Indicates the initial species composition. If NULL, rep(100, n_species) is used.

names_species	Character: names of species. If NULL, paste0("sp", seq_len(n_species)) is used. (default: names_species = NULL)
migration_p	Numeric: the probability/frequency of migration from a metacommunity. (default: migration_p = 0.01)
metacommunity_probability	Numeric: Normalized probability distribution of the likelihood that species from the metacommunity can enter the community during the simulation. If NULL, rdirichlet(1, alpha = rep(1,n_species)) is used. (default: metacommunity_probability = NULL)
k_events	Integer scalar. Indicates the number of events to simulate before updating the sampling distributions. (Default: 1)
growth_rates	Numeric scalar. Indicates the maximum growth rates(mu) of species. If NULL, rep(1, n_species) is used. (Default: NULL)
error_variance	Numeric: the variance of measurement error. By default it equals to 0, indicating that the result won't contain any measurement error. This value should be non-negative. (default: error_variance = 0)
norm	Logical: whether the time series should be returned with the abundances as proportions (norm = TRUE) or the raw counts (default: norm = FALSE) (default: norm = FALSE)
t_end	Numeric: the end time of the simulationTimes, defining the modeled time length of the community. (default: t_end = 1000)
...	additional parameters, see utils to know more.

Value

simulateHubbellRates returns a TreeSummarizedExperiment class object

References

Rosindell, James et al. "The unified neutral theory of biodiversity and biogeography at age ten." Trends in ecology & evolution vol. 26,7 (2011).

Examples

```
set.seed(42)
tse <- simulateHubbellRates(n_species = 5)

miaViz::plotSeries(tse, assay.type = "counts",
    time.col = "time", colour.by  = "rownames")

# no migration, all stochastic birth and death
set.seed(42)
tse1 <- simulateHubbellRates(n_species = 5, migration_p = 0)

# all migration, no stochastic birth and death
set.seed(42)
tse2 <- simulateHubbellRates(
    n_species = 5,
```

```
    migration_p = 1,
    metacommunity_probability = c(0.1, 0.15, 0.2, 0.25, 0.3),
    t_end = 20,
    t_store = 200
)

# all migration, no stochastic birth and death, but with measurement errors
set.seed(42)
tse3 <- simulateHubbellRates(
    n_species = 5,
    migration_p = 1,
    metacommunity_probability = c(0.1, 0.15, 0.2, 0.25, 0.3),
    t_end = 20,
    t_store = 200,
    error_variance = 100
)

# model with specified inputs
set.seed(42)
tse4 <- simulateHubbellRates(
    n_species = 5,
    migration_p = 0.1,
    metacommunity_probability = c(0.1, 0.15, 0.2, 0.25, 0.3),
    t_end = 200,
    t_store = 1000,
    k_events = 5,
    growth_rates = c(1.1, 1.05, 1, 0.95, 0.9)
)
```

`simulateRicker` *Generate time series with the Ricker model*

Description

The Ricker model is a discrete version of the generalized Lotka-Volterra model and is implemented here as proposed by Fisher and Mehta in PLoS ONE 2014.

Usage

```
simulateRicker(
  n_species,
  A,
  names_species = NULL,
  x0 = runif(n_species),
  carrying_capacities = runif(n_species),
  error_variance = 0.05,
  explosion_bound = 10^8,
  t_end = 1000,
```

```
  norm = FALSE,
  ...
)
```

Arguments

n_species	Integer: number of species
A	interaction matrix
names_species	Character: names of species. If NULL, paste0("sp", seq_len(n_species)) is used. (default: names_species = NULL)
x0	Numeric scalar. Indicates the initial abundances of simulated species. If NULL, runif(n = n_species, min = 0, max = 1) is used.
carrying_capacities	Numeric scalar. Indicates carrying capacities. If NULL, runif(n = n_species, min = 0, max = 1) is used.
error_variance	Numeric scalar. Specifies the variance of measurement error. By default it equals to 0, indicating that the result won't contain any measurement error. This value should be non-negative. (Default: 0.05)
explosion_bound	Numeric scalar. Specifies the boundary for explosion. (Default: 10^8)
t_end	Integer scalar. Indicates simulations to be simulated
norm	Logical scalar. Whether normalised abundances (proportions in each generation) is returned. (Default: FALSE)
...	additional parameters, see utils to know more.

Value

simulateRicker returns a TreeSummarizedExperiment class object

References

Fisher & Mehta (2014). Identifying Keystone Species in the Human Gut Microbiome from Metagenomic Timeseries using Sparse Linear Regression. PLoS One 9:e102451

Examples

```
A <- powerlawA(10, alpha = 1.01)
tse <- simulateRicker(n_species = 10, A, t_end = 100)
```

simulateSOI *Self-Organised Instability model (SOI) simulation*

Description

Generate time-series with The Self-Organised Instability (SOI) model. Implements a K-leap method for accelerating stochastic simulation.

Usage

```
simulateSOI(
  n_species,
  x0 = NULL,
  names_species = NULL,
  carrying_capacity = 1000,
  A = NULL,
  k_events = 5,
  t_end = 1000,
  metacommunity_probability = runif(n_species, min = 0.1, max = 0.8),
  death_rates = runif(n_species, min = 0.01, max = 0.08),
  norm = FALSE
)
```

Arguments

n_species	Integer: number of species
x0	Numeric scalar. Specifies initial community abundances If NULL, based on migration rates. (Default: NULL)
names_species	Character: names of species. If NULL, paste0("sp", seq_len(n_species)) is used. (default: names_species = NULL)
carrying_capacity	Integer scalar. Indicates community size, number of available sites (individuals). (Default: 1000)
A	Matrix. Defines the positive and negative interactions between n_species. If NULL, powerlawA(n_species) is used. (Default: NULL)
k_events	Integer scalar. Indicates the number of transition events that are allowed to take place during one leap. Higher values reduce runtime, but also accuracy of the simulation. (Default: 5).
t_end	Numeric scalar. Specifies the end time of the simulation, defining the modeled time length of the community. (Default: 1000)
metacommunity_probability	Numeric scalar: Indicates the normalized probability distribution of the likelihood that species from the metacommunity can enter the community during the simulation. (Default: runif(n_species, min = 0.1, max = 0.8))

death_rates Numeric scalar. Indicates the death rates of each species. (Default: runif(n_species, min = 0.01, max = 0.08))

norm Logical scalar. Whether the time series should be returned with the abundances as proportions (norm = TRUE) or the raw counts. (Default: FALSE)

Value

simulateSOI returns a TreeSummarizedExperiment class object

Examples

```
# Generate interaction matrix
A <- miaSim::powerlawA(10, alpha = 1.2)
# Simulate data from the SOI model
tse <- simulateSOI(
    n_species = 10, carrying_capacity = 1000, A = A,
    k_events = 5, x0 = NULL, t_end = 150, norm = TRUE
)
```

---

simulateStochasticLogistic

Stochastic Logistic simulation

Description

Simulates time series with the (stochastic) logistic model

Usage

```
simulateStochasticLogistic(
  n_species,
  names_species = NULL,
  growth_rates = NULL,
  carrying_capacities = NULL,
  death_rates = NULL,
  x0 = NULL,
  sigma_drift = 0.001,
  sigma_epoch = 0.1,
  sigma_external = 0.3,
  sigma_migration = 0.01,
  epoch_p = 0.001,
  t_external_events = NULL,
  t_external_durations = NULL,
  migration_p = 0.01,
  metacommunity_probability = NULL,
  stochastic = TRUE,
  error_variance = 0,
```

```
  norm = FALSE,
  t_end = 1000,
  ...
)
```

Arguments

n_species	Integer: number of species
names_species	Character: names of species. If NULL, paste0("sp", seq_len(n_species)) is used. (default: names_species = NULL)
growth_rates	Numeric scalar. Specifies the growth rates of simulated species. If NULL, runif(n = n_species, min = 0.1, max = 0.2) is used. (Default: NULL)
carrying_capacities	Numeric scalar. Indicates the max population of species supported in the community. If NULL, runif(n = n_species, min = 1000, max = 2000) is used. (Default: NULL)
death_rates	Numeric scalar. Indicates the death rates of each species. If NULL, runif(n = n_species, min = 0.0005, max = 0.0025) is used. (Default: NULL)
x0	Numeric scalar. Indicates the initial abundances of simulated species. If NULL, runif(n = n_species, min = 0.1, max = 10) is used. (Default: NULL)
sigma_drift	Numeric: standard deviation of a normally distributed noise applied in each time step (t_step) (default: sigma_drift = 0.001)
sigma_epoch	Numeric: standard deviation of a normally distributed noise applied to random periods of the community composition with frequency defined by the epoch_p parameter (default: sigma_epoch = 0.1)
sigma_external	Numeric: standard deviation of a normally distributed noise applied to user-defined external events/disturbances (default: sigma_external = 0.3)
sigma_migration	Numeric: standard deviation of a normally distributed variable that defines the intensity of migration at each time step (t_step) (default: sigma_migration = 0.01)
epoch_p	Numeric: the probability/frequency of random periodic changes introduced to the community composition (default: epoch_p = 0.001)
t_external_events	Numeric: the starting time points of defined external events that introduce random changes to the community composition (default: t_external_events = NULL)
t_external_durations	Numeric: respective duration of the external events that are defined in the 't_external_events' (times) and sigma_external (std). (default: t_external_durations = NULL)
migration_p	Numeric: the probability/frequency of migration from a metacommunity. (default: migration_p = 0.01)
metacommunity_probability	Numeric: Normalized probability distribution of the likelihood that species from the metacommunity can enter the community during the simulation. If NULL,

	rdirichlet(1, alpha = rep(1,n_species)) is used. (default: metacommunity_probability = NULL)
stochastic	Logical scalar. Whether to introduce noise in the simulation. If False, sigma_drift, sigma_epoch, and sigma_external are ignored. (Default: TRUE)
error_variance	Numeric: the variance of measurement error. By default it equals to 0, indicating that the result won't contain any measurement error. This value should be non-negative. (default: error_variance = 0)
norm	Logical: whether the time series should be returned with the abundances as proportions (norm = TRUE) or the raw counts (default: norm = FALSE) (default: norm = FALSE)
t_end	Numeric: the end time of the simulationTimes, defining the modeled time length of the community. (default: t_end = 1000)
...	additional parameters, see utils to know more.

Details

The change rate of the species was defined as dx/dt = b*x*(1-(x/k))*rN - dr*x, where b is the vector of growth rates, x is the vector of initial species abundances, k is the vector of maximum carrying capacities, rN is a random number ranged from 0 to 1 which changes in each time step, dr is the vector of constant death rates. Also, the vectors of initial dead species abundances can be set. The number of species will be set to 0 if the dead species abundances surpass the alive species abundances.

Value

simulateStochasticLogistic returns a TreeSummarizedExperiment class object

Examples

```
# Example of logistic model without stochasticity, death rates, or external
# disturbances
set.seed(42)
tse <- simulateStochasticLogistic(
    n_species = 5,
    stochastic = FALSE, death_rates = rep(0, 5)
)

# Adding a death rate
set.seed(42)
tse1 <- simulateStochasticLogistic(
    n_species = 5,
    stochastic = FALSE, death_rates = rep(0.01, 5)
)

# Example of stochastic logistic model with measurement error
set.seed(42)
tse2 <- simulateStochasticLogistic(
    n_species = 5,
    error_variance = 1000
```

```
)

# example with all the initial parameters defined by the user
set.seed(42)
tse3 <- simulateStochasticLogistic(
    n_species = 2,
    names_species = c("species1", "species2"),
    growth_rates = c(0.2, 0.1),
    carrying_capacities = c(1000, 2000),
    death_rates = c(0.001, 0.0015),
    x0 = c(3, 0.1),
    sigma_drift = 0.001,
    sigma_epoch = 0.3,
    sigma_external = 0.5,
    sigma_migration = 0.002,
    epoch_p = 0.001,
    t_external_events = c(100, 200, 300),
    t_external_durations = c(0.1, 0.2, 0.3),
    migration_p = 0.01,
    metacommunity_probability = miaSim::rdirichlet(1, alpha = rep(1, 2)),
    stochastic = TRUE,
    error_variance = 0,
    norm = FALSE, # TRUE,
    t_end = 400,
    t_start = 0, t_step = 0.01,
    t_store = 1500
)
```

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