Package: TiPS (via r-universe)

Type Package

Title Trajectories and Phylogenies Simulator

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Description Generates stochastic time series and genealogies
associated with a population dynamics model. Times series are
simulated using the Gillespie exact and approximate algorithms
and a new algorithm we introduce that uses both approaches to
optimize the time execution of the simulations. Genealogies are
simulated from a trajectory using a backwards-in-time based
approach. Methods are described in Danesh G et al (2022)
<doi:10.1111/2041-210X.14038>.

License GPL (>= 2)

Depends R (>= 3.5.0)

Imports graphics, grDevices, gtools, inline, methods, Rcpp (>=
0.12.14), stats, stringr, utils

Suggests knitr, rmarkdown, ape, testthat (>= 3.0.0)

LinkingTo Rcpp

VignetteBuilder knitr

NeedsCompilation yes

RoxygenNote 7.1.1

Encoding UTF-8

BugReports https://gitlab.in2p3.fr/ete/tips/-/issues

URL https://gitlab.in2p3.fr/ete/tips/

Config/testthat/edition 3

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Repository https://gonchedanesh.r-universe.dev

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Contents

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build_simulator	*Build a simulator of dynamics of population-model*

Description

A simulator is built by supplying reactions of the model described by our formalism or described by differential equations The returned function will be used to simulate trajectories, that can further be used to simulate phylogenies.

Usage

```
build_simulator(reactions, functions = NULL)
```

Arguments

reactions	A character vector of reactions describing the input model.
functions	A named vector where functions are defined.

Value

An object of class `simulation`, which is a function that can be used to simulate trajectories from the model.

Author(s)

Gonche Danesh

Examples

```
## Not run:
# Build a simulator for an SIR model
reactions <- c('S [beta * S * I] -> I',
               'I [gamma * I] -> R')

sir.simu <- build_simulator(reactions = reactions)

# Run a simulation of a trajectory
sir_traj <- sir.simu(paramValues = c(gamma = 1, beta = 2e-4),
                     initialStates = c(I = 1, S = 9999, R = 0),
                     times = c(0, 20), ,
                     method = "exact",
                     seed = 166)

# The output is a named list containing the trajectory, the algorithm used,
# the parameter values and the reactions of the model.
names(sir_traj)

# Print head of the simulated trajectory
head(sir_traj$traj)

# Plot the trajectory
plot(sir_traj)

## End(Not run)
```

---

plot.simutraj   *Plot an object of class* simutraj.

Description

Plot an object of class simutraj.

Usage

```
## S3 method for class 'simutraj'
plot(x, ...)
```

Arguments

x   An object of simutraj resulting from running a simulator of trajectories built
            using the build_simulator function.

...   Arguments to be passed to methods, such as graphical parameters

Author(s)

Gonche Danesh

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simulate_tree | *Simulates a phylogeny using a beackward-in-time process using sampling dates and a trajectory*

Description

Simulates a phylogeny using a beackward-in-time process using sampling dates and a trajectory

Usage

```
simulate_tree(
  simuResults,
  dates,
  deme,
  sampled,
  root,
  isFullTrajectory = FALSE,
  nTrials = 1,
  addInfos = FALSE,
  resampling = FALSE,
  verbose = FALSE,
  seed = 0,
  outFile = "",
  format = "newick"
)
```

Arguments

simuResults	Object of class `simutraj` resulting from running a simulator of trajectories built using the `build_simulator` function.
dates	Contains the sampling dates. Can be a vector (for example using `seq` function), can be a named list or a file with header.
deme	A vector with the compartments that contribute to the simulation of phylogeny.
sampled	A named vector with the proportions of sampling for each compartment. This is used in case there are multiple deme compartments where the sampling dates will be randomly associated to a compartment to sample. Sum of `sampled` must be 1.
root	Name of the compartment from which the phylogeny is rooted.
isFullTrajectory	
	Boolean to define if death events generate or not leaves. By default, `isFullTrajectory=FALSE`.
nTrials	Integer indicating the number of unsuccessful simulation trials allowed before giving up.
addInfos	Boolean to define if each internal node' name will be the reaction. By default, `addInfos=FALSE`.

resampling	Boolean to allow a sampled individual to transmit the pathogen once again. By default, `resampling=FALSE`.
verbose	Boolean to allow printing time execution of simulation
seed	Seed to initialize the random generator, for better reproducibility. By default, `seed=0` and the seed value is randomly generated.
outFile	Output file name to write tree. By default, tree is not written in output file.
format	Output tree format if output file is given. Values are either `format = "newick"` ou `format = "nexus"`. By default, `format = "newick"`

Value

An object of class `ape::phylo`.

Author(s)

Gonche Danesh

Examples

```
## Not run:
# A multi-type birth-death model with birth rate beta,
# death rate gamma, mutation rates m1 and m2
# and I1 and I2 the number of infected individuals of each type.
# With parameter beta varying over 2 time intervals.
reactions <- c("0 [beta1 * I1] -> I1","I1 [gamma1 * I1] -> 0",
"I1 [mu1 * I1] -> I2","0 [beta2 * I2] -> I2",
"I2 [gamma2 * I2] -> 0","I2 [mu2 * I2] -> I1")

BD_simu <- build_simulator(reactions)
initialStates <- c(I1 = 0, I2 = 1)
times <- c(1975, 1998, 2018)
theta <- list(gamma1 = c(0.2, 0.09), gamma2 = 0.1, mu1 = 0.025,
mu2 = 0.021, beta1 = c(0.26,0.37), beta2 = 0.414)
BDres <- BD_simu(paramValues = theta,
                 initialStates = initialStates,
                 times = times,
                 tau = 0.08,
                 method = "approximate",
        seed = 994543)
# Let's generate 100 sampling dates from 2015 and 2018
dates_bd <- seq(from=2015, to=2018, length.out=100)
BD_tree <- simulate_tree(simuResults = BDres,
                         dates = dates,
                         deme = c("I"),
                         sampled = c(I=1),
                         root = "I",
                         isFullTrajectory = FALSE,
                         seed = 973360)
BD_tree$seed
# Plot the simulated phylogeny using the \code{ape::plot.phylo} function.
ape::plot.phylo(BD_tree)
```

```
## End(Not run)
```

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