Package ‘TiPS’

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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 (2020) <doi:10.1101/2020.11.09.373795>.
License GPL (>= 2)
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**build_simulator**  
*Builds 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. The mandatory arguments of the returned function are the following:

- `paramValues`  
  numerical list : values of parameters of the model

- `initialStates`  
  numerical vector : values of initial number of individuals

- `times`  
  numerical vector : time intervals.

- `nTrials`  
  integer : number of trials of simulation.

- `seed`  
  integer : seed for reproducible simulations.

- `verbose`  
  logical: whether to print some information

**Author(s)**

Gonche Danesh
# 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 = list(gamma = 1, beta = 2e-4),
                      initialStates = c(I = 1, S = 9999, R = 0),
                      times = c(0, 20),
                      nTrials = 10,
                      seed=166)

# The output is a list with the trajectory, the algorithm, the parameter values and the reactions
names(sir_traj)

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

# Plot the trajectory
plot(sir_traj)

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

### Description
Plot an object of class simutraj.

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

### Arguments
- `x`  
  An object of simutraj class resulting from running a simulator of trajectories built using the `build_simulator` function.
- `...`  
  Further arguments to be passed to `plot` or to `plot.simutraj`.

### Value
`plot.simutraj` returns a graphical plot of the trajectory, i.e the number if individuals of each compartment through time.

### Author(s)
Gonche Danesh
**simulate_tree**

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

### Description

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

### Usage

```r
simulate_tree(
  simuResults,
  dates,
  deme,
  sampled,
  root,
  isFullTrajectory = FALSE,
  nTrials = 1,
  addInfos = FALSE,
  resampling = FALSE,
  verbose = FALSE
)
```

### 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`: Vector containing the compartment names that contribute directly or indirectly to the 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`: logical: whether to simulate complete phylogeny where all death events generate leaves. By default, `isFullTrajectory=FALSE`.
- `addInfos`: logical: whether to define each internal node’s name by the reaction. By default, `addInfos=FALSE`.
- `resampling`: logical: whether to allow a sampled individual to transmit the pathogen once again. By default, `resampling=FALSE`.
- `nTrials`: Number of trials of simulations if the simulation fails, meaning that the simulation ends before the final time asked as input. By default, `nTrials=1`.
- `verbose`: logical: whether to print some information.
simulate_tree

Value
An object of class ape::phylo.

Author(s)
Gonche Danesh
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