

# Package ‘TiPS’

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**Type** Package

**Title** Trajectories and Phylogenies Simulator

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**Maintainer** Gonche Danesh <gonche.danesh@gmail.com>

**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](https://doi.org/10.1101/2020.11.09.373795)>.

**License** GPL (>= 2)

**SystemRequirements** C++11

**Depends** R (>= 3.2.0)

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

**Suggests** knitr, rmarkdown, ape

**LinkingTo** Rcpp

**VignetteBuilder** knitr

**NeedsCompilation** yes

**RoxygenNote** 7.1.0

**Encoding** UTF-8

**Author** Gonche Danesh [aut, cre, cph],  
Emma Saulnier [aut, cph],  
Marc Choisy [aut, cph, ths],  
Samuel Alizon [aut, cph, ths]

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build_simulator	<i>Builds a simulator of dynamics of population-model</i>
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### 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.
verbose	logical: whether to print some information

### Author(s)

Gonche Danesh

**Examples**

```
# 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)

# 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.*

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**Description**

Plot an object of class simutraj.

**Usage**

```
## 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 of individuals of each compartment through time.

**Author(s)**

Gonche Danesh

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simulate_tree	<i>Simulates a phylogeny using a backward-in-time process using sampling dates and a trajectory</i>
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### Description

Simulates a phylogeny using a backward-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
)
```

### Arguments

simuResults	Object of class <code>simutraj</code> resulting from running a simulator of trajectories built using the <code>build_simulator</code> function.
dates	Contains the sampling dates. Can be a vector (for example using <code>seq</code> 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 <code>sampled</code> 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, <code>isFullTrajectory=FALSE</code> .
addInfos	logical: whether to define each internal node's name by the reaction. By default, <code>addInfos=FALSE</code> .
resampling	logical: whether to allow a sampled individual to transmit the pathogen once again. By default, <code>resampling=FALSE</code> .
nTrials	Number of trials of simulations if the simulation fails, meaning that the simulation ends before the final time asked as input. By default, <code>nTrials=1</code> .
verbose	logical: whether to print some information

*simulate\_tree*

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**Value**

An object of class `ape::phylo`.

**Author(s)**

Gonche Danesh

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