

# Package: nosoi (via r-universe)

September 7, 2024

**Type** Package

**Title** A Forward Agent-Based Transmission Chain Simulator

**Version** 1.1.2

**Description** The aim of 'nosoi' (pronounced no.si) is to provide a flexible agent-based stochastic transmission chain/epidemic simulator (Lequime et al. Methods in Ecology and Evolution 11:1002-1007). It is named after the daimones of plague, sickness and disease that escaped Pandora's jar in the Greek mythology. 'nosoi' is able to take into account the influence of multiple variable on the transmission process (e.g. dual-host systems (such as arboviruses), within-host viral dynamics, transportation, population structure), alone or taken together, to create complex but relatively intuitive epidemiological simulations.

**URL** <https://github.com/slequime/nosoi>,  
<https://slequime.github.io/nosoi/>

**BugReports** <https://github.com/slequime/nosoi/issues>

**Language** en-US

**License** GPL-3

**Encoding** UTF-8

**RoxygenNote** 7.2.3

**Depends** data.table (>= 1.12.0), R (>= 3.5.0)

**Imports** stats (>= 3.5.2), methods (>= 3.5.2), raster (>= 2.8-19)

**Suggests** testthat (>= 2.1.0), knitr, rmarkdown, igraph, ggplot2, ggnetwork, intergraph, viridis, gifski, png, gganimate, ape (>= 5.3), tidytree (>= 0.3.3), treeio (>= 1.14.0), ggtree (>= 2.4.0), magrittr (>= 1.5), dplyr (>= 0.8.0), covr

**VignetteBuilder** knitr

**Repository** <https://slequime.r-universe.dev>

**RemoteUrl** <https://github.com/slequime/nosoi>

**RemoteRef** HEAD

**RemoteSha** e2b8bc7964f0ca211f0e14dbc08c11dcdaeba742

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dualContinuous	<i>Dual-host pathogen in structured (continuous) hosts populations</i>
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## Description

This function runs a dual-host transmission chain simulation, with structured hosts populations (such as spatial features) in a shared continuous space. The simulation stops either at the end of given time (specified by `length.sim`) or when the number of hosts infected threshold (`max.infected`) is passed. The movement of hosts on the continuous space map is a random walk (Brownian motion) that can be modified towards a biased random walk where hosts tend to be attracted to higher values of the environmental variable defined by the raster.

## Usage

```
dualContinuous(
  length.sim,
  max.infected.A,
  max.infected.B,
  init.individuals.A,
  init.individuals.B,
  init.structure.A,
  init.structure.B,
  structure.raster.A,
  structure.raster.B,
  pExit.A,
  param.pExit.A,
```

```
timeDep.pExit.A = FALSE,
diff.pExit.A = FALSE,
hostCount.pExit.A = FALSE,
pMove.A,
param.pMove.A,
timeDep.pMove.A = FALSE,
diff.pMove.A = FALSE,
hostCount.pMove.A = FALSE,
sdMove.A,
param.sdMove.A,
diff.sdMove.A = FALSE,
timeDep.sdMove.A = FALSE,
hostCount.sdMove.A = FALSE,
attracted.by.raster.A = FALSE,
nContact.A,
param.nContact.A,
timeDep.nContact.A = FALSE,
diff.nContact.A = FALSE,
hostCount.nContact.A = FALSE,
pTrans.A,
param.pTrans.A,
timeDep.pTrans.A = FALSE,
diff.pTrans.A = FALSE,
hostCount.pTrans.A = FALSE,
prefix.host.A = "H",
pExit.B,
param.pExit.B,
timeDep.pExit.B = FALSE,
diff.pExit.B = FALSE,
hostCount.pExit.B = FALSE,
pMove.B,
param.pMove.B,
timeDep.pMove.B = FALSE,
diff.pMove.B = FALSE,
hostCount.pMove.B = FALSE,
sdMove.B,
param.sdMove.B,
diff.sdMove.B = FALSE,
timeDep.sdMove.B = FALSE,
hostCount.sdMove.B = FALSE,
attracted.by.raster.B = FALSE,
nContact.B,
param.nContact.B,
timeDep.nContact.B = FALSE,
diff.nContact.B = FALSE,
hostCount.nContact.B = FALSE,
pTrans.B,
param.pTrans.B,
```

```

timeDep.pTrans.B = FALSE,
diff.pTrans.B = FALSE,
hostCount.pTrans.B = FALSE,
prefix.host.B = "V",
print.progress = TRUE,
print.step = 10
)

```

### Arguments

`length.sim` specifies the length (in unit of time) over which the simulation should be run.

`max.infected.A` specifies the maximum number of individual hosts A that can be infected in the simulation.

`max.infected.B` specifies the maximum number of individual hosts B that can be infected in the simulation.

`init.individuals.A`  
number of initially infected individuals (hosts A).

`init.individuals.B`  
number of initially infected individuals (hosts B).

`init.structure.A`  
in which location the initially infected host-A individuals are located. A vector of coordinates in the same coordinate space as the raster (NA if `init.individual.A` is 0).

`init.structure.B`  
in which location the initially infected host-B individuals are located. A vector of coordinates in the same coordinate space as the raster (NA if `init.individual.B` is 0).

`structure.raster.A`  
raster object defining the environmental variable for host-type A.

`structure.raster.B`  
raster object defining the environmental variable for host B.

`pExit.A` function that gives the probability to exit the simulation for an infected host A (either moving out, dying, etc.).

`param.pExit.A` parameter names (list of functions) for the `pExit` for host-type A.

`timeDep.pExit.A`  
is `pExit` of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?

`diff.pExit.A` does `pExit` of host-type A depend on the environmental variable (set by the raster) (TRUE/FALSE).

`hostCount.pExit.A`  
does `pExit` of host-type A vary with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); if TRUE, `diff.pExit.A` should be TRUE.

`pMove.A` function that gives the probability of a host moving as a function of time for host-type A.

`param.pMove.A` parameter names (list of functions) for the `pMove` for host-type A.

`timeDep.pMove.A`  
is `pMove` of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?

<code>diff.pMove.A</code>	does pMove of host-type A depend on the environmental variable (set by the raster) (TRUE/FALSE).A.
<code>hostCount.pMove.A</code>	does pMove of host-type A vary with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.pMove.A</code> should be TRUE.
<code>sdMove.A</code>	function that gives the distance traveled for host-type A (based on coordinates); output is the standard deviation value for the Brownian motion.
<code>param.sdMove.A</code>	parameter names (list of functions) for sdMove for host-type A.
<code>diff.sdMove.A</code>	does sdMove of host-type A depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>timeDep.sdMove.A</code>	is sdMove of host-type A dependent on the absolute time of the simulation (TRUE/FALSE) ?
<code>hostCount.sdMove.A</code>	does sdMove varies with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); <code>diff.sdMove.A</code> should be TRUE.
<code>attracted.by.raster.A</code>	should the host-type A be attracted by higher values in the environmental raster? (TRUE/FALSE).
<code>nContact.A</code>	function that gives the number of potential transmission events per unit of time for host-type A.
<code>param.nContact.A</code>	parameter names (list of functions) for param.nContact for host-type A.
<code>timeDep.nContact.A</code>	is nContact of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?
<code>diff.nContact.A</code>	does nContact of host-type A depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>hostCount.nContact.A</code>	does nContact vary with the host count (of either host-type A or B) in each raster cell?? (TRUE/FALSE); <code>diff.nContact.A</code> should be TRUE.
<code>pTrans.A</code>	function that gives the probability of transmit a pathogen as a function of time since infection for host A.
<code>param.pTrans.A</code>	parameter names (list of functions) for the pExit for host A.
<code>timeDep.pTrans.A</code>	is pTrans of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?
<code>diff.pTrans.A</code>	does pTrans of host-type A depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>hostCount.pTrans.A</code>	does pTrans vary with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); <code>diff.pTrans.A</code> should be TRUE.
<code>prefix.host.A</code>	character(s) to be used as a prefix for the host A identification number.

<code>pExit.B</code>	function that gives the probability to exit the simulation for an infected host B (either moving out, dying, etc.).
<code>param.pExit.B</code>	parameter names (list of functions) for the <code>pExit</code> for host-type B.
<code>timeDep.pExit.B</code>	is <code>pExit</code> of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
<code>diff.pExit.B</code>	does <code>pExit</code> of host-type B depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>hostCount.pExit.B</code>	does <code>pExit</code> of host-type B vary with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.pExit.B</code> should be TRUE.
<code>pMove.B</code>	function that gives the probability of a host moving as a function of time for host-type B.
<code>param.pMove.B</code>	parameter names (list of functions) for the <code>pMove</code> for host-type B.
<code>timeDep.pMove.B</code>	is <code>sdMove</code> of host-type B dependent on the absolute time of the simulation (TRUE/FALSE) for host-type B.
<code>diff.pMove.B</code>	does <code>pMove</code> of host-type B depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>hostCount.pMove.B</code>	does <code>pMove</code> of host-type B vary with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.pMove.B</code> should be TRUE.
<code>sdMove.B</code>	function that gives the distance traveled for host-type B (based on coordinates); output is the standard deviation value for the Brownian motion.
<code>param.sdMove.B</code>	parameter names (list of functions) for <code>sdMove</code> for host-type B.
<code>diff.sdMove.B</code>	does <code>sdMove</code> of host-type B depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>timeDep.sdMove.B</code>	is <code>sdMove</code> of host-type B dependent on the absolute time of the simulation (TRUE/FALSE) ?
<code>hostCount.sdMove.B</code>	does <code>sdMove</code> of host-type B vary with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.sdMove.B</code> should be TRUE.
<code>attracted.by.raster.B</code>	should the host-type B be attracted by higher values in the environmental raster? (TRUE/FALSE)
<code>nContact.B</code>	function that gives the number of potential transmission events per unit of time for host B.
<code>param.nContact.B</code>	parameter names (list of functions) for <code>param.nContact</code> for host-type B.
<code>timeDep.nContact.B</code>	is <code>nContact</code> of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
<code>diff.nContact.B</code>	does <code>nContact</code> of host-type B depend on the environmental variable (set by the raster) (TRUE/FALSE).

<code>hostCount.nContact.B</code>	does <code>nContact</code> of host-type B vary with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.nContact.B</code> should be TRUE.
<code>pTrans.B</code>	function that gives the probability of transmit a pathogen as a function of time since infection for host B.
<code>param.pTrans.B</code>	parameter names (list of functions) for the <code>pExit</code> for host-type B.
<code>timeDep.pTrans.B</code>	is <code>pTrans</code> of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
<code>diff.pTrans.B</code>	does <code>pTrans</code> of host-type B depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>hostCount.pTrans.B</code>	does <code>pTrans</code> of host-type B vary with the host count (of either host-type A or B) in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.pTrans.B</code> should be TRUE.
<code>prefix.host.B</code>	character(s) to be used as a prefix for the host B identification number.
<code>print.progress</code>	if TRUE, displays a progress bar (current time/length.sim).
<code>print.step</code>	<code>print.progress</code> is TRUE, step with which the progress message will be printed.

## Details

The `pExit` and `pTrans` functions should return a single probability (a number between 0 and 1), and `nContact` a positive natural number (positive integer) or 0.

The `param` arguments should be a list of functions or NA. Each item name in the parameter list should have the same name as the argument in the corresponding function.

The use of `timeDep` (switch to TRUE) makes the corresponding function use the argument `preTime` (for "present time").

## Value

An object of class `nosoiSim`, containing all results of the simulation.

## Raster

The structure `raster(s)` provided should be of class `raster`. High values of the environmental variable can attract hosts if `attracted.by.raster` is TRUE. Raster have to share the same space (i.e. also the same cell size and ID).

## Order of Arguments

The user specified function's arguments should follow this order: `t` (mandatory), `preTime` (optional, only if `timeDep` is TRUE), `current.env.value` (optional, only if `diff` is TRUE), `host.count.A` or `host.count.B` (optional, only if `hostCount` is TRUE) and parameters specified in the list.

### Structure Parameters

The `pMove` function should return a single probability (a number between 0 and 1), and `sdMove` a real number (keep in mind this number is related to your coordinate space).

The use of `diff` (switch to TRUE) makes the corresponding function use the argument `current.env.value` (for "current environmental value").

The use of `hostCount` (switch to TRUE) makes the corresponding function use the argument `host.count`.

### Suffixes

The suffix `.A` or `.B` specifies if the considered function or parameter concerns host type A or B.

### See Also

For simulations with a discrete structure, see [dualDiscrete](#). For simulations without any structures, see [dualNone](#).

### Examples

```
library(raster)

#Generating a raster for the movement
set.seed(860)

test.raster <- raster(nrows=100, ncols=100, xmn=-50, xmx=50, ymn=-50, ymx=50)
test.raster[] <- runif(10000, -80, 180)
test.raster <- focal(focal(test.raster, w=matrix(1, 5, 5), mean), w=matrix(1, 5, 5), mean)

t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Move_fct <- function(t){return(0.1)}

sdMove_fct = function(t,current.env.value){return(100/(current.env.value+1))}

p_Exit_fct <- function(t){return(0.08)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact = function(t){round(rnorm(1, 3, 1), 0)}

start.pos <- c(0,0)

set.seed(805)
test.nosoi <- nosoiSim(type="dual", popStructure="continuous",
  length.sim=200,
  max.infected.A=500,
  max.infected.B=500,
  init.individuals.A=1,
```



```

init.individuals.B=0,
init.structure.A=start.pos,
init.structure.B=NA,
structure.raster.A=test.raster,
structure.raster.B=test.raster,
pExit.A=p_Exit_fct,
param.pExit.A=NA,
timeDep.pExit.A=FALSE,
diff.pExit.A=FALSE,
pMove.A=p_Move_fct,
param.pMove.A=NA,
timeDep.pMove.A=FALSE,
diff.pMove.A=FALSE,
diff.sdMove.A=TRUE,
sdMove.A=sdMove_fct,
param.sdMove.A=NA,
attracted.by.raster.A=TRUE,
nContact.A=time_contact,
param.nContact.A=NA,
timeDep.nContact.A=FALSE,
diff.nContact.A=FALSE,
pTrans.A=proba,
param.pTrans.A=list(p_max=p_max_fct,
                    t_incub=t_incub_fct),
timeDep.pTrans.A=FALSE,
diff.pTrans.A=FALSE,
prefix.host.A="H",
pExit.B=p_Exit_fct,
param.pExit.B=NA,
timeDep.pExit.B=FALSE,
diff.pExit.B=FALSE,
pMove.B=p_Move_fct,
param.pMove.B=NA,
timeDep.pMove.B=FALSE,
diff.pMove.B=FALSE,
diff.sdMove.B=TRUE,
sdMove.B=sdMove_fct,
param.sdMove.B=NA,
attracted.by.raster.B=TRUE,
nContact.B=time_contact,
param.nContact.B=NA,
timeDep.nContact.B=FALSE,
diff.nContact.B=FALSE,
pTrans.B=proba,
param.pTrans.B=list(p_max=p_max_fct,
                    t_incub=t_incub_fct),
timeDep.pTrans.B=FALSE,
diff.pTrans.B=FALSE,
prefix.host.B="V")

```

test.nosoi

---

dualDiscrete

*Dual-host pathogen in structured (discrete) hosts populations*


---

### Description

This function, that can be wrapped within `nosoiSim`, runs a dual-host transmission chain simulation, with discrete hosts populations structures (e.g. spatial, socio-economic, etc.). The simulation stops either at the end of given time (specified by `length.sim`) or when the number of hosts infected threshold (`max.infected`) is crossed.

### Usage

```
dualDiscrete(
  length.sim,
  max.infected.A,
  max.infected.B,
  init.individuals.A,
  init.individuals.B,
  init.structure.A,
  init.structure.B,
  structure.matrix.A,
  structure.matrix.B,
  pExit.A,
  param.pExit.A,
  timeDep.pExit.A = FALSE,
  diff.pExit.A = FALSE,
  hostCount.pExit.A = FALSE,
  pMove.A,
  param.pMove.A,
  timeDep.pMove.A = FALSE,
  diff.pMove.A = FALSE,
  hostCount.pMove.A = FALSE,
  nContact.A,
  param.nContact.A,
  timeDep.nContact.A = FALSE,
  diff.nContact.A = FALSE,
  hostCount.nContact.A = FALSE,
  pTrans.A,
  param.pTrans.A,
  timeDep.pTrans.A = FALSE,
  diff.pTrans.A = FALSE,
  hostCount.pTrans.A = FALSE,
  prefix.host.A = "H",
  pExit.B,
  param.pExit.B,
  timeDep.pExit.B = FALSE,
  diff.pExit.B = FALSE,
```

```

    hostCount.pExit.B = FALSE,
    pMove.B,
    param.pMove.B,
    timeDep.pMove.B = FALSE,
    diff.pMove.B = FALSE,
    hostCount.pMove.B = FALSE,
    nContact.B,
    param.nContact.B,
    timeDep.nContact.B = FALSE,
    diff.nContact.B = FALSE,
    hostCount.nContact.B = FALSE,
    pTrans.B,
    param.pTrans.B,
    timeDep.pTrans.B = FALSE,
    diff.pTrans.B = FALSE,
    hostCount.pTrans.B = FALSE,
    prefix.host.B = "V",
    print.progress = TRUE,
    print.step = 10
)

```

### Arguments

`length.sim` specifies the length (in unit of time) over which the simulation should be run.

`max.infected.A` specifies the maximum number of individual hosts A that can be infected in the simulation.

`max.infected.B` specifies the maximum number of individual hosts B that can be infected in the simulation.

`init.individuals.A`  
number of initially infected individuals (hosts A).

`init.individuals.B`  
number of initially infected individuals (hosts B).

`init.structure.A`  
in which state (e.g. location) the initially infected individuals of host-type A are located (NA if `init.individual.A` is 0)?

`init.structure.B`  
in which state (e.g. location) the initially infected individuals of host-type B are located (NA if `init.individual.B` is 0)?

`structure.matrix.A`  
transition matrix (probabilities) to go from location A (row) to B (column) for host-type A.

`structure.matrix.B`  
transition matrix (probabilities) to go from location A (row) to B (column) for host-type B.

`pExit.A` function that gives the probability to exit the simulation for an infected host A (either moving out, dying, etc.).

`param.pExit.A` parameter names (list of functions) for the `pExit` for host-type A.

timeDep.pExit.A	is pExit of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?
diff.pExit.A	is pExit of host-type A different between states of the structured population (TRUE/FALSE)?
hostCount.pExit.A	does pExit of host-type A vary with the host count (of either host-type A or B) in the state? (TRUE/FALSE); diff.pExit.A should be TRUE.
pMove.A	function that gives the probability of a host moving as a function of time for host-type A.
param.pMove.A	parameter names (list of functions) for the pMove for host-type A.
timeDep.pMove.A	is pMove of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?
diff.pMove.A	is pMove of host-type A different between states of the structured population (TRUE/FALSE)?
hostCount.pMove.A	does pMove of host-type A vary with the host count (of either host A or B) in the state? (TRUE/FALSE); diff.pMove.A should be TRUE.
nContact.A	function that gives the number of potential transmission events per unit of time for host-type A.
param.nContact.A	parameter names (list of functions) for param.nContact for host-type A.
timeDep.nContact.A	is nContact of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?
diff.nContact.A	is nContact of host-type A different between states of the structured population (TRUE/FALSE)?
hostCount.nContact.A	does nContact of host-type A vary with the host count (of either host A or B) in the state? (TRUE/FALSE); diff.nContact.A should be TRUE.
pTrans.A	function that gives the probability of transmit a pathogen as a function of time since infection for host A.
param.pTrans.A	parameter names (list of functions) for the pExit for host A.
timeDep.pTrans.A	is pTrans of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?
diff.pTrans.A	is pTrans of host-type A different between states of the structured population (TRUE/FALSE)?
hostCount.pTrans.A	does pTrans of host-type A vary with the host count (of either host A or B) in the state? (TRUE/FALSE); diff.pTrans.A should be TRUE.
prefix.host.A	character(s) to be used as a prefix for the host A identification number.
pExit.B	function that gives the probability to exit the simulation for an infected host B (either moving out, dying, etc.).
param.pExit.B	parameter names (list of functions) for the pExit for host-type B.

timeDep.pExit.B	is pExit of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
diff.pExit.B	is pExit of host-type B different between states of the structured population (TRUE/FALSE)?
hostCount.pExit.B	does pExit of host-type B vary with the host count (of either host A or B) in the state? (TRUE/FALSE); diff.pExit.B should be TRUE.
pMove.B	function that gives the probability of a host moving as a function of time for host-type B.
param.pMove.B	parameter names (list of functions) for the pMove for host-type B.
timeDep.pMove.B	is sdMove of host-type B dependent on the absolute time of the simulation (TRUE/FALSE) for host-type B.
diff.pMove.B	is pMove of host-type B different between states of the structured population (TRUE/FALSE)?
hostCount.pMove.B	does pMove of host-type B vary with the host count (of either host A or B) in the state? (TRUE/FALSE); diff.pMove.B should be TRUE.
nContact.B	function that gives the number of potential transmission events per unit of time for host B.
param.nContact.B	parameter names (list of functions) for param.nContact for host-type B.
timeDep.nContact.B	is nContact of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
diff.nContact.B	is nContact of host-type B different between states of the structured population (TRUE/FALSE)?
hostCount.nContact.B	does nContact of host-type B vary with the host count (of either host A or B) in the state? (TRUE/FALSE); diff.nContact.B should be TRUE.
pTrans.B	function that gives the probability of transmit a pathogen as a function of time since infection for host B.
param.pTrans.B	parameter names (list of functions) for the pExit for host-type B.
timeDep.pTrans.B	is pTrans of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
diff.pTrans.B	is pTrans host-type B different between states of the structured population (TRUE/FALSE)?
hostCount.pTrans.B	does pTrans of host-type B vary with the host count (of either host A or B) in the state? (TRUE/FALSE); diff.pTrans.B should be TRUE.
prefix.host.B	character(s) to be used as a prefix for the host B identification number.
print.progress	if TRUE, displays a progress bar (current time/length.sim).
print.step	print.progress is TRUE, step with which the progress message will be printed.

## Details

The `pExit` and `pTrans` functions should return a single probability (a number between 0 and 1), and `nContact` a positive natural number (positive integer) or 0.

The `param` arguments should be a list of functions or NA. Each item name in the parameter list should have the same name as the argument in the corresponding function.

The use of `timeDep` (switch to TRUE) makes the corresponding function use the argument `preTime` (for "present time").

## Value

An object of class `nosoiSim`, containing all results of the simulation.

## Structure Matrix

The structure/transition matrix provided should be of class `matrix`, with the same number of rows and columns, rows representing departure state and column the arrival state. All rows should add to 1. Probability values can be different for hosts A and B (so two different matrices), but the name of the column and the rows should be shared.

## Order of Arguments

The user specified function's arguments should follow this order: `t` (mandatory), `preTime` (optional, only if `timeDep` is TRUE), `current.in` (optional, only if `diff` is TRUE), `host.count.A` or `host.count.B` (optional, only if `hostCount` is TRUE) and parameters specified in the list.

## Structure Parameters

The `pMove` function should return a single probability (a number between 0 and 1).

The use of `diff` (switch to TRUE) makes the corresponding function use the argument `current.in` (for "currently in"). Your function should in that case give a result for every possible discrete state.

The use of `hostCount` (switch to TRUE) makes the corresponding function use the argument `host.count`.

## Suffixes

The suffix `.A` or `.B` specifies if the considered function or parameter concerns host type A or B.

## See Also

For simulations with a structure in continuous space, see [dualContinuous](#). For simulations without any structures, see [dualNone](#).

## Examples

```
#Host A
t_infectA_fct <- function(x){rnorm(x,mean = 12,sd=3)}
pTrans_hostA <- function(t,t_infectA){
  if(t/t_infectA <= 1){p=sin(pi*t/t_infectA)}
  if(t/t_infectA > 1){p=0}
  return(p)}

```

```

}

p_Move_fctA <- function(t){return(0.1)}

p_Exit_fctA <- function(t,t_infectA){
  if(t/t_infectA <= 1){p=0}
  if(t/t_infectA > 1){p=1}
  return(p)
}

time_contact_A = function(t){sample(c(0,1,2),1,prob=c(0.2,0.4,0.4))}

t_incub_fct_B <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct_B <- function(x){rbeta(x,shape1 = 5,shape2=2)}

p_Exit_fct_B <- function(t,current.in){
  if(current.in=="A"){return(0.1)}
  if(current.in=="B"){return(0.2)}
  if(current.in=="C"){return(1)}
}

pTrans_hostB <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact_B = function(t){round(rnorm(1, 3, 1), 0)}

transition.matrix = matrix(c(0,0.2,0.4,0.5,0,0.6,0.5,0.8,0),
  nrow = 3, ncol = 3,
  dimnames=list(c("A", "B", "C"),c("A", "B", "C")))

set.seed(6262)
test.nosoi <- nosoiSim(type="dual", popStructure="discrete",
  length.sim=40,
  max.infected.A=100,
  max.infected.B=200,
  init.individuals.A=1,
  init.individuals.B=0,
  init.structure.A="A",
  init.structure.B=NA,
  structure.matrix.A=transition.matrix,
  structure.matrix.B=transition.matrix,
  pExit.A = p_Exit_fctA,
  param.pExit.A = list(t_infectA = t_infectA_fct),
  pMove.A=p_Move_fctA,
  param.pMove.A=NA,
  timeDep.pMove.A=FALSE,
  diff.pMove.A=FALSE,
  timeDep.pExit.A=FALSE,
  nContact.A = time_contact_A,
  param.nContact.A = NA,
  timeDep.nContact.A=FALSE,

```

```

pTrans.A = pTrans_hostA,
param.pTrans.A = list(t_infectA=t_infectA_fct),
timeDep.pTrans.A=FALSE,
prefix.host.A="H",
pExit.B = p_Exit_fct_B,
param.pExit.B = NA,
timeDep.pExit.B=FALSE,
diff.pExit.B=TRUE,
pMove.B=NA,
param.pMove.B=NA,
timeDep.pMove.B=FALSE,
diff.pMove.B=FALSE,
nContact.B = time_contact_B,
param.nContact.B = NA,
timeDep.nContact.B=FALSE,
pTrans.B = pTrans_hostB,
param.pTrans.B = list(p_max=p_max_fct_B,
                      t_incub=t_incub_fct_B),
timeDep.pTrans.B=FALSE,
prefix.host.B="V")

```

```
test.nosoi
```

---

dualNone

---

*Dual-host pathogen in homogeneous hosts populations*


---

### Description

This function, that can be wrapped within `nosoiSim`, runs a dual-host transmission chain simulation, without any structure features in both hosts populations. The simulation stops either at the end of given time (specified by `length.sim`) or when the number of hosts infected threshold (`max.infected`) is crossed.

### Usage

```

dualNone(
  length.sim,
  max.infected.A,
  max.infected.B,
  init.individuals.A,
  init.individuals.B,
  pExit.A,
  param.pExit.A,
  timeDep.pExit.A = FALSE,
  nContact.A,
  param.nContact.A,
  timeDep.nContact.A = FALSE,
  pTrans.A,

```



```

    param.pTrans.A,
    timeDep.pTrans.A = FALSE,
    prefix.host.A = "H",
    pExit.B,
    param.pExit.B,
    timeDep.pExit.B = FALSE,
    nContact.B,
    param.nContact.B,
    timeDep.nContact.B = FALSE,
    pTrans.B,
    param.pTrans.B,
    timeDep.pTrans.B = FALSE,
    prefix.host.B = "V",
    print.progress = TRUE,
    print.step = 10
)

```

### Arguments

`length.sim` specifies the length (in unit of time) over which the simulation should be run.

`max.infected.A` specifies the maximum number of individual hosts A that can be infected in the simulation.

`max.infected.B` specifies the maximum number of individual hosts B that can be infected in the simulation.

`init.individuals.A`  
number of initially infected individuals (hosts A).

`init.individuals.B`  
number of initially infected individuals (hosts B).

`pExit.A` function that gives the probability to exit the simulation for an infected host A (either moving out, dying, etc.).

`param.pExit.A` parameter names (list of functions) for the `pExit` for host-type A.

`timeDep.pExit.A`  
is `pExit` of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?

`nContact.A` function that gives the number of potential transmission events per unit of time for host-type A.

`param.nContact.A`  
parameter names (list of functions) for `param.nContact` for host-type A.

`timeDep.nContact.A`  
is `nContact` of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?

`pTrans.A` function that gives the probability of transmit a pathogen as a function of time since infection for host A.

`param.pTrans.A` parameter names (list of functions) for the `pExit` for host A.

`timeDep.pTrans.A`  
is `pTrans` of host-type A dependent on the absolute time of the simulation (TRUE/FALSE)?

<code>prefix.host.A</code>	character(s) to be used as a prefix for the host A identification number.
<code>pExit.B</code>	function that gives the probability to exit the simulation for an infected host B (either moving out, dying, etc.).
<code>param.pExit.B</code>	parameter names (list of functions) for the <code>pExit</code> for host-type B.
<code>timeDep.pExit.B</code>	is <code>pExit</code> of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
<code>nContact.B</code>	function that gives the number of potential transmission events per unit of time for host B.
<code>param.nContact.B</code>	parameter names (list of functions) for <code>param.nContact</code> for host-type B.
<code>timeDep.nContact.B</code>	is <code>nContact</code> of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
<code>pTrans.B</code>	function that gives the probability of transmit a pathogen as a function of time since infection for host B.
<code>param.pTrans.B</code>	parameter names (list of functions) for the <code>pExit</code> for host-type B.
<code>timeDep.pTrans.B</code>	is <code>pTrans</code> of host-type B dependent on the absolute time of the simulation (TRUE/FALSE)?
<code>prefix.host.B</code>	character(s) to be used as a prefix for the host B identification number.
<code>print.progress</code>	if TRUE, displays a progress bar (current time/length.sim).
<code>print.step</code>	<code>print.progress</code> is TRUE, step with which the progress message will be printed.

### Details

The `pExit` and `pTrans` functions should return a single probability (a number between 0 and 1), and `nContact` a positive natural number (positive integer) or 0.

The `param` arguments should be a list of functions or NA. Each item name in the parameter list should have the same name as the argument in the corresponding function.

The use of `timeDep` (switch to TRUE) makes the corresponding function use the argument `prestime` (for "present time").

### Value

An object of class `nosoiSim`, containing all results of the simulation.

### Suffixes

The suffix `.A` or `.B` specifies if the considered function or parameter concerns host type A or B.

### Order of Arguments

The user specified function's arguments should follow this order: `t` (mandatory), `prestime` (optional, only if `timeDep` is TRUE), parameters specified in the list.

**See Also**

For simulations with a discrete structured host population, see [dualDiscrete](#). For simulations with a structured population in continuous space, [dualContinuous](#)

**Examples**

```

#Host A
t_infectA_fct <- function(x){rnorm(x,mean = 12,sd=3)}
pTrans_hostA <- function(t,t_infectA){
  if(t/t_infectA <= 1){p=sin(pi*t/t_infectA)}
  if(t/t_infectA > 1){p=0}
  return(p)
}

p_Exit_fctA <- function(t,t_infectA){
  if(t/t_infectA <= 1){p=0}
  if(t/t_infectA > 1){p=1}
  return(p)
}

time_contact_A = function(t){sample(c(0,1,2),1,prob=c(0.2,0.4,0.4))}

#Host B
t_incub_fct_B <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct_B <- function(x){rbeta(x,shape1 = 5,shape2=2)}

p_Exit_fct_B <- function(t,prestime){(sin(prestime/12)+1)/5}

pTrans_hostB <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact_B = function(t){round(rnorm(1, 3, 1), 0)}

set.seed(90)
test.nosoi <- nosoiSim(type="dual", popStructure="none",
  length.sim=40,
  max.infected.A=100,
  max.infected.B=200,
  init.individuals.A=1,
  init.individuals.B=0,
  pExit.A = p_Exit_fctA,
  param.pExit.A = list(t_infectA = t_infectA_fct),
  timeDep.pExit.A=FALSE,
  nContact.A = time_contact_A,
  param.nContact.A = NA,
  timeDep.nContact.A=FALSE,
  pTrans.A = pTrans_hostA,
  param.pTrans.A = list(t_infectA=t_infectA_fct),
  timeDep.pTrans.A=FALSE,

```

```

prefix.host.A="H",
pExit.B = p_Exit_fct_B,
param.pExit.B = NA,
timeDep.pExit.B=TRUE,
nContact.B = time_contact_B,
param.nContact.B = NA,
timeDep.nContact.B=FALSE,
pTrans.B = pTrans_hostB,
param.pTrans.B = list(p_max=p_max_fct_B,
                      t_incub=t_incub_fct_B),
timeDep.pTrans.B=FALSE,
prefix.host.B="V")

test.nosoi

```

---

getCumulative	<i>Gets the cumulative number of infected hosts for the full length of the simulation</i>
---------------	-------------------------------------------------------------------------------------------

---

### Description

This function computes from the output of a `nosoiSim` simulation the cumulative count of infected hosts at each time step of the simulation. The output is a [data.table](#).

### Usage

```
getCumulative(nosoi.output)
```

### Arguments

`nosoi.output` Output of a `nosoi` simulation (object of class `nosoiSim`).

### Value

The output is a [data.table](#) with the following structure:

**t** Time-step (integer).

**Count** Cumulative number of infected hosts at given time-step.

**type** Host-type, identified by its user-defined prefix.

### See Also

[summary.nosoiSim](#)

---

getDynamic	<i>Gets the current number of infected hosts for the full length of the simulation</i>
------------	----------------------------------------------------------------------------------------

---

### Description

This function computes from the output of a `nosoiSim` simulation the dynamic count of infected hosts at each time step (and each state if discrete structure) of the simulation. The output is a [data.table](#).

### Usage

```
getDynamic(nosoi.output)
```

### Arguments

`nosoi.output` Output of a `nosoi` simulation (object of class [nosoiSim](#)).

### Value

The output is a [data.table](#) with the following structure:

**state** (only when discrete structure) Given state

**Count** Current number of infected hosts at given time-step.

**type** Host-type, identified by its user-defined prefix.

**t** Time-step (integer).

### See Also

[summary.nosoiSim](#)

---

getHostData	<i>Extracts specific data from a nosoiSim object</i>
-------------	------------------------------------------------------

---

### Description

This function extracts data user-defined data (i.e. `table.hosts`, `N.infected`, `table.state` or `popStructure`) from a [nosoiSim](#) object.

### Usage

```
getHostData(  
  nosoi.output,  
  what = c("table.hosts", "N.infected", "table.state", "popStructure"),  
  pop = "A"  
)
```

**Arguments**

`nosoi.output` an object of class `nosoiSim`

`what` the data to get, among `table.hosts`, `N.infected`, `table.state` or `popStructure`.

`pop` the population to be extracted (one of "A" or "B")

**Value**

Returns a [data.table](#) with the requested data.

**See Also**

To directly extract `table.hosts` or `table.state`, you can also use [getTableHosts](#) and [getTableState](#) respectively.

**Examples**

```
t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Exit_fct <- function(t){return(0.08)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact <- function(t){round(rnorm(1, 3, 1), 0)}

test.nosoi <- nosoiSim(type="single", popStructure="none",
  length=40,
  max.infected=100,
  init.individuals=1,
  nContact=time_contact,
  param.nContact=NA,
  pTrans = proba,
  param.pTrans = list(p_max=p_max_fct,
    t_incub=t_incub_fct),
  pExit=p_Exit_fct,
  param.pExit=NA)

data.extracted <- getHostData(test.nosoi, "table.hosts", "A")
```

---

getR0	<i>Gets R0 from a nosoi simulation</i>
-------	----------------------------------------

---

### Description

Gets an estimate of secondary cases (what R0 usually tries to estimate) and its distribution from the output of a nosoiSim simulation. The actual calculation is based on inactive hosts at the end of the simulation to avoid bias introduced by hosts that have not finished their transmission potential.

### Usage

```
getR0(nosoi.output)
```

### Arguments

`nosoi.output` Output of a nosoi simulation (object of class [nosoiSim](#)).

### Details

Current getR0 (after and including version 1.1.0) is a corrected version. In previous versions (prior to 1.1.0), the output included in its computation hosts that should not have been counted (still active).

### Value

A list with the following items:

**N.inactive** Number of inactive hosts at the end of the simulation.

**R0.mean** Mean R0 based on the distribution (see below).

**R0.dist** Distribution for each host of the secondary cases it generated (in case of dual-hosts, then the secondary cases of the same host-type).

### See Also

[summary.nosoiSim](#)

---

getTableHosts	<i>Extracts table.hosts from a nosoiSim object</i>
---------------	----------------------------------------------------

---

### Description

This function extracts the `table.hosts` for the request host-type from a `nosoiSim` object.

### Usage

```
getTableHosts(nosoi.output, pop = "A")
```

### Arguments

<code>nosoi.output</code>	an object of class <code>nosoiSim</code>
<code>pop</code>	the host-type to be extracted (either "A" or "B", if not dual-host, then "A")

### Value

Returns a `data.table` with the requested data. The `table.hosts` (class `data.table`) contains informations about each host that has been simulated (one row is one host). The structure of the table is the following:

**hosts.ID** Unique identifier for the host, based on user-defined prefix and an integer.

**inf.by** Unique identifier for the host that infected the current one.

**inf.in** (only if structure is present) State or coordinates (in that case `inf.in.x` and `inf.in.y`) in which the host was infected.

**current.in** (only if structure is present) State or coordinates (in that case `current.in.x` and `current.in.y`) in which the host is at the end of the simulation.

**current.env.value** (only if continuous structure is present) Environmental value (raster cell value) in which the host is at the end of the simulation.

**current.cell.raster** (only if continuous structure is present) Raster cell numeric ID in which the host is at the end of the simulation.

**host.count** (only if structure is present) Host count in the current state or raster cell (beware, updated only if used).

**inf.time** When did the host enter the simulation (infection time).

**out.time** When did the host exit the simulation (NA if still active).

**active** Is the host still active at the end of the simulation (TRUE for YES, FALSE for NO)?

**parameters** The remaining columns are the sampled values for the individual-based parameters (if any) specified by the user.



---

getTableState	<i>Extracts table.state from a nosoiSim object</i>
---------------	----------------------------------------------------

---

### Description

This function extracts the `table.state` for the request host-type from a `nosoiSim` object. `table.state` is present only if there is any structure (discrete or continuous) used.

### Usage

```
getTableState(nosoi.output, pop = "A")
```

### Arguments

<code>nosoi.output</code>	an object of class <code>nosoiSim</code>
<code>pop</code>	the host-type to be extracted (either "A" or "B", if not dual-host, then "A")

### Value

Returns a `data.table` with the requested data. The `table.state` (class `data.table`) contains informations the location of each host during time (one row is one host at one location). The structure of the table is the following:

**hosts.ID** Unique identifier for the host, based on user-defined prefix and an integer.

**state** State or coordinates (in that case `state.x` and `state.y`) in which the host is during that time interval.

**current.env.value** (only if continuous structure is present) Environmental value (raster cell value) in which the host is at the end of the simulation.

**current.cell.raster** (only if continuous structure is present) Raster cell numeric ID in which the host is at the end of the simulation.

**time.from** Time-step at which the host moved to the location.

**time.to** Time-step at which the host exited the location (either by exiting the simulation or moving somewhere else).

---

getTransmissionTree	<i>Gets the full transmission tree (phylogenetic tree-like) from a nosoi simulation</i>
---------------------	-----------------------------------------------------------------------------------------

---

### Description

From a `nosoi` simulated epidemics, this function extracts the full transmission tree in a form mimicking a phylogenetic tree.

**Usage**

```
getTransmissionTree(nosoiInf)
```

**Arguments**

nosoiInf            an object of class `nosoiSim`

**Details**

This function uses packages **tidytree** and **treeio**, that rely on [ape](#).

**Value**

A tree of class `treedata`, containing a phylogenetic tree based on the transmission chain and the mapped data at all the nodes.

**See Also**

For exporting the annotated tree to other software packages, see functions in **treeio** (e.g. [write.beast](#)).

To sub-sample this tree, see functions [sampleTransmissionTree](#) and [sampleTransmissionTreeFromExiting](#)

**Examples**

```
t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Exit_fct <- function(t){return(0.08)}
p_Move_fct <- function(t){return(0.1)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact = function(t){round(rnorm(1, 3, 1), 0)}

transition.matrix = matrix(c(0, 0.2, 0.4, 0.5, 0, 0.6, 0.5, 0.8, 0),
                           nrow = 3, ncol = 3,
                           dimnames = list(c("A", "B", "C"), c("A", "B", "C")))

set.seed(805)
test.nosoi <- nosoiSim(type="single", popStructure="discrete",
                      length=20,
                      max.infected=100,
                      init.individuals=1,
                      init.structure="A",
                      structure.matrix=transition.matrix,
                      pMove=p_Move_fct,
                      param.pMove=NA,
                      nContact=time_contact,
                      param.nContact=NA,
```

```

        pTrans = proba,
        param.pTrans = list(p_max=p_max_fct,
                           t_incub=t_incub_fct),
        pExit=p_Exit_fct,
        param.pExit=NA
    )

## Make sure all needed packages are here
if (requireNamespace("ape", quietly = TRUE) &&
    requireNamespace("tidytree", quietly = TRUE) &&
    requireNamespace("treeio", quietly = TRUE)) {
  library(ape)
  library(tidytree)
  library(treeio)

  #' ## Full transmission tree
  ttreedata <- getTransmissionTree(test.nosoi)
  plot(ttreedata@phylo)

  ## Sampling "non dead" individuals
  hID <- c("H-1", "H-7", "H-15", "H-100")
  samples <- data.table(hosts = hID,
                       times = c(5.2, 9.3, 10.2, 16),
                       labels = paste0(hID, "-s"))

  sampledTree <- sampleTransmissionTree(test.nosoi, ttreedata, samples)
  plot(sampledTree@phylo)

  ## Sampling "dead" individuals
  sampledDeadTree <- sampleTransmissionTreeFromExiting(ttreedata, hID)
  plot(sampledDeadTree@phylo)
}

```

---

nosoiSim

*Top-level function to use nosoi.*

---

## Description

This function determines which general settings the user wants to use for his simulation. All other arguments are passed down to the chosen simulator itself, such as [singleNone](#), [singleDiscrete](#), [singleContinuous](#), [dualNone](#), [dualDiscrete](#) or [dualContinuous](#).

## Usage

```
nosoiSim(type = "single", popStructure = "none", ...)
```

**Arguments**

<code>type</code>	specifies which type of pathogen we are interested in, either "single" or "dual"-host (e.g. arboviruses).
<code>popStructure</code>	specifies if the population in which the transmission is to occur is structured ("none", "discrete" or "continuous").
<code>...</code>	arguments to be passed on to the chosen simulator itself, such as <a href="#">singleNone</a> , <a href="#">singleDiscrete</a> , <a href="#">singleContinuous</a> , <a href="#">dualNone</a> , <a href="#">dualDiscrete</a> or <a href="#">dualContinuous</a> .

**Value**

An object of class `nosoiSim`, containing all results of the simulation. Class `nosoiSim` object have the following slots:

**total.time** Number of time steps the simulation ran (integer).

**type** String giving the simulation type ("single" or "dual" host).

**host.info.A: object of class nosoiSimOne** **N.infected** Number of infected hosts (integer).

**table.hosts** Table containing the results of the simulation (see [getTableHosts](#) for more details on the table).

**table.state** Table containing the results of the simulation, focusing on the movement history of each host (see [getTableState](#) for more details on the table).

**prefix.host** String containing the prefix used to name hosts (character string).

**popStructure** String giving the population structure (one of "none", "discrete" or "continuous").

**host.info.B: object of class nosoiSimOne** Same structure as `host.info.A`, but for host B (if it exists).

**See Also**

**Individual simulation functions:** [singleNone](#), [singleDiscrete](#), [singleContinuous](#), [dualNone](#), [dualDiscrete](#) and [dualContinuous](#).

**Functions to extract the results:** [getTableHosts](#), [getTableState](#)

**Summary statistics functions:** [nosoiSummary](#), [getCumulative](#), [getDynamic](#), [getR0](#)

**Examples**

```
t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Exit_fct <- function(t){return(0.08)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact = function(t){round(rnorm(1, 3, 1), 0)}
```

```

test.nosoi <- nosoiSim(type="single", popStructure="none",
                      length=40,
                      max.infected=100,
                      init.individuals=1,
                      nContact=time_contact,
                      param.nContact=NA,
                      pTrans = proba,
                      param.pTrans = list(p_max=p_max_fct,
                                           t_incub=t_incub_fct),
                      pExit=p_Exit_fct,
                      param.pExit=NA)

test.nosoi

```

---

nosoiSummary

*Summarizes the epidemiological features of a nosoi simulation*


---

### Description

This function provides summary information about the simulation (number of infected hosts,  $R_0$ , etc.) as a list.

### Usage

```

nosoiSummary(object)

## S3 method for class 'nosoiSim'
summary(object, ...)

```

### Arguments

**object** Output of a nosoi simulation (object of class [nosoiSim](#)).

**...** further arguments passed to or from other methods.

### Value

All computed data is provided in a list:

**R0** Provides a sublist with number of inactive hosts at the end of the simulation `N.inactive`, mean `R0.R0.mean`, and `R0` distribution `R0.dist`. For more details, see [getR0](#).

**dynamics** [data.table](#) with the count of currently infected (i.e. active) hosts at each time step of the simulation (by state if the simulation was in a discrete structured host population). For more details, see [getDynamic](#).

**cumulative** [data.table](#) with the cumulative count of infected hosts at each time step of the simulation. For more details, see [getCumulative](#).

**See Also**

You can directly compute each elements of the list without using the summarise function. See [getR0](#), [getDynamic](#) and [getCumulative](#).

**Examples**

```
t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Exit_fct <- function(t){return(0.08)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact <- function(t){round(rnorm(1, 3, 1), 0)}

test.nosoi <- nosoiSim(type="single", popStructure="none",
  length=40,
  max.infected=100,
  init.individuals=1,
  nContact=time_contact,
  param.nContact=NA,
  pTrans = proba,
  param.pTrans = list(p_max=p_max_fct,
    t_incub=t_incub_fct),
  pExit=p_Exit_fct,
  param.pExit=NA)

nosoiSummary(test.nosoi)
```

---

sampleTransmissionTree

*Sample the transmission tree (phylogenetic tree-like)*

---

**Description**

Sample a full transmission tree. This function allows for sampling multiple times on the same lineage. When this happens, the sampled ancestor is a tip with length zero.

**Usage**

```
sampleTransmissionTree(nosoiInf, tree, samples)
```

**Arguments**

nosoiInf	an object of class <code>nosoiSim</code>
tree	a <code>treedata</code> object created by function <code>getTransmissionTree</code>
samples	a <code>data.table</code> object with the following entries: <b>hosts</b> Host ID of the individuals to be sampled <b>times</b> Times at which each host is sampled <b>labels</b> label for the corresponding tip in the tree

**Details**

The tree needs to be produced by function `getTransmissionTree` applied on the same `nosoiSim` object.

**Value**

A tree of class `treedata`, containing a phylogenetic tree based on the transmission chain and the mapped data at all the nodes.

**See Also**

For exporting the annotated tree to other software packages, see functions in **treeio** (e.g. `write.beast`).

To get the full transmission matrix, see `getTransmissionTree`.

For sampling only dead individuals, see `sampleTransmissionTreeFromExiting`.

**Examples**

```
t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Exit_fct <- function(t){return(0.08)}
p_Move_fct <- function(t){return(0.1)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact = function(t){round(rnorm(1, 3, 1), 0)}

transition.matrix = matrix(c(0, 0.2, 0.4, 0.5, 0, 0.6, 0.5, 0.8, 0),
                           nrow = 3, ncol = 3,
                           dimnames = list(c("A", "B", "C"), c("A", "B", "C")))

set.seed(805)
test.nosoi <- nosoiSim(type="single", popStructure="discrete",
                      length=20,
                      max.infected=100,
                      init.individuals=1,
                      init.structure="A",
```

```

        structure.matrix=transition.matrix,
        pMove=p_Move_fct,
        param.pMove=NA,
        nContact=time_contact,
        param.nContact=NA,
        pTrans = proba,
        param.pTrans = list(p_max=p_max_fct,
                           t_incub=t_incub_fct),
        pExit=p_Exit_fct,
        param.pExit=NA
    )

## Make sure all needed packages are here
if (requireNamespace("ape", quietly = TRUE) &&
    requireNamespace("tidytree", quietly = TRUE) &&
    requireNamespace("treeio", quietly = TRUE)) {
  library(ape)
  library(tidytree)
  library(treeio)

#' ## Full transmission tree
ttreedata <- getTransmissionTree(test.nosoi)
plot(ttreedata@phylo)

## Sampling "non dead" individuals
hID <- c("H-1", "H-7", "H-15", "H-100")
samples <- data.table(hosts = hID,
                      times = c(5.2, 9.3, 10.2, 16),
                      labels = paste0(hID, "-s"))

sampledTree <- sampleTransmissionTree(test.nosoi, ttreedata, samples)
plot(sampledTree@phylo)

## Sampling "dead" individuals
sampledDeadTree <- sampleTransmissionTreeFromExiting(ttreedata, hID)
plot(sampledDeadTree@phylo)
}

```

---

```
sampleTransmissionTreeFromExiting
```

*Sample the transmission tree (phylogenetic tree-like) among the exited hosts*

---

### Description

Sample a full transmission tree. This function allows for sampling only exited (i.e. inactive) individuals (e.g. when the sampling procedure is destructive or cuts the hosts from the population). Beware because it does not influence the epidemiological process, it only means that the host has been sampled when exiting the simulation.



**Usage**

```
sampleTransmissionTreeFromExiting(tree, hosts)
```

**Arguments**

tree            a [treedata](#) object created by function [getTransmissionTree](#)  
 hosts          a vector of dead hosts to sample

**Details**

The tree needs to be produced by function [getTransmissionTree](#) applied on the same `nosoiSim` object.

**Value**

A tree of class [treedata](#), containing a phylogenetic tree based on the transmission chain and the mapped data at all the nodes.

**See Also**

For exporting the annotated tree to other software packages, see functions in **treeio** (e.g. [write.beast](#)).

To get the full transmission matrix, see [getTransmissionTree](#).

For sampling among non-dead individuals, see [sampleTransmissionTree](#).

**Examples**

```
t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Exit_fct <- function(t){return(0.08)}
p_Move_fct <- function(t){return(0.1)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact = function(t){round(rnorm(1, 3, 1), 0)}

transition.matrix = matrix(c(0, 0.2, 0.4, 0.5, 0, 0.6, 0.5, 0.8, 0),
  nrow = 3, ncol = 3,
  dimnames = list(c("A", "B", "C"), c("A", "B", "C")))

set.seed(805)
test.nosoi <- nosoiSim(type="single", popStructure="discrete",
  length=20,
  max.infected=100,
  init.individuals=1,
  init.structure="A",
  structure.matrix=transition.matrix,
```

```

        pMove=p_Move_fct,
        param.pMove=NA,
        nContact=time_contact,
        param.nContact=NA,
        pTrans = proba,
        param.pTrans = list(p_max=p_max_fct,
                            t_incub=t_incub_fct),
        pExit=p_Exit_fct,
        param.pExit=NA
    )

## Make sure all needed packages are here
if (requireNamespace("ape", quietly = TRUE) &&
    requireNamespace("tidytree", quietly = TRUE) &&
    requireNamespace("treeio", quietly = TRUE)) {
  library(ape)
  library(tidytree)
  library(treeio)

  #' ## Full transmission tree
  ttreedata <- getTransmissionTree(test.nosoi)
  plot(ttreedata@phylo)

  ## Sampling "non dead" individuals
  hID <- c("H-1", "H-7", "H-15", "H-100")
  samples <- data.table(hosts = hID,
                        times = c(5.2, 9.3, 10.2, 16),
                        labels = paste0(hID, "-s"))

  sampledTree <- sampleTransmissionTree(test.nosoi, ttreedata, samples)
  plot(sampledTree@phylo)

  ## Sampling "dead" individuals
  sampledDeadTree <- sampleTransmissionTreeFromExiting(ttreedata, hID)
  plot(sampledDeadTree@phylo)
}

```

---

singleContinuous

*Single-host pathogen in a structured (continuous) host population*


---

### Description

This function runs a single-host transmission chain simulation, with a structured host population (such as spatial features) in a continuous space. The simulation stops either at the end of given time (specified by `length.sim`) or when the number of hosts infected threshold (`max.infected`) is passed. The movement of hosts on the continuous space map is a random walk (Brownian motion) that can be modified towards a biased random walk where hosts tend to be attracted to higher values of the environmental variable defined by the raster.

**Usage**

```

singleContinuous(
  length.sim,
  max.infected,
  init.individuals,
  init.structure,
  structure.raster,
  diff.pExit = FALSE,
  timeDep.pExit = FALSE,
  hostCount.pExit = FALSE,
  pExit,
  param.pExit,
  diff.pMove = FALSE,
  timeDep.pMove = FALSE,
  hostCount.pMove = FALSE,
  pMove,
  param.pMove,
  diff.sdMove = FALSE,
  timeDep.sdMove = FALSE,
  hostCount.sdMove = FALSE,
  sdMove,
  param.sdMove,
  attracted.by.raster = FALSE,
  diff.nContact = FALSE,
  timeDep.nContact = FALSE,
  hostCount.nContact = FALSE,
  nContact,
  param.nContact,
  diff.pTrans = FALSE,
  timeDep.pTrans = FALSE,
  hostCount.pTrans = FALSE,
  pTrans,
  param.pTrans,
  prefix.host = "H",
  print.progress = TRUE,
  print.step = 10
)

```

**Arguments**

`length.sim` specifies the length (in unit of time) over which the simulation should be run.

`max.infected` specifies the maximum number of hosts that can be infected in the simulation.

`init.individuals` number of initially infected individuals.

`init.structure` in which location the initially infected individuals are located. A vector of coordinates in the same coordinate space as the raster.

`structure.raster` raster object defining the environmental variable.

<code>diff.pExit</code>	does pExit depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>timeDep.pExit</code>	is pExit dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>hostCount.pExit</code>	does pExit vary with the host count in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.pExit</code> should be TRUE.
<code>pExit</code>	function that gives the probability to exit the simulation for an infected host (either moving out, dying, etc.).
<code>param.pExit</code>	parameter names (list of functions) for the pExit.
<code>diff.pMove</code>	does pMove depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>timeDep.pMove</code>	does pMove depend on the absolute time of the simulation (TRUE/FALSE).
<code>hostCount.pMove</code>	does pMove vary with the host count in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.pMove</code> should also be TRUE.
<code>pMove</code>	function that gives the probability of a host moving as a function of time.
<code>param.pMove</code>	parameter names (list of functions) for the pMove.
<code>diff.sdMove</code>	does sdMove depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>timeDep.sdMove</code>	does sdMove depend on the absolute time of the simulation (TRUE/FALSE).
<code>hostCount.sdMove</code>	does sdMove vary with the host count in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.sdMove</code> should be TRUE.
<code>sdMove</code>	function that gives the distance traveled (based on coordinates); output is the standard deviation value for the Brownian motion.
<code>param.sdMove</code>	parameter names (list of functions) for sdMove.
<code>attracted.by.raster</code>	should the hosts be attracted by higher values in the environmental raster? (TRUE/FALSE).
<code>diff.nContact</code>	does nContact depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>timeDep.nContact</code>	is nContact dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>hostCount.nContact</code>	does nContact vary with the host count in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.nContact</code> should be TRUE.
<code>nContact</code>	function that gives the number of potential transmission events per unit of time.
<code>param.nContact</code>	parameter names (list of functions) for param.nContact.
<code>diff.pTrans</code>	does pTrans depend on the environmental variable (set by the raster) (TRUE/FALSE).
<code>timeDep.pTrans</code>	is pTrans dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>hostCount.pTrans</code>	does pTrans vary with the host count in each raster cell? (TRUE/FALSE); if TRUE, <code>diff.pTrans</code> should be TRUE.
<code>pTrans</code>	function that gives the probability of transmit a pathogen as a function of time since infection.
<code>param.pTrans</code>	parameter names (list of functions) for the pExit.
<code>prefix.host</code>	character(s) to be used as a prefix for the hosts identification number.
<code>print.progress</code>	if TRUE, displays a progress bar (current time/length.sim).
<code>print.step</code>	<code>print.progress</code> is TRUE, step with which the progress message will be printed.

**Details**

The `pExit` and `pTrans` functions should return a single probability (a number between 0 and 1), and `nContact` a positive natural number (positive integer) or 0.

The `param` arguments should be a list of functions or NA. Each item name in the parameter list should have the same name as the argument in the corresponding function.

The use of `timeDep` (switch to TRUE) makes the corresponding function use the argument `preTime` (for "present time").

**Value**

An object of class `nosoiSim`, containing all results of the simulation.

**Raster**

The structure raster provided should be of class `raster`. High values of the environmental variable can attract hosts if `attracted.by.raster` is TRUE.

**Structure Parameters**

The `pMove` function should return a single probability (a number between 0 and 1), and `sdMove` a real number (keep in mind this number is related to your coordinate space).

The use of `diff` (switch to TRUE) makes the corresponding function use the argument `current.env.value` (for "current environmental value").

The use of `hostCount` (switch to TRUE) makes the corresponding function use the argument `host.count`.

**Order of Arguments**

The user specified function's arguments should follow this order: `t` (mandatory), `preTime` (optional, only if `timeDep` is TRUE), `current.env.value` (optional, only if `diff` is TRUE), `host.count` (optional, only if `hostCount` is TRUE) and parameters specified in the list.

**See Also**

For simulations with a discrete structure, see [singleDiscrete](#). For simulations without any structures, see [singleNone](#).

**Examples**

```
library(raster)
#Generating a raster for the movement
set.seed(860)

test.raster <- raster(nrows=100, ncols=100, xmn=-50, xmx=50, ymn=-50, ymx=50)
test.raster[] <- runif(10000, -80, 180)
test.raster <- focal(focal(test.raster, w=matrix(1, 5, 5), mean), w=matrix(1, 5, 5), mean)
plot(test.raster)

t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
```

```

p_Move_fct <- function(t){return(0.1)}

sdMove_fct = function(t,current.env.value){return(100/(current.env.value+1))}

p_Exit_fct <- function(t){return(0.08)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact = function(t){round(rnorm(1, 3, 1), 0)}

start.pos <- c(0,0)

test.nosoiA <- nosoiSim(type="single", popStructure="continuous",
  length=200,
  max.infected=500,
  init.individuals=1,
  init.structure=start.pos,
  structure.raster=test.raster,
  pMove=p_Move_fct,
  param.pMove=NA,
  diff.sdMove=TRUE,
  sdMove=sdMove_fct,
  param.sdMove=NA,
  attracted.by.raster=TRUE,
  nContact=time_contact,
  param.nContact=NA,
  pTrans = proba,
  param.pTrans = list(p_max=p_max_fct,
                     t_incub=t_incub_fct),
  pExit=p_Exit_fct,
  param.pExit=NA)

```

---

singleDiscrete

*Single-host pathogen in a structured (discrete) host population*


---

### Description

This function, that can be wrapped within `nosoiSim`, runs a single-host transmission chain simulation, with a discrete host population structure (e.g. spatial, socio-economic, etc.). The simulation stops either at the end of given time (specified by `length.sim`) or when the number of hosts infected threshold (`max.infected`) is crossed.

### Usage

```
singleDiscrete(
```

```

length.sim,
max.infected,
init.individuals,
init.structure,
structure.matrix,
diff.pExit = FALSE,
timeDep.pExit = FALSE,
hostCount.pExit = FALSE,
pExit,
param.pExit,
diff.pMove = FALSE,
timeDep.pMove = FALSE,
hostCount.pMove = FALSE,
pMove,
param.pMove,
diff.nContact = FALSE,
timeDep.nContact = FALSE,
hostCount.nContact = FALSE,
nContact,
param.nContact,
diff.pTrans = FALSE,
timeDep.pTrans = FALSE,
hostCount.pTrans = FALSE,
pTrans,
param.pTrans,
prefix.host = "H",
print.progress = TRUE,
print.step = 10
)

```

### Arguments

<code>length.sim</code>	specifies the length (in unit of time) over which the simulation should be run.
<code>max.infected</code>	specifies the maximum number of hosts that can be infected in the simulation.
<code>init.individuals</code>	number of initially infected individuals.
<code>init.structure</code>	in which state (e.g. location) the initially infected individuals are located.
<code>structure.matrix</code>	transition matrix (probabilities) to go from location A (row) to B (column)
<code>diff.pExit</code>	is pExit different between states of the structured population (TRUE/FALSE)
<code>timeDep.pExit</code>	is pExit dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>hostCount.pExit</code>	does pExit varies with the host count in the state? (TRUE/FALSE); <code>diff.pExit</code> should be TRUE.
<code>pExit</code>	function that gives the probability to exit the simulation for an infected host (either moving out, dying, etc.).

<code>param.pExit</code>	parameter names (list of functions) for the <code>pExit</code> .
<code>diff.pMove</code>	is <code>pMove</code> different between states of the structured population (TRUE/FALSE)
<code>timeDep.pMove</code>	is <code>pMove</code> dependent on the absolute time of the simulation (TRUE/FALSE)
<code>hostCount.pMove</code>	does <code>pMove</code> varies with the host count in the state? (TRUE/FALSE); <code>diff.pMove</code> should be TRUE.
<code>pMove</code>	function that gives the probability of a host moving as a function of time.
<code>param.pMove</code>	parameter names (list of functions) for the <code>pMove</code> .
<code>diff.nContact</code>	is <code>nContact</code> different between states of the structured population (TRUE/FALSE)
<code>timeDep.nContact</code>	is <code>nContact</code> dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>hostCount.nContact</code>	does <code>nContact</code> varies with the host count in the state? (TRUE/FALSE); <code>diff.nContact</code> should be TRUE.
<code>nContact</code>	function that gives the number of potential transmission events per unit of time.
<code>param.nContact</code>	parameter names (list of functions) for <code>param.nContact</code> .
<code>diff.pTrans</code>	is <code>pTrans</code> different between states of the structured population (TRUE/FALSE)
<code>timeDep.pTrans</code>	is <code>pTrans</code> dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>hostCount.pTrans</code>	does <code>pTrans</code> varies with the host count in the state? (TRUE/FALSE); <code>diff.pTrans</code> should be TRUE.
<code>pTrans</code>	function that gives the probability of transmit a pathogen as a function of time since infection.
<code>param.pTrans</code>	parameter names (list of functions) for the <code>pExit</code> .
<code>prefix.host</code>	character(s) to be used as a prefix for the hosts identification number.
<code>print.progress</code>	if TRUE, displays a progress bar (current time/length.sim).
<code>print.step</code>	<code>print.progress</code> is TRUE, step with which the progress message will be printed.

### Details

The `pExit` and `pTrans` functions should return a single probability (a number between 0 and 1), and `nContact` a positive natural number (positive integer) or 0.

The `param` arguments should be a list of functions or NA. Each item name in the parameter list should have the same name as the argument in the corresponding function.

The use of `timeDep` (switch to TRUE) makes the corresponding function use the argument `prestime` (for "present time").

### Value

An object of class `nosoiSim`, containing all results of the simulation.

### Structure Matrix

The structure matrix provided should of class `matrix`, with the same number of rows and columns, rows representing departure state and column the arrival state. All rows should add to 1.



### Structure Parameters

The `pMove` function should return a single probability (a number between 0 and 1).

The use of `diff` (switch to TRUE) makes the corresponding function use the argument `current.in` (for "currently in"). Your function should in that case give a result for every possible discrete state.

The use of `hostCount` (switch to TRUE) makes the corresponding function use the argument `host.count`.

### Order of Arguments

The user specified function's arguments should follow this order: `t` (mandatory), `prestime` (optional, only if `timeDep` is TRUE), `current.in` (optional, only if `diff` is TRUE), `host.count` (optional, only if `hostCount` is TRUE) and parameters specified in the list.

### See Also

For simulations with a structure in continuous space, see [singleContinuous](#). For simulations without any structures, see [singleNone](#).

### Examples

```
t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Exit_fct <- function(t){return(0.08)}
p_Move_fct <- function(t){return(0.1)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact = function(t){round(rnorm(1, 3, 1), 0)}

transition.matrix = matrix(c(0,0.2,0.4,0.5,0,0.6,0.5,0.8,0),
  nrow = 3, ncol = 3,
  dimnames=list(c("A","B","C"),c("A","B","C")))

set.seed(805)
test.nosoiA <- nosoiSim(type="single", popStructure="discrete",
  length=20,
  max.infected=100,
  init.individuals=1,
  init.structure="A",
  structure.matrix=transition.matrix,
  pMove=p_Move_fct,
  param.pMove=NA,
  nContact=time_contact,
  param.nContact=NA,
  pTrans = proba,
  param.pTrans = list(p_max=p_max_fct,
    t_incub=t_incub_fct),
  pExit=p_Exit_fct,
```

```
param.pExit=NA)
```

---

singleNone

*Single-host pathogen in a homogeneous host population*

---

### Description

This function, that can be wrapped within `nosoiSim`, runs a single-host transmission chain simulation, without any structure features in the host population. The simulation stops either at the end of given time (specified by `length.sim`) or when the number of hosts infected threshold (`max.infected`) is crossed.

### Usage

```
singleNone(
  length.sim,
  max.infected,
  init.individuals,
  pExit,
  param.pExit,
  timeDep.pExit = FALSE,
  nContact,
  param.nContact,
  timeDep.nContact = FALSE,
  pTrans,
  param.pTrans,
  timeDep.pTrans = FALSE,
  prefix.host = "H",
  print.progress = TRUE,
  print.step = 10
)
```

### Arguments

<code>length.sim</code>	specifies the length (in unit of time) over which the simulation should be run.
<code>max.infected</code>	specifies the maximum number of hosts that can be infected in the simulation.
<code>init.individuals</code>	number of initially infected individuals.
<code>pExit</code>	function that gives the probability to exit the simulation for an infected host (either moving out, dying, etc.).
<code>param.pExit</code>	parameter names (list of functions) for the <code>pExit</code> .
<code>timeDep.pExit</code>	is <code>pExit</code> dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>nContact</code>	function that gives the number of potential transmission events per unit of time.
<code>param.nContact</code>	parameter names (list of functions) for <code>param.nContact</code> .

<code>timeDep.nContact</code>	is <code>nContact</code> dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>pTrans</code>	function that gives the probability of transmit a pathogen as a function of time since infection.
<code>param.pTrans</code>	parameter names (list of functions) for the <code>pExit</code> .
<code>timeDep.pTrans</code>	is <code>pTrans</code> dependent on the absolute time of the simulation? (TRUE/FALSE)
<code>prefix.host</code>	character(s) to be used as a prefix for the hosts identification number.
<code>print.progress</code>	if TRUE, displays a progress bar (current time/length.sim).
<code>print.step</code>	<code>print.progress</code> is TRUE, step with which the progress message will be printed.

### Details

The `pExit` and `pTrans` functions should return a single probability (a number between 0 and 1), and `nContact` a positive natural number (positive integer) or 0.

The `param` arguments should be a list of functions or NA. Each item name in the parameter list should have the same name as the argument in the corresponding function.

The use of `timeDep` (switch to TRUE) makes the corresponding function use the argument `prestime` (for "present time").

### Value

An object of class `nosoiSim`, containing all results of the simulation.

### Order of Arguments

The user specified function's arguments should follow this order: `t` (mandatory), `prestime` (optional, only if `timeDep` is TRUE), parameters specified in the list.

### See Also

For simulations with a discrete structured host population, see [singleDiscrete](#). For simulations with a structured population in continuous space, [singleContinuous](#)

### Examples

```
t_incub_fct <- function(x){rnorm(x,mean = 5,sd=1)}
p_max_fct <- function(x){rbeta(x,shape1 = 5,shape2=2)}
p_Exit_fct <- function(t){return(0.08)}

proba <- function(t,p_max,t_incub){
  if(t <= t_incub){p=0}
  if(t >= t_incub){p=p_max}
  return(p)
}

time_contact <- function(t){round(rnorm(1, 3, 1), 0)}

test.nosoi <- nosoiSim(type="single", popStructure="none",
```

```
length=40,  
max.infected=100,  
init.individuals=1,  
nContact=time_contact,  
param.nContact=NA,  
pTrans = proba,  
param.pTrans = list(p_max=p_max_fct,  
                    t_incub=t_incub_fct),  
pExit=p_Exit_fct,  
param.pExit=NA)
```

```
test.nosoi
```

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