Package 'phylopomp'

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as.data.frame *Coerce to a Data Frame*

Description

Functions to coerce an object to a data frame.

Usage

```
## S3 method for class 'gplin'
as.data.frame(x, ...)
```

Arguments

x	any R object.
...	additional arguments to be passed to or from methods.

Details

An object of class 'gplin' is coerced to a data frame by means of as.data.frame.

curtail *Curtail a genealogy to the given time*

Description

Discards all nodes beyond the given time.

Usage

```
curtail(object, time = NA, troot = NA)
```

Arguments

object	gpsim object.
time	logical; return the current time?
troot	new root time for curtailed genealogy

Value

A curtailed genealogy object.

Examples

```
library(ggplot2)

simulate("SIIR",time=5) -> x

plot_grid(
  x |>
    plot(prune=FALSE,points=TRUE),
  x |>
    curtail(time=3) |>
    plot(prune=FALSE,points=TRUE)+
    expand_limits(x=5),
  ncol=1,align="h",axis="tblr"
)

plot_grid(
  x |>
    plot(prune=TRUE,points=TRUE)+
    geom_vline(xintercept=3),
  x |> curtail(time=3) |>
    plot(prune=TRUE,points=TRUE)+
    geom_vline(xintercept=3)+
    expand_limits(x=5),
  ncol=1,align="h",axis="tblr"
)
```

---

diagram *Genealogy process diagram*

Description

Produces a diagram of the genealogy process state.

Usage

```
diagram(
  object,
  prune = TRUE,
  obscure = TRUE,
  m = NULL,
  n = NULL,
  ...,
  digits = 1,
  palette = scales::hue_pal(l = 80, c = 20, h = c(220, 580))
)

## S3 method for class 'gpdiag'
print(x, newpage = is.null(vp), vp = NULL, ...)
```

Arguments

object	gpsim object.
prune	logical; prune the genealogy?
obscure	logical; obscure the demes?
m	width of plotting window, in nodes. By default, the nodes will be adjusted in width to fit the window.
n	height of the pockets, in balls. By default, the balls will be adjusted in size to fit the space available.
...	other arguments, ignored.
digits	non-negative integer; number of decimal digits to print in the node time
palette	color palette for indicating demes. This can be furnished either as a function or a vector of colors. If this is a function, it should take a single integer argument, the number of colors required. If it is a vector, it should have at least as many elements as there are demes in the genealogy.
x	An R object.
newpage	draw new empty page first?
vp	viewport to draw plot in

Value

A **grid** graphics object (grob), invisibly.

Examples

```
runSIR(Beta=3,gamma=0.1,psi=0.2,S0=100,I0=5,R0=0,time=2,t0=0) -> x
plot(x,points=TRUE,prune=FALSE)
plot_grid(plotlist=list(plot(x,points=TRUE),diagram(x)),
  ncol=1,rel_heights=c(4,1))
```

---

gendat *Genealogy as a data frame*

Description

Converts a given genealogy to a data frame.

Usage

```
gendat(object, obscure = TRUE)
```

Arguments

object	a 'gpgen' object.
obscure	logical; obscure the demes?

Value

A list of objects containing the information pertinent for filtering.

`geneal` *Bare genealogy*

Description

Extracts the bare genealogy from a Markov genealogy process simulation

Usage

```
geneal(object)
```

Arguments

`object`	a 'gpgen' object.

Value

A bare genealogy object.

`genealogy diagram internals`
Diagramming internals

Description

Facilities to produce diagrammatic representations of genealogy process states.

Usage

```
genealogyGrob(object, m = NULL, n = NULL, vp = NULL, palette, ...)

nodeGrob(object, digits = 1, palette, n = NULL, vp = NULL)

pocketGrob(object, n, vp = NULL)

ballGrob(object, vp = NULL)

resizingTextGrob(..., vp = NULL)

## S3 method for class 'resizingTextGrob'
drawDetails(x, recording = TRUE)
```

```
## S3 method for class 'resizingTextGrob'
preDrawDetails(x)

## S3 method for class 'resizingTextGrob'
postDrawDetails(x)

## S3 method for class 'ballGrob'
drawDetails(x, recording = TRUE)

## S3 method for class 'ballGrob'
preDrawDetails(x)

## S3 method for class 'ballGrob'
postDrawDetails(x)

## S3 method for class 'gpsim'
print(x, ...)

## S3 method for class 'gpgen'
print(x, ...)

## S3 method for class 'gpyaml'
print(x, ...)
```

Arguments

object	list; pocket structure
m	width of plotting window, in nodes. By default, the nodes will be adjusted in width to fit the window.
n	length of longest genealogy
vp	viewport to draw plot in
palette	color palette for indicating demes. This can be furnished either as a function or a vector of colors. If this is a function, it should take a single integer argument, the number of colors required. If it is a vector, it should have at least as many elements as there are demes in the genealogy.
...	arguments to be passed to textGrob.
digits	non-negative integer; number of decimal digits to print in the node time
x	An R object.
recording	A logical value indicating whether a grob is being added to the display list or redrawn from the display list.

Details

Code for the resizing text adapted from a blog post by Mark Heckmann (https://ryouready.wordpress.com/2012/08/01/creating
a-text-grob-that-automatically-adjusts-to-viewport-size/).

getInfo *getInfo*

Description

Retrieve information from genealogy process simulation

Usage

```
getInfo(
  object,
  prune = TRUE,
  obscure = TRUE,
  t0 = FALSE,
  time = FALSE,
  description = FALSE,
  structure = FALSE,
  yaml = FALSE,
  ndeme = FALSE,
  lineages = FALSE,
  newick = FALSE,
  nsample = FALSE,
  genealogy = FALSE,
  gendat = FALSE
)
```

Arguments

object	gpsim object.
prune	logical; prune the genealogy?
obscure	logical; obscure the demes?
t0	logical; return the zero-time?
time	logical; return the current time?
description	logical; return the description?
structure	logical; return the structure in R list format?
yaml	logical; return the structure in YAML format?
ndeme	logical; return the number of demes?
lineages	logical; return the lineage-count function?
newick	logical; return a Newick-format description of the tree?
nsample	logical; return the number of samples?
genealogy	logical; return the lineage-traced genealogy?
gendat	logical; return the data-frame format?

Value

A list containing the requested elements, including any or all of:

t0 the initial time (a numeric scalar)

time the final time (a numeric scalar)

ndeme the number of demes (an integer)

nsample the number of samples (an integer)

newick the genealogical tree, in Newick format

description a human readable description of the state of the genealogy process

yaml the state of the genealogy process in YAML format

structure the state of the genealogy process in R list format

lineages a `tibble` containing the lineage count function through time

gendat a `tibble` containing the (obscured) genealogy in a data-frame format

genealogy the lineage-traced genealogy (as a raw vector)

Examples

```
simulate("SIIR",time=3,psi1=1,psi2=0) |>
  simulate(Beta1=2,gamma=2,time=10,psi1=10,psi2=1) |>
  plot()

runSIIR(Beta1=10,Beta2=8,
  S0=200,I1_0=10,I2_0=8,R0=0,time=0,t0=-1) |>
  simulate(psi1=10,time=2) |>
  plot(points=TRUE,obscure=FALSE)

simulate("SIIR",Beta1=2,Beta2=50,gamma=1,psi1=2,
  S0=300,I1_0=20,I2_0=2,time=5) |>
  lineages() |>
  plot()
```

---

lbdp *Linear birth-death-sampling model*

Description

The genealogy process induced by a simple linear birth-death process with constant-rate sampling.

Usage

```
runLBDP(time, t0 = 0, lambda = 2, mu = 1, psi = 1, n0 = 5)

continueLBDP(object, time, lambda = NA, mu = NA, psi = NA)

lbdp_pomp(x, lambda, mu, psi, n0 = 1, t0 = 0)

lbdp_exact(x, lambda, mu, psi, n0 = 1)
```

Arguments

time	final time
t0	initial time
lambda	per capita birth rate
mu	per capita death rate
psi	per capita sampling rate
n0	population size at time t0
object	either the name of the model to simulate *or* a previously computed 'gpsim' object
x	genealogy in **phylopomp** format (i.e., an object that inherits from 'gpgen').

Details

`lbdp_pomp` constructs a **pomp** object containing a given set of data and a linear birth-death-sampling process.

`lbdp_exact` gives the exact log likelihood of a linear birth-death process, conditioned on the population size at time 0.

Value

`runLBDP` and `continueLBDP` return objects of class 'gpsim' with 'model' attribute "LBDP".

`lbdp_exact` returns the log likelihood of the genealogy. Note that the time since the most recent sample is informative.

References

A. A. King, Q. Lin, and E. L. Ionides. Exact phylodynamic likelihood via structured Markov genealogy processes. *arXiv* 2405.17032, 2024. doi:10.48550/arxiv.2405.17032.

A. A. King, Q. Lin, and E. L. Ionides. Markov genealogy processes. *Theoretical Population Biology* **143**, 77–91, 2022. doi:10.1016/j.tpb.2021.11.003.

T. Stadler. Sampling-through-time in birth-death trees. *Journal of Theoretical Biology* **267**, 396–404, 2010. doi:10.1016/j.jtbi.2010.09.010.

T. Stadler. Sampling-through-time in birth-death trees. *Journal of Theoretical Biology* **267**, 396–404, 2010. doi:10.1016/j.jtbi.2010.09.010.

A. A. King, Q. Lin, and E. L. Ionides. Exact phylodynamic likelihood via structured Markov genealogy processes. *arXiv* 2405.17032, 2024. doi:10.48550/arxiv.2405.17032.

See Also

More example genealogy processes: `moran`, `s2i2r2`, `seir`, `si2r`, `siir`, `simulate()`, `sir`, `strains`, `twospecies`, `twoundead`

Examples

```
simulate("LBDP",time=4) |> plot(points=TRUE)

simulate("LBDP",lambda=2,mu=1,psi=3,n0=1,time=1) |>
  simulate(time=10,lambda=1) |>
  plot()

simulate("LBDP",time=4) |>
  lineages() |>
  plot()
```

`lineages` *Lineage-count function*

Description

Lineage-counts, saturations, and event-codes.

Usage

```
lineages(object, prune = TRUE, obscure = TRUE)

## S3 method for class 'gplin'
plot(x, ..., palette = scales::hue_pal(l = 30, h = c(220, 580)))
```

Arguments

`object`	`gpsim` object.
`prune`	logical; prune the genealogy?
`obscure`	logical; obscure the demes?
`x`	object of class 'gpgen'
`...`	passed to `theme`.
`palette`	color palette for branches. This can be furnished either as a function or a vector of colors. If this is a function, it should take a single integer argument, the number of colors required. If it is a vector, it should have at least as many elements as there are demes in the genealogy.

Details

This function extracts from the specified genealogy several important time-varying quantities. These include:

lineages number of lineages through time

saturation the number of lineages emerging from the event

event_type an integer coding the type of event

If the genealogy has been obscured (the default), the number in the `lineages` returned is the total number of lineages present at the specified time and the saturation is the total saturation. If the genealogy has not been obscured (`obscure = FALSE`), the deme-specific data are returned. In this case, the `deme` column specifies the pertinent deme.

The event types are:

0 no event,

-1 a root,

1 a sample event,

2 a non-sample event,

3 the end of the time interval, which may or may not coincide with the latest tip of the genealogy.

Value

A `tibble` containing information about the genealogy. See Details for specifics. The `tibble` returned by `lineages` has a `plot` method.

Examples

```
library(tidyverse)

pal <- c("#00274c","#ffcb05")

simulate("SIIR",time=3) -> x
plot_grid(
  x |> plot(),
  x |> lineages() |> plot(),
  x |> plot(obscure=FALSE,palette=pal),
  x |> lineages(obscure=FALSE) |>
    plot(palette=pal,legend.position=c(0.8,0.9)),
  align="v",axis="b",
  ncol=2,byrow=FALSE
)
```

---

moran *The classical Moran model*

Description

The Markov genealogy process induced by the classical Moran process, in which birth/death events occur at a constant rate and the population size remains constant.

Usage

```
runMoran(time, t0 = 0, mu = 1, psi = 1, n = 100)

continueMoran(object, time, mu = NA, psi = NA)

moran_exact(x, n = 100, mu = 1, psi = 1)
```

Arguments

time	final time
t0	initial time
mu	per capita event rate
psi	per capita sampling rate
n	population size
object	either the name of the model to simulate *or* a previously computed 'gpsim' object
x	genealogy in **phylopomp** format (i.e., an object that inherits from 'gpgen').

Details

moran_exact gives the exact log likelihood of a genealogy under the uniformly-sampled Moran process.

Value

runMoran and continueMoran return objects of class 'gpsim' with 'model' attribute "Moran".

moran_exact returns the log likelihood of the genealogy.

References

P.A.P. Moran. Random processes in genetics. *Mathematical Proceedings of the Cambridge Philosophical Society* **54**, 60–71, 1958. doi:10.1017/s0305004100033193.

See Also

More example genealogy processes: lbdp, s2i2r2, seir, si2r, siir, simulate(), sir, strains, twospecies, twoundead

---

newick *Newick output*

Description

Extract a Newick-format description of a genealogy.

Usage

```
newick(object, prune = TRUE, obscure = TRUE)
```

Arguments

object	gpsim object.
prune	logical; prune the genealogy?
obscure	logical; obscure the demes?

Value

A string in Newick format.

Examples

```
simulate("SIIR",time=1) |> newick()
```

---

parse_newick *parse a Newick string*

Description

Parses a Newick description and returns a binary version of the genealogy.

Usage

```
parse_newick(x, t0 = 0, tf = NA)
```

Arguments

x	character; the Newick description. See Details for specifics.
t0	numeric; the root time.
tf	numeric; the current or final time.

Details

parse_newick can only handle a subset of the full Newick specification. In particular, labels are assumed to be of the form <TYPE>_<DEME>_<LABEL>, i.e., each label has three parts, separated by underscores ('_'). The parts are as follows.

- TYPE must be a single character from among the following: 'b', 'g', 'm', 'o'.
  - 'b' signifies a sample.
  - 'g' signifies an internal node.
  - 'm' signifies a root.
  - 'o' indicates an extant lineage.
- DEME must be a non-negative integer, specifying the deme in which the branch resides. If deme information is not present, use 0.
- LABEL is ignored and may be left out.

Value

An object of class "gpgen".

phylopomp *Phylodynamics for POMP models*

Description

Simulation and inference of Markov genealogy processes.

Author(s)

Aaron A. King, Qianying Lin

References

A. A. King, Q. Lin, and E. L. Ionides. Exact phylodynamic likelihood via structured Markov genealogy processes. *arXiv* 2405.17032, 2024. doi:10.48550/arxiv.2405.17032.

A. A. King, Q. Lin, and E. L. Ionides. Markov genealogy processes. *Theoretical Population Biology* **143**, 77–91, 2022. doi:10.1016/j.tpb.2021.11.003.

reexports *Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

cowplot plot_grid

foreach %dopar%, foreach, registerDoSEQ

grid viewport

pomp bake, freeze, stew

yaml as.yaml, read_yaml

s2i2r2 *Two-host infection model with waning, immigration, and demography.*

Description

The population is structured by infection progression and host species.

Usage

```
runS2I2R2(
  time,
  t0 = 0,
  Beta11 = 4,
  Beta12 = 0,
  Beta22 = 4,
  gamma1 = 1,
  gamma2 = 1,
  psi1 = 1,
  psi2 = 0,
  omega1 = 0,
  omega2 = 0,
  b1 = 0,
  b2 = 0,
  d1 = 0,
  d2 = 0,
  iota1 = 0,
  iota2 = 0,
  S1_0 = 100,
  S2_0 = 100,
  I1_0 = 0,
  I2_0 = 10,
  R1_0 = 0,
  R2_0 = 0
)

continueS2I2R2(
  object,
  time,
  Beta11 = NA,
  Beta12 = NA,
  Beta22 = NA,
  gamma1 = NA,
  gamma2 = NA,
  psi1 = NA,
  psi2 = NA,
  omega1 = NA,
  omega2 = NA,
```

```
  b1 = NA,
  b2 = NA,
  d1 = NA,
  d2 = NA,
  iota1 = NA,
  iota2 = NA
)
```

Arguments

time	final time
t0	initial time
Beta11, Beta22	transmission rates within species 1 and 2, respectively
Beta12	transmission from species 2 to species 1
gamma1, gamma2	recovery rates for species 1 and 2, respectively
psi1, psi2	per capita sampling rates
omega1, omega2	rates of waning of immunity
b1, b2	per capita birth rates
d1, d2	per capita death rates
iota1, iota2	infection importation rates
S1_0, S2_0	initial sizes of susceptible populations
I1_0, I2_0	initial sizes of infected populations
R1_0, R2_0	initial sizes of immune populations
object	either the name of the model to simulate *or* a previously computed 'gpsim' object

Value

runS2I2R2 and continueS2I2R2 return objects of class 'gpsim' with 'model' attribute "S2I2R2".

See Also

More example genealogy processes: lbdp, moran, seir, si2r, siir, simulate(), sir, strains, twospecies, twoundead

---

seir *Classical susceptible-exposed-infected-recovered model*

Description

The population is structured by infection progression.

Usage

```
runSEIR(
  time,
  t0 = 0,
  Beta = 4,
  sigma = 1,
  gamma = 1,
  psi = 1,
  omega = 0,
  S0 = 100,
  E0 = 5,
  I0 = 5,
  R0 = 0
)

runSEIRS(
  time,
  t0 = 0,
  Beta = 4,
  sigma = 1,
  gamma = 1,
  psi = 1,
  omega = 0,
  S0 = 100,
  E0 = 5,
  I0 = 5,
  R0 = 0
)

continueSEIR(
  object,
  time,
  Beta = NA,
  sigma = NA,
  gamma = NA,
  psi = NA,
  omega = NA
)

continueSEIRS(
  object,
  time,
  Beta = NA,
  sigma = NA,
  gamma = NA,
  psi = NA,
  omega = NA
)
```

```
seirs_pomp(x, Beta, sigma, gamma, psi, omega = 0, S0, E0, I0, R0)
```

Arguments

time	final time
t0	initial time
Beta	transmission rate
sigma	progression rate
gamma	recovery rate
psi	per capita sampling rate
omega	rate of waning of immunity
S0, E0, I0, R0	initial sizes of S, E, I, R compartments, respectively.
object	either the name of the model to simulate *or* a previously computed 'gpsim' object
x	genealogy in **phylopomp** format.

Details

seirs_pomp constructs a 'pomp' object containing a given set of data and an SEIRS model.

Value

runSEIR and continueSEIR return objects of class 'gpsim' with 'model' attribute "SEIR".

seirs_pomp returns a 'pomp' object.

References

A. A. King, Q. Lin, and E. L. Ionides. Exact phylodynamic likelihood via structured Markov genealogy processes. *arXiv* 2405.17032, 2024. doi:10.48550/arxiv.2405.17032.

See Also

More example genealogy processes: lbdp, moran, s2i2r2, si2r, siir, simulate(), sir, strains, twospecies, twoundead

Examples

```
simulate("SEIR",Beta=2,sigma=2,gamma=1,psi=2,S0=1000,I0=5,time=5) |>
  simulate(Beta=5,gamma=2,time=10,psi=3) |>
  plot()

runSEIR(Beta=3,gamma=1,psi=2,S0=20,I0=5,R0=0,time=5,t0=-1) |>
  plot(points=TRUE,obscure=FALSE)

runSEIR(Beta=3,gamma=0.1,psi=0.2,S0=100,I0=5,R0=0,time=2,t0=0) -> x
plot_grid(plotlist=list(plot(x,points=TRUE),diagram(x)),
  ncol=1,rel_heights=c(4,1))
```

```
simulate("SEIR",sigma=1,omega=1,time=20,I0=4) |> plot(obscure=FALSE)

simulate("SEIR",sigma=1,omega=1,time=20,I0=4) |>
  lineages(obscure=FALSE) |>
  plot()
```

---

si2r *Two-deme model of superspreading*

Description

Deme 2 consists of "superspreaders" who engender clusters of infection in "superspreading events".

Usage

```
runSI2R(
  time,
  t0 = 0,
  Beta = 5,
  mu = 5,
  gamma = 1,
  omega = 0,
  psi1 = 1,
  psi2 = 0,
  sigma12 = 1,
  sigma21 = 3,
  S0 = 500,
  I0 = 10,
  R0 = 0
)

continueSI2R(
  object,
  time,
  Beta = NA,
  mu = NA,
  gamma = NA,
  omega = NA,
  psi1 = NA,
  psi2 = NA,
  sigma12 = NA,
  sigma21 = NA
)
```

Arguments

time	final time
t0	initial time
Beta	transmission rate
mu	mean superspreading-event cluster size
gamma	recovery rate
omega	rate of waning of immunity
psi1, psi2	sampling rates for demes 1 and 2, respectively
sigma12, sigma21	movement rates from deme 1 to 2 and 2 to 1, respectively
S0	initial size of susceptible population
I0	initial size of I1 population (I2 = 0 at t = 0)
R0	initial size of recovered population
object	either the name of the model to simulate *or* a previously computed 'gpsim' object

Details

Superspreaders (deme 2) behave differently than ordinary infections: transmission events occur at the same rate (Beta), but at each event, a superspreader infects N individuals, where

$$N \sim 1 + \text{Geometric}(1/\mu).$$

Thus, assuming susceptibles are not limiting, the mean number of infections resulting from a superspreading event is μ and the variance in this number is $\mu^2 - \mu$. If susceptibles are limiting, i.e., if the number of susceptibles is not greater than N, then all remaining susceptibles are infected.

Value

runSI2R and continueSI2R return objects of class 'gpsim' with 'model' attribute "SI2R".

See Also

More example genealogy processes: lbdp, moran, s2i2r2, seir, siir, simulate(), sir, strains, twospecies, twoundead

Examples

```
simulate("SI2R",time=1) |>
  plot(obscure=FALSE)

runSI2R(Beta=10,S0=2000,time=1,psi1=0) |>
  simulate(time=2,psi1=1) |>
  plot(points=TRUE,obscure=FALSE)

simulate("SI2R",time=5) |>
  lineages() |>
```

```
  plot()

simulate("SI2R",time=2) |>
  diagram(m=30)

simulate("SI2R",time=20,omega=0.2,mu=20) -> x
plot_grid(
  x |> plot(obscure=FALSE),
  x |> lineages(obscure=FALSE) |> plot(),
  ncol=1,
  align="v",axis="b"
)
```

`siir` *Two-strain SIR model.*

Description

Two distinct pathogen strains compete for susceptibles.

Usage

```
runSIIR(
  time,
  t0 = 0,
  Beta1 = 5,
  Beta2 = 5,
  gamma = 1,
  psi1 = 1,
  psi2 = 0,
  sigma12 = 0,
  sigma21 = 0,
  omega = 0,
  S0 = 500,
  I1_0 = 10,
  I2_0 = 10,
  R0 = 0
)

continueSIIR(
  object,
  time,
  Beta1 = NA,
  Beta2 = NA,
  gamma = NA,
  psi1 = NA,
  psi2 = NA,
  sigma12 = NA,
```

```
  sigma21 = NA,
  omega = NA
)
```

Arguments

time	final time
t0	initial time
Beta1, Beta2	transmission rates from each of the infectious classes.
gamma	recovery rate.
psi1, psi2	sampling rates.
sigma12, sigma21	movement rates from deme 1 to 2 and 2 to 1, respectively
omega	rate of loss of immunity
S0	initial size of susceptible population.
I1_0	initial size of I2 population.
I2_0	initial size of I2 population.
R0	initial size of recovered population.
object	either the name of the model to simulate *or* a previously computed 'gpsim' object

Value

runSIIR and continueSIIR return objects of class 'gpsim' with 'model' attribute "SIIR".

See Also

More example genealogy processes: lbdp, moran, s2i2r2, seir, si2r, simulate(), sir, strains, twospecies, twoundead

Examples

```
simulate("SIIR",time=3,psi1=1,psi2=0) |>
  simulate(Beta1=2,gamma=2,time=10,psi1=10,psi2=1) |>
  plot()

runSIIR(Beta1=10,Beta2=8,
  S0=200,I1_0=10,I2_0=8,R0=0,time=0,t0=-1) |>
  simulate(psi1=10,time=2) |>
  plot(points=TRUE,obscure=FALSE)

simulate("SIIR",Beta1=2,Beta2=50,gamma=1,psi1=2,
  S0=300,I1_0=20,I2_0=2,time=5) |>
  lineages() |>
  plot()
```

`simulate` *simulate*

Description

Simulate Markov genealogy processes

Usage

```
simulate(object, ...)

## Default S3 method:
simulate(object, ...)

## S3 method for class 'character'
simulate(object, time, ...)

## S3 method for class 'gpsim'
simulate(object, time, ...)
```

Arguments

`object`	either the name of the model to simulate *or* a previously computed 'gpsim' object
`...`	additional arguments to the model-specific simulation functions
`time`	end timepoint of simulation

Details

When `object` is of class 'gpsim', i.e., the result of a genealogy-process simulation, `simulate` acts to continue the simulation to a later timepoint. Note that, one cannot change initial conditions or `t0` when continuing a simulation.

Value

An object of 'gpsim' class.

References

A. A. King, Q. Lin, and E. L. Ionides. Exact phylodynamic likelihood via structured Markov genealogy processes. *arXiv* 2405.17032, 2024. doi:10.48550/arxiv.2405.17032.

A. A. King, Q. Lin, and E. L. Ionides. Markov genealogy processes. *Theoretical Population Biology* **143**, 77–91, 2022. doi:10.1016/j.tpb.2021.11.003.

See Also

More example genealogy processes: `lbdp`, `moran`, `s2i2r2`, `seir`, `si2r`, `siir`, `sir`, `strains`, `twospecies`, `twoundead`

sir *Classical susceptible-infected-recovered model*

Description

A single, unstructured population of hosts.

Usage

```
runSIR(
  time,
  t0 = 0,
  Beta = 2,
  gamma = 1,
  psi = 1,
  omega = 0,
  S0 = 100,
  I0 = 2,
  R0 = 0
)

runSIRS(
  time,
  t0 = 0,
  Beta = 2,
  gamma = 1,
  psi = 1,
  omega = 0,
  S0 = 100,
  I0 = 2,
  R0 = 0
)

continueSIR(object, time, Beta = NA, gamma = NA, psi = NA, omega = NA)

runSIRS(
  time,
  t0 = 0,
  Beta = 2,
  gamma = 1,
  psi = 1,
  omega = 0,
  S0 = 100,
  I0 = 2,
  R0 = 0
)
```

```
continueSIRS(object, time, Beta = NA, gamma = NA, psi = NA, omega = NA)

sir_pomp(x, Beta, gamma, psi, omega = 0, S0, I0, R0)

sirs_pomp(x, Beta, gamma, psi, omega = 0, S0, I0, R0)
```

Arguments

time	final time
t0	initial time
Beta	transmission rate.
gamma	recovery rate.
psi	sampling rate.
omega	immunity waning rate
S0, I0, R0	initial sizes of susceptible, infected, and recovered populations, respectively.
object	either the name of the model to simulate *or* a previously computed 'gpsim' object
x	genealogy in **phylopomp** format (i.e., an object that inherits from 'gpgen').

Details

sir_pomp constructs a 'pomp' object containing a given set of data and a SIR model.

Value

runSIR and continueSIR return objects of class 'gpsim' with 'model' attribute "SIR".

sir_pomp and sirs_pomp return 'pomp' objects.

References

A. A. King, Q. Lin, and E. L. Ionides. Exact phylodynamic likelihood via structured Markov genealogy processes. *arXiv* 2405.17032, 2024. doi:10.48550/arxiv.2405.17032.

A. A. King, Q. Lin, and E. L. Ionides. Markov genealogy processes. *Theoretical Population Biology* **143**, 77–91, 2022. doi:10.1016/j.tpb.2021.11.003.

See Also

More example genealogy processes: lbdp, moran, s2i2r2, seir, si2r, siir, simulate(), strains, twospecies, twoundead

Examples

```
simulate("SIR",Beta=2,gamma=1,psi=2,S0=1000,I0=5,time=5) |>
  simulate(Beta=5,gamma=2,time=10,psi=3) |>
  plot()

runSIR(Beta=3,gamma=1,psi=2,S0=20,I0=5,R0=0,time=5,t0=-1) |>
```

```
  plot(points=TRUE)

runSIR(Beta=3,gamma=0.1,psi=0.2,S0=100,I0=5,R0=0,time=2,t0=0) -> x
plot_grid(plotlist=list(plot(x,points=TRUE),diagram(x)),
  ncol=1,rel_heights=c(4,1))

simulate("SIRS",omega=1,time=20,I0=4) |> plot()
simulate("SIRS",omega=1,time=20,I0=4) |> lineages() |> plot()
```

`strains` *Three strains compete for a single susceptible pool.*

Description

The three demes are three distinct pathogen strains that compete for susceptibles.

Usage

```
runStrains(
  time,
  t0 = 0,
  Beta1 = 5,
  Beta2 = 5,
  Beta3 = 5,
  gamma = 1,
  psi1 = 1,
  psi2 = 0,
  psi3 = 0,
  S0 = 10000,
  I1_0 = 10,
  I2_0 = 10,
  I3_0 = 10,
  R0 = 0
)

continueStrains(
  object,
  time,
  Beta1 = NA,
  Beta2 = NA,
  Beta3 = NA,
  gamma = NA,
  psi1 = NA,
  psi2 = NA,
  psi3 = NA
)

strains_pomp(
```

```
  x,
  Beta1,
  Beta2,
  Beta3,
  gamma,
  psi1,
  psi2,
  psi3,
  S0,
  I1_0,
  I2_0,
  I3_0,
  R0
)
```

Arguments

`time`	final time
`t0`	initial time
`Beta1`, `Beta2`, `Beta3`	transmission rate for strains 1, 2, 3, respectively
`gamma`	recovery rate
`psi1`, `psi2`, `psi3`	sampling rates
`S0`	initial size of susceptible population
`I1_0`, `I2_0`, `I3_0`	initial numbers of strain-specific infections
`R0`	initial size of immune population
`object`	either the name of the model to simulate *or* a previously computed 'gpsim' object
`x`	genealogy in **phylopomp** format (i.e., an object that inherits from 'gpgen').

Details

`strains_pomp` constructs a 'pomp' object containing a given set of data and the Strains model.

Value

`runStrains` and `continueStrains` return objects of class 'gpsim' with 'model' attribute "Strains".

`strains_pomp` returns a 'pomp' object.

See Also

More example genealogy processes: `lbdp`, `moran`, `s2i2r2`, `seir`, `si2r`, `siir`, `simulate()`, `sir`, `twospecies`, `twoundead`

`treeplot` *Fancy tree plotter*

Description

Plots a genealogical tree.

Usage

```
## S3 method for class 'gpgen'
plot(x, ..., time, t0, prune = TRUE, obscure = TRUE)

treeplot(
  tree,
  time = NULL,
  t0 = 0,
  ladderize = TRUE,
  points = FALSE,
  ...,
  palette = scales::hue_pal(l = 30, h = c(220, 580))
)
```

Arguments

`x`	object of class 'gpgen'
`...`	`plot` passes extra arguments to `treeplot`. `treeplot` passes extra arguments to `theme`.
`time`	numeric; time of the genealogy.
`t0`	numeric; root time.
`prune`	logical; prune the genealogy?
`obscure`	logical; obscure the demes?
`tree`	character; tree representation in Newick format.
`ladderize`	Ladderize?
`points`	Show nodes and tips?
`palette`	color palette for branches. This can be furnished either as a function or a vector of colors. If this is a function, it should take a single integer argument, the number of colors required. If it is a vector, it should have at least as many elements as there are demes in the genealogy.

Value

A printable `ggplot` object.

Examples

```
## Not run:

  library(ggplot2)
  library(phylopomp)
  times <- seq(from=0,to=8,by=0.1)[-1]

  png_files <- sprintf(
    file.path(tempdir(),"frame%05d.png"),
    seq_len(2*length(times))
  )

  pb <- utils::txtProgressBar(0,2*length(times),0,style=3)
  x <- simulate("SIIR",time=0,Beta1=5,Beta2=10,gamma=1,omega=0.5,
    psi1=0.2,psi2=0.1,sigma12=1,sigma21=1,S0=200,I1_0=3,I2_0=2)

  img <- 1
  for (k in seq.int(from=1,to=length(times),by=1)) {
    x <- simulate(x,time=times[k])
    ggsave(
      filename=png_files[img],
      plot=plot(
        x, t0=0, time=max(times),
        points=FALSE, prune=FALSE, obscure=FALSE,
        palette=c("#ffcb05","#dddddd"),
        axis.line=element_line(color="white"),
        axis.ticks=element_line(color="white"),
        axis.text=element_blank(),
        plot.background=element_rect(fill=NA,color=NA),
        panel.background=element_rect(fill=NA,color=NA)
      ),
      device="png",dpi=300,
      height=2,width=3,units="in"
    )
    setTxtProgressBar(pb,img)
    img <- img+1
  }

  for (k in seq.int(from=length(times),to=1,by=-1)) {
    x <- curtail(x,time=times[k])
    ggsave(
      filename=png_files[img],
      plot=plot(
        x, t0=0, time=max(times),
        points=FALSE, prune=FALSE, obscure=FALSE,
        palette=c("#ffcb05","#dddddd"),
        axis.line=element_line(color="white"),
        axis.ticks=element_line(color="white"),
        axis.text=element_blank(),
        plot.background=element_rect(fill=NA,color=NA),
        panel.background=element_rect(fill=NA,color=NA)
      ),
```

```
    device="png",dpi=300,
    height=2,width=3,units="in"
  )
  setTxtProgressBar(pb,img)
  img <- img+1
}

library(gifski)
gif_file <- "movie1.gif"
gifski(png_files,gif_file,delay=0.08,loop=TRUE)
unlink(png_files)


## End(Not run)
```

`twospecies` *Two-host infection model with waning, immigration, demography, and spillover. Hosts are culled upon sampling with a given probability.*

Description

The population is structured by infection progression and host species.

Usage

```
runTwoSpecies(
  time,
  t0 = 0,
  Beta11 = 4,
  Beta12 = 0,
  Beta21 = 0,
  Beta22 = 4,
  gamma1 = 1,
  gamma2 = 1,
  psi1 = 1,
  psi2 = 0,
  c1 = 1,
  c2 = 1,
  omega1 = 0,
  omega2 = 0,
  b1 = 0,
  b2 = 0,
  d1 = 0,
  d2 = 0,
  iota1 = 0,
  iota2 = 0,
  S1_0 = 100,
  S2_0 = 100,
```

```
  I1_0 = 0,
  I2_0 = 10,
  R1_0 = 0,
  R2_0 = 0
)

continueTwoSpecies(
  object,
  time,
  Beta11 = NA,
  Beta12 = NA,
  Beta21 = NA,
  Beta22 = NA,
  gamma1 = NA,
  gamma2 = NA,
  psi1 = NA,
  psi2 = NA,
  c1 = NA,
  c2 = NA,
  omega1 = NA,
  omega2 = NA,
  b1 = NA,
  b2 = NA,
  d1 = NA,
  d2 = NA,
  iota1 = NA,
  iota2 = NA
)

twospecies_pomp(
  x,
  Beta11,
  Beta12,
  Beta21,
  Beta22,
  gamma1,
  gamma2,
  psi1,
  psi2,
  c1,
  c2,
  omega1,
  omega2,
  b1,
  b2,
  d1,
  d2,
  S1_0,
```

```
  S2_0,
  I1_0,
  I2_0,
  R1_0,
  R2_0
)
```

Arguments

time	final time
t0	initial time
Beta11	transmission rate within species 1
Beta12	transmission from species 2 to species 1
Beta21	transmission from species 1 to species 2
Beta22	transmission rate within species 2
gamma1	species 1 recovery rate
gamma2	species 2 recovery rate
psi1	per capita sampling rate for species 1
psi2	per capita sampling rate for species 2
c1	probability that a sampled (positive) host of species 1 is culled
c2	probability that a sampled (positive) host of species 2 is culled
omega1	rate of waning of immunity for species 1
omega2	rate of waning of immunity for species 2
b1	per capita birth rate for species 1
b2	per capita birth rate for species 2
d1	per capita death rate for species 1
d2	per capita death rate for species 2
iota1	imported infections for species 1
iota2	imported infections for species 2
S1_0	initial size of species 1 susceptible population
S2_0	initial size of species 2 susceptible population
I1_0	initial size of species 1 infected population
I2_0	initial size of species 2 infected population
R1_0	initial size of species 1 immune population
R2_0	initial size of species 2 immune population
object	either the name of the model to simulate *or* a previously computed 'gpsim' object
x	genealogy in **phylopomp** format.

Details

twospecies_pomp constructs a 'pomp' object containing a given set of data and a TwoSpecies model. Note that, for the moment, twospecies_pomp assumes that there is no importation of infection into the populations (i.e., iota1 = iota2 = 0).

Value

runTwoSpecies and continueTwoSpecies return objects of class 'gpsim' with 'model' attribute "TwoSpecies".

twospecies_pomp returns a 'pomp' object.

See Also

More example genealogy processes: lbdp, moran, s2i2r2, seir, si2r, siir, simulate(), sir, strains, twoundead

---

twoundead — *Two-host infection model with waning, immigration, demography, and spillover. Hosts are culled upon sampling with a given probability. This is identical to the TwoSpecies model with the exception that dead lineages are not pruned. Instead, they become *ghosts*.*

Description

The population is structured by infection progression and host species.

Usage

```
runTwoUndead(
  time,
  t0 = 0,
  Beta11 = 4,
  Beta12 = 0,
  Beta21 = 0,
  Beta22 = 4,
  gamma1 = 1,
  gamma2 = 1,
  psi1 = 1,
  psi2 = 0,
  c1 = 1,
  c2 = 1,
  omega1 = 0,
  omega2 = 0,
  b1 = 0,
  b2 = 0,
  d1 = 0,
```

```
  d2 = 0,
  iota1 = 0,
  iota2 = 0,
  S1_0 = 100,
  S2_0 = 100,
  I1_0 = 0,
  I2_0 = 10,
  R1_0 = 0,
  R2_0 = 0
)

continueTwoUndead(
  object,
  time,
  Beta11 = NA,
  Beta12 = NA,
  Beta21 = NA,
  Beta22 = NA,
  gamma1 = NA,
  gamma2 = NA,
  psi1 = NA,
  psi2 = NA,
  c1 = NA,
  c2 = NA,
  omega1 = NA,
  omega2 = NA,
  b1 = NA,
  b2 = NA,
  d1 = NA,
  d2 = NA,
  iota1 = NA,
  iota2 = NA
)
```

Arguments

time	final time
t0	initial time
Beta11	transmission rate within species 1
Beta12	transmission from species 2 to species 1
Beta21	transmission from species 1 to species 2
Beta22	transmission rate within species 2
gamma1	species 1 recovery rate
gamma2	species 2 recovery rate
psi1	per capita sampling rate for species 1
psi2	per capita sampling rate for species 2

c1	probability that a sampled (positive) host of species 1 is culled
c2	probability that a sampled (positive) host of species 2 is culled
omega1	rate of waning of immunity for species 1
omega2	rate of waning of immunity for species 2
b1	per capita birth rate for species 1
b2	per capita birth rate for species 2
d1	per capita death rate for species 1
d2	per capita death rate for species 2
iota1	imported infections for species 1
iota2	imported infections for species 2
S1_0	initial size of species 1 susceptible population
S2_0	initial size of species 2 susceptible population
I1_0	initial size of species 1 infected population
I2_0	initial size of species 2 infected population
R1_0	initial size of species 1 immune population
R2_0	initial size of species 2 immune population
object	either the name of the model to simulate *or* a previously computed 'gpsim' object

Value

`runTwoUndead` and `continueTwoUndead` return objects of class 'gpsim' with 'model' attribute "TwoUndead".

See Also

More example genealogy processes: `lbdp`, `moran`, `s2i2r2`, `seir`, `si2r`, `siir`, `simulate()`, `sir`, `strains`, `twospecies`

`yaml` *YAML output*

Description

Human- and machine-readable description.

Usage

```
yaml(object)
```

Arguments

object	`gpsim` object.

Value

A string in YAML format, with class “gpyaml”.

Examples

```
simulate("SIIR",time=1) |> yaml()
```

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