

Package ‘phylopomp’

December 28, 2021

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phylopomp-package	<i>Phylodynamics for POMP models</i>
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Description

Super cool.

Author(s)

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diagram	<i>Genealogy process diagram</i>
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Description

Produces a diagram of the genealogy process state.

Usage

```
diagram(
  object,
  prune = TRUE,
  obscure = TRUE,
  m = NULL,
  n = NULL,
  ...,
  digits = 1
)

## 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.
...	graphical parameter settings, suitable for passing to gpar .
digits	non-negative integer; number of decimal digits to print in the node time
x	An R object.
vp	a viewport object (or NULL).

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,compact=FALSE)
plot_grid(plotlist=list(plot(x,points=TRUE)[[1]],diagram(x)),
  ncol=1,rel_heights=c(4,1))
```

genealogyGrob

*Diagramming internals***Description**

Facilities to produce diagrammatic representations of genealogy process states.

Usage

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

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

```
pocketGrob(object, n = NULL, 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, ...)
```

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	a viewport object (or NULL).
...	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	<i>getInfo</i>
---------	----------------

Description

Retrieve information from genealogy process simulation

Usage

```
getInfo(
  object,
  prune = TRUE,
  obscure = TRUE,
  t0 = FALSE,
  time = FALSE,
  description = FALSE,
  structure = FALSE,
  yaml = FALSE,
  lineages = FALSE,
  tree = FALSE,
  compact = TRUE
)
```

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?

<code>yaml</code>	logical; return the structure in YAML format?
<code>lineages</code>	logical; return the lineage-count function?
<code>tree</code>	logical; return the tree?
<code>compact</code>	logical; return the tree in compact representation?

Value

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

t0 the initial time

time the current time

tree 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

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)
```

Arguments

<code>time</code>	final time
<code>t0</code>	initial time
<code>lambda</code>	per capita birth rate
<code>mu</code>	per capita recovery rate.
<code>psi</code>	per capita sampling rate.
<code>n0</code>	initial population size
<code>object</code>	either the name of the model to simulate <i>or</i> a previously computed ‘gpsim’ object

Value

An object of class ‘gpsim’ with ‘model’ attribute “LBDP”.

See Also

More example genealogy processes: [moran](#), [si2r](#), [siir](#), [simulate\(\)](#), [sir](#)

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

The number of lineages through time

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 'gpsim'
...	passed to treeplot
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,

Value

A [tibble](#) containing the lineage count function. If the genealogy has been obscured (the default), the number in the lineages column is the total number of lineages present at the times in the time column. If the genealogy has not been obscured (obscure = FALSE), the deme-specific lineage counts are returned.

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, n = 100, mu = 1, psi = 1)

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

Arguments

time	final time
t0	initial time
n	population size
mu	event rate
psi	sampling rate.
object	either the name of the model to simulate <i>or</i> a previously computed ‘gpsim’ object

Value

An object of class ‘gpsim’ with ‘model’ attribute “Moran”.

See Also

More example genealogy processes: [lbdp](#), [si2r](#), [siir](#), [simulate\(\)](#), [sir](#)

newick2df

Convert a tree in Newick format to data frame

Description

Convert a genealogical tree in Newick format to a data frame suitable for use with **pomp**.

Usage

```
newick2df(tree, time = NA, root_time = 0)
```

Arguments

tree	tree data in Newick format.
time	time of the genealogy.
root_time	time of the root.

Details

If time is furnished, it is assumed that the absence of samples between the latest leaf and time is informative.

Invisible nodes (labeled ‘X_’ for any X) are dropped.

Value

A data frame suitable for use as pomp input, containing three columns:

time numeric; time of the genealogy event.

lineages integer; the value of the lineage-count function at the specified time. Note that this function is right-continuous with left limits, and constant on the inter-event intervals.

code integer; a code describing the nature of the event. 1 indicates a coalescence; 0 indicates a dead sample; -1 indicates a live sample; 2 indicates the root.

Examples

```
runSIR(Beta=2,gamma=1,psi=2,S0=100,I0=2,R0=0,time=5,t0=0) |>
  getInfo(tree=TRUE) |>
  getElement("tree") |>
  newick2df()
```

plot	<i>Fancy tree plotter</i>
------	---------------------------

Description

Plots a genealogical tree.

Usage

```
## S3 method for class 'gpsim'
plot(x, ..., time, t0, prune = TRUE, obscure = TRUE, compact = 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 ‘gpsim’
...	passed to <code>treeplot</code>
time	numeric; time of the genealogy.
t0	numeric; time of the root.
prune	logical; prune the genealogy?

obscure	logical; obscure the demes?
compact	logical; return the tree in compact representation?
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,

Value

A printable ggplot object.

Examples

```
## Not run:
library(ggplot2)
times <- seq(from=0,to=8,by=0.1)[-1]

png_files <- sprintf(
  file.path(tempdir(),"frame%05d.png"),
  seq_along(times)
)

pb <- utils::txtProgressBar(0,length(times),0,style=3)
x <- simulate("SIIR",time=0,Beta1=5,Beta2=10,gamma=1,
  psi1=0.2,psi2=0.1,sigma12=1,sigma21=1,S0=500,I1_0=3,I2_0=2)
for (k in seq_len(length(times))) {
  x <- simulate(x,time=times[k])
  ggsave(
    filename=png_files[k],
    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,k)
}

library(gifski)
gif_file <- "movie1.gif"
gifski(png_files,gif_file,delay=0.02,loop=TRUE)
```

```
unlink(png_files)

## End(Not run)
```

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](#)

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,
  delta = 0,
  psi1 = 1,
  psi2 = 0,
  sigma12 = 1,
  sigma21 = 3,
  S0 = 500,
  I0 = 10,
  R0 = 0
)

continueSI2R(
```

```

    object,
    time,
    Beta = NA,
    mu = NA,
    gamma = NA,
    delta = NA,
    psi1 = NA,
    psi2 = NA,
    sigma21 = NA,
    sigma12 = NA
  )

```

Arguments

time	final time
t0	initial time
Beta	transmission rate
mu	mean superspreading-event cluster size
gamma	recovery rate
delta	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 <i>or</i> 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

An object of class ‘gpsim’ with ‘model’ attribute “SI2R”.

See Also

More example genealogy processes: [lbdp](#), [moran](#), [siir](#), [simulate\(\)](#), [sir](#)

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,delta=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 = psi1,
  sigma12 = 0,
  sigma21 = 0,
  S0 = 100,
  I1_0 = 10,
  I2_0 = 10,
  R0 = 0
)
```

```

continueSIIR(
  object,
  time,
  Beta1 = NA,
  Beta2 = NA,
  gamma = NA,
  psi1 = NA,
  psi2 = NA,
  sigma21 = NA,
  sigma12 = 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
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 <i>or</i> a previously computed ‘gpsim’ object

Value

An object of class ‘gpsim’ with ‘model’ attribute “SIIR”.

See Also

More example genealogy processes: [lbdp](#), [moran](#), [si2r](#), [simulate\(\)](#), [sir](#)

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 <i>or</i> 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.

See Also

More example genealogy processes: [lbdp](#), [moran](#), [si2r](#), [siir](#), [sir](#)

sir

*Classical susceptible-infected-recovered model***Description**

A single, unstructured population of hosts.

Usage

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

```
continueSIR(object, time, Beta = NA, gamma = NA, psi = NA, delta = NA)
```

```
sir_pomp(data, Beta, gamma, psi, delta = 0, S0, I0, R0, t0 = 0)
```

Arguments

time	final time
t0	initial time
Beta	transmission rate.
gamma	recovery rate.
psi	sampling rate.
delta	immunity waning rate
S0	initial size of susceptible population.
I0	initial size of infected population.
R0	initial size of recovered population.
object	either the name of the model to simulate <i>or</i> a previously computed ‘gpsim’ object
data	data frame containing the genealogy in the format returned by newick2df .

Details

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

Value

An object of class 'gpsim' with 'model' attribute "SIR".

See Also

More example genealogy processes: [lbdp](#), [moran](#), [si2r](#), [siir](#), [simulate\(\)](#)

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

yml	<i>YAML output</i>
-----	--------------------

Description

Human- and machine-readable description

Usage

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

Arguments

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

Value

A string in yml format.

Examples

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

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