Package 'phylopomp'

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R topics documented:

`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.

---

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
)

## 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
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)[[1]],diagram(x)),
  ncol=1,rel_heights=c(4,1))
```

---

genealogy diagram internals

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	viewport to draw plot in
...	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,
  lineages = FALSE,
  tree = 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?
`lineages`	logical; return the lineage-count function?
`tree`	logical; return the tree?

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)

lbdp_exact(data, lambda, mu, psi, n0 = 1)

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

Arguments

time	final time
t0	initial time
lambda	per capita birth rate
mu	per capita recovery rate.
psi	per capita sampling rate.
n0	initial population size
object	either the name of the model to simulate *or* a previously computed 'gpsim' object
data	data frame containing the genealogy event times.

Details

lbdp_exact gives the exact log likelihood of a linear birth-death process, conditioned on $n_0 = 0$ (Stadler, 2010, Thm 3.5). The derivation is also given in comments in the code.

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

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

T. Stadler. Sampling-through-time in birth-death trees. *Journal of Theoretical Biology* **267**, 396–404, 2010.

See Also

More example genealogy processes: moran, seir, 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

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 'gpsim'
...	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, ...

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

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

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

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 *or* a previously computed 'gpsim' object
`data`	data frame containing the genealogy event times.

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.

See Also

More example genealogy processes: `lbdp`, `seir`, `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, t0 = 0)
```

Arguments

tree	tree data in Newick format.
t0	time of the root.

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 a root.

Examples

```
runSIR(Beta=2,gamma=1,psi=2,S0=100,I0=2,R0=0,time=10,t0=0) |>
  getInfo(tree=TRUE) |>
  getElement("tree") |>
  newick2df()
```

parse_newick *parse_newick*

Description

Parse a Newick description and extract various equivalent representations.

Usage

```
parse_newick(
  x,
  prune = TRUE,
  obscure = TRUE,
  t0 = 0,
  time = FALSE,
  description = FALSE,
  structure = FALSE,
  yaml = FALSE,
  lineages = TRUE,
  tree = FALSE
)
```

Arguments

x	character; the Newick description. See Details for specifics.
prune	logical; prune the genealogy?
obscure	logical; obscure the demes?
t0	numeric; the root 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?
lineages	logical; return the lineage-count function?
tree	logical; return the tree?

Value

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

time the current time

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

tree the genealogical tree, in Newick format

phylopomp *Phylodynamics for POMP models*

Description

Simulation and inference of Markov genealogy processes.

Author(s)

Aaron A. King, Qianying Lin

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

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,
  delta = 0,
  S0 = 100,
```

```
  E0 = 5,
  I0 = 5,
  R0 = 0
)

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

Arguments

time	final time
t0	initial time
Beta	transmission rate
sigma	progression rate
gamma	recovery rate
psi	per capita sampling rate
delta	rate of waning of immunity
S0	initial size of susceptible population
E0	initial size of exposed population
I0	initial size of infected population
R0	initial size of immune population
object	either the name of the model to simulate *or* a previously computed 'gpsim' object

Value

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

See Also

More example genealogy processes: `lbdp`, `moran`, `si2r`, `siir`, `simulate()`, `sir`

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,delta=1,time=20,I0=4) |> plot(obscure=FALSE)

simulate("SEIR",sigma=1,delta=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,
  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,
  sigma12 = NA,
  sigma21 = 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 *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`, `seir`, `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 = 0,
  sigma12 = 0,
  sigma21 = 0,
  delta = 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,
```

```
  delta = 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
`delta`	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`, `seir`, `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 *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.

See Also

More example genealogy processes: lbdp, moran, seir, 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
)

runSIRS(
  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)

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

```
)

continueSIRS(object, time, Beta = NA, gamma = NA, psi = NA, delta = NA)

sirs_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 *or* a previously computed 'gpsim' object
data	data frame containing the lineage count function

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".

See Also

More example genealogy processes: lbdp, moran, seir, 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()
```

`treeplot` *Fancy tree plotter*

Description

Plots a genealogical tree.

Usage

```
## S3 method for class 'gpsim'
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 'gpsim'
`...`	`plot` passes extra arguments to `treeplot`. `treeplot` passes extra arguments to `theme`.
`time`	numeric; time of the genealogy.
`t0`	numeric; time of the root.
`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, ...

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,delta=0.5,
    psi1=0.2,psi2=0.1,sigma12=1,sigma21=1,S0=200,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)
```

---

yaml *YAML output*

Description

Human- and machine-readable description

Usage

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

Arguments

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

Value

A string in yaml format.

Examples

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

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