

# Package ‘phylopomp’

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|               |                               |
|---------------|-------------------------------|
| as.data.frame | <i>Coerce to a Data Frame</i> |
|---------------|-------------------------------|

---

## 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, prune = TRUE, obscure = TRUE)
```

**Arguments**

`object` gpsim object.

`time` logical; return the current time?

`prune` logical; prune the genealogy?

`obscure` logical; obscure the demes?

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

---

geneal

*Bare genealogy*

---

**Description**

Extracts the bare genealogy from a Markov genealogy process simulation

**Usage**

```
geneal(object)
```

**Arguments**

object            a 'gpger' 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 <a href="#">textGrob</a> .   |
| 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
)
```

**Arguments**

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

**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  
**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 | <i>Linear birth-death-sampling model</i> |
|------|--|

---

### 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(x, lambda, mu, psi, n0 = 1)

lbdp_pomp(x, 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 <i>or</i> a previously computed ‘gpsim’ object |
| x      | genealogy in <b>phylopomp</b> format (i.e., an object that inherits from ‘gpgen’).      |

### 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 | <i>Lineage-count function</i> |
|----------|-------------------------------|

---

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 <a href="#">theme</a> .  |
| 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, n = 100, mu = 1, psi = 1)
```

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

```
moran_exact(x, 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 <i>or</i> a previously computed ‘gpsim’ object |
| x      | genealogy in <b>phylopomp</b> 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.

## See Also

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

---

|        |                      |
|--------|----------------------|
| newick | <i>Newick output</i> |
|--------|----------------------|

---

**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 | <i>parse a Newick string</i> |
|--------------|------------------------------|

---

**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.                           |

**Value**

An object of class “gpngen”.

---

phylopomp

*Phylogenetics 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,
  omega = 0,
  S0 = 100,
```

```

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

  continueSEIR(
    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     | 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 <i>or</i> a previously computed ‘gpsim’ object |
| x      | genealogy in <b>phylopomp</b> 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”.

### 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,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 <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  $\mu$  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,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 <i>or</i> 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 <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](#), [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,  
  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)
```

```
sir_pomp(x, Beta, gamma, psi, omega = 0, S0, I0, R0, t0 = 0)
```

```
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)

sirs_pomp(x, Beta, gamma, psi, omega = 0, S0, I0, R0, t0 = 0)
```

### Arguments

|        |   |
|--------|---|
| time   | final time  |
| t0     | initial time  |
| Beta   | transmission rate.  |
| gamma  | recovery rate.  |
| psi    | sampling rate.  |
| omega  | 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 |
| x      | genealogy in <b>phylopomp</b> format (i.e., an object that inherits from ‘gpngen’).     |

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

treeplot

*Fancy tree plotter***Description**

Plots a genealogical tree.

**Usage**

```
## S3 method for class 'gp-gen'
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 'gp-gen'   |
| ...       | plot passes extra arguments to <a href="#">treeplot</a> . treeplot passes extra arguments to <a href="#">theme</a> .   |
| 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, 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)
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,omega=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)
```

**Arguments**

object                  gpsim object.

**Value**

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

**Examples**

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



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