Package 'epiworldR'

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Type Package

Title Fast Agent-Based Epi Models

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Description A flexible framework for Agent-Based Models (ABM), the 'epiworldR' package provides methods for prototyping disease outbreaks and transmission models using a 'C++' backend, making it very fast. It supports multiple epidemiological models, including the Susceptible-Infected-Susceptible (SIS), Susceptible-Infected-Removed (SIR), Susceptible-Exposed-Infected-Removed (SEIR), and others, involving arbitrary mitigation policies and multiple-disease models. Users can specify infectiousness/susceptibility rates as a function of agents' features, providing great complexity for the model dynamics. Furthermore, 'epiworldR' is ideal for simulation studies featuring large populations.

URL https://github.com/UofUEpiBio/epiworldR,
https://uofuepibio.github.io/epiworldR/,
https://uofuepibio.github.io/epiworldR-workshop/

BugReports https://github.com/UofUEpiBio/epiworldR/issues

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R **topics documented:**

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epiworldR-package   *epiworldR*

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for prototyping disease outbreaks and transmission models using a 'C++' backend, making it very
fast. It supports multiple epidemiological models, including the Susceptible-Infected-Susceptible
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tions.

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See Also

Useful links:

- `https://github.com/UofUEpiBio/epiworldR`
- `https://uofuepibio.github.io/epiworldR/`
- `https://uofuepibio.github.io/epiworldR-workshop/`
- Report bugs at `https://github.com/UofUEpiBio/epiworldR/issues`

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agents_smallworld   *Load agents to a model*

Description

These functions provide access to the network of the model. The network is represented by an
edgelist. The `agents_smallworld` function generates a small world network with the Watts-
Strogatz algorithm. The `agents_from_edgelist` function loads a network from an edgelist. The
`get_network` function returns the edgelist of the network.

Usage

```
agents_smallworld(model, n, k, d, p)

agents_from_edgelist(model, source, target, size, directed)

get_network(model)

get_agents_states(model)
```

```
add_virus_agent(agent, model, virus, state_new = -99, queue = -99)

add_tool_agent(agent, model, tool, state_new = -99, queue = -99)

has_virus(agent, virus)

has_tool(agent, tool)

change_state(agent, model, state_new, queue = -99)

get_agents_tools(model)
```

Arguments

`model`	Model object of class [epiworld_model]().
`n, size`	Number of individuals in the population.
`k`	Number of ties in the small world network.
`d, directed`	Logical scalar. Whether the graph is directed or not.
`p`	Probability of rewiring.
`source, target`	Integer vectors describing the source and target of in the edgelist.
`agent`	Agent object of class epiworld_agent.
`virus`	Virus object of class epiworld_virus.
`state_new`	Integer scalar. New state of the agent after the action is executed.
`queue`	Integer scalar. Change in the queuing system after the action is executed.
`tool`	Tool object of class epiworld_tool.

Details

The `new_state` and queue parameters are optional. If they are not provided, the agent will be updated with the default values of the virus/tool.

Value

- The 'agents_smallworld' function returns a model with the agents loaded.

- The `agents_from_edgelist` function returns an empty model of class epiworld_model.

- The `get_network` function returns a data frame with two columns (`source` and `target`) describing the edgelist of the network.

- `get_agents_states` returns an character vector with the states of the agents by the end of the simulation.

- The function `add_virus_agent` adds a virus to an agent and returns the agent invisibly.

- The function `add_tool_agent` adds a tool to an agent and returns the agent invisibly.

- The functions `has_virus` and `has_tool` return a logical scalar indicating whether the agent has the virus/tool or not.

- `get_agents_tools` returns a list of class `epiworld_agents_tools` with `epiworld_tools` (list of lists).

Examples

```
# Initializing SIR model with agents_smallworld
sir <- ModelSIR(name = "COVID-19", prevalence = 0.01, transmission_rate = 0.9,
                recovery_rate = 0.1)
agents_smallworld(
   sir,
   n = 1000,
   k = 5,
   d = FALSE,
   p = .01
 )
run(sir, ndays = 100, seed = 1912)
sir

# We can also retrieve the network
net <- get_network(sir)
head(net)

# Simulating a bernoulli graph
set.seed(333)
n <- 1000
g <- matrix(runif(n ^ 2) < .01, nrow = n)
diag(g) <- FALSE
el <- which(g, arr.ind = TRUE) - 1L


# Generating an empty model
sir <- ModelSIR("COVID-19", .01, .8, .3)
agents_from_edgelist(
  sir,
  source = el[,1],
  target = el[,2],
  size   = n,
  directed = TRUE
)

# Running the simulation
run(sir, 50)

plot(sir)
```

---

epiworld-data   *Accessing the database of epiworld*

Description

Models in `epiworld` are stored in a database. This database can be accessed using the functions described in this manual page. Some elements of the database are: the transition matrix, the incidence matrix, the reproductive number, the generation time, and daily incidence at the virus and tool level.

Usage

```
get_hist_total(x)

get_today_total(x)

get_hist_virus(x)

get_hist_tool(x)

get_transition_probability(x)

get_reproductive_number(x)

## S3 method for class 'epiworld_repnum'
plot(
  x,
  y = NULL,
  ylab = "Average Rep. Number",
  xlab = "Day (step)",
  main = "Reproductive Number",
  type = "b",
  plot = TRUE,
  ...
)

plot_reproductive_number(x, ...)

get_hist_transition_matrix(x, skip_zeros = FALSE)

## S3 method for class 'epiworld_hist_transition'
as.array(x, ...)

plot_incidence(x, ...)

## S3 method for class 'epiworld_hist_transition'
plot(
  x,
```

```
  type = "b",
  xlab = "Day (step)",
  ylab = "Counts",
  main = "Daily incidence",
  plot = TRUE,
  ...
)

get_transmissions(x)

get_generation_time(x)

## S3 method for class 'epiworld_generation_time'
plot(
  x,
  type = "b",
  xlab = "Day (step)",
  ylab = "Avg. Generation Time",
  main = "Generation Time",
  plot = TRUE,
  ...
)

plot_generation_time(x, ...)
```

Arguments

x	An object of class [epiworld_sir](#), [epiworld_seir](#), etc. any model.
y	Ignored.
ylab, xlab, main, type	
	Further parameters passed to [graphics::plot()](#)
plot	Logical scalar. If TRUE (default), the function will the desired statistic.
...	In the case of plot methods, further arguments passed to [graphics::plot.](#)
skip_zeros	Logical scalar. When FALSE it will return all the entries in the transition matrix.

Details

The plot_reproductive_number function is a wrapper around [get_reproductive_number](#) that plots the result.

The plot_incidence function is a wrapper between [get_hist_transition_matrix](#) and it's plot method.

The plot method for the epiworld_hist_transition class plots the daily incidence of each state. The function returns the data frame used for plotting.

Value

- The get_hist_total function returns an object of class [epiworld_hist_total](#).

- The `get_today_total` function returns a named vector with the total number of individuals in each state at the end of the simulation.

- The `get_hist_virus` function returns an object of class epiworld_hist_virus.

- The `get_hist_tool` function returns an object of epiworld_hist_virus.

- The `get_transition_probability` function returns an object of class `matrix`.

- The `get_reproductive_number` function returns an object of class epiworld_repnum.

- The `plot` function returns a plot of the reproductive number over time.

- `get_hist_transition_matrix` returns a data.frame with four columns: "state_from", "state_to", "date", and "counts."

- The `as.array` method for `epiworld_hist_transition` objects turns the `data.frame` returned by `get_hist_transition_matrix` into an array of `nstates x nstates x (ndays + 1)` entries, where the first entry is the initial state.

- The `plot_incidence` function returns a plot originating from the object `get_hist_transition_matrix`.

- The `plot` function returns a plot which originates from the `epiworld_hist_transition` object.

- The function `get_transmissions` returns a `data.frame` with the following columns: `date`, `source`, `target`, `virus_id`, `virus`, and `source_exposure_date`.

- The function `get_generation_time` returns a `data.frame` with the following columns: "agent", "virus_id", "virus", "date", and "gentime".

- The function `plot_generation_time` is a wrapper for plot and get_generation_time.

See Also

Other Models: `ModelDiffNet()`, `ModelSEIR()`, `ModelSEIRCONN()`, `ModelSEIRD()`, `ModelSEIRDCONN()`, `ModelSIR()`, `ModelSIRCONN()`, `ModelSIRD()`, `ModelSIRDCONN()`, `ModelSIRLogit()`, `ModelSIS()`, `ModelSISD()`, `ModelSURV()`

Examples

```
# SEIR Connected
seirconn <- ModelSEIRCONN(
  name              = "Disease",
  n                 = 10000,
  prevalence        = 0.1,
  contact_rate      = 2.0,
  transmission_rate = 0.8,
  incubation_days   = 7.0,
  recovery_rate     = 0.3
)
```

```
# Running the simulation for 50 steps (days)
set.seed(937)
run(seirconn, 50)

# Retrieving the transition probability
get_transition_probability(seirconn)

# Retrieving date, state, and counts dataframe including any added tools
get_hist_tool(seirconn)

# Retrieving overall date, state, and counts dataframe
head(get_hist_total(seirconn))

# Retrieving date, state, and counts dataframe by variant
head(get_hist_virus(seirconn))

# Retrieving (and plotting) the reproductive number
rp <- get_reproductive_number(seirconn)
plot(rp) # Also equivalent to plot_reproductive_number(seirconn)

# We can go further and get all the history
t_hist <- get_hist_transition_matrix(seirconn)

head(t_hist)

# And turn it into an array
as.array(t_hist)[,,1:3]

# We cam also get (and plot) the incidence, as well as
# the generation time
inci <- plot_incidence(seirconn)
gent <- plot_generation_time(seirconn)
```

---

epiworld-methods   *Methods for epiworldR objects*

Description

The functions described in this section are methods for objects of class `epiworld_model`. Besides of printing and plotting, other methods provide access to manipulate model parameters, getting information about the model and running the simulation.

Usage

```
queuing_on(x)

queuing_off(x)

verbose_off(x)
```

```
verbose_on(x)

run(model, ndays, seed = sample.int(10000, 1))

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

get_states(x)

get_param(x, pname)

set_param(x, pname, pval)

set_name(x, mname)

get_name(x)

get_n_viruses(x)

get_n_tools(x)

get_ndays(x)

get_n_replicates(x)

size(x)

set_agents_data(model, data)

get_agents_data_ncols(model)

get_virus(model, virus_pos)

get_tool(model, tool_pos)

initial_states(model, proportions)

clone_model(model)
```

Arguments

x	An object of class epiworld_model.
model	Model object.
ndays	Number of days (steps) of the simulation.
seed	Seed to set for initializing random number generator.
object	Object of class epiworld_model.

...	Additional arguments.
pname	String. Name of the parameter.
pval	Numeric. Value of the parameter.
mname	String. Name of the model.
data	A numeric matrix.
virus_pos	Integer. Relative location (starting from 0) of the virus in the model
tool_pos	Integer. Relative location (starting from 0) of the tool in the model
proportions	Numeric vector. Proportions in which agents will be distributed (see details).

Details

The verbose_on and verbose_off functions activate and deactivate printing progress on screen, respectively. Both functions return the model (x) invisibly.

epiworld_model objects are pointers to an underlying C++ class in epiworld. To generate a copy of a model, use clone_model, otherwise, the assignment operator will only copy the pointer.

Value

- The verbose_on and verbose_off functions return the same model, however verbose_off returns the model with no progress bar.

- The run function returns the simulated model of class epiworld_model.

- The summary function prints a more detailed view of the model, and returns the same model invisibly.

- The get_states function returns the unique states found in a model.

- The get_param function returns a selected parameter from the model object of class epiworld_model.

- The set_param function does not return a value but instead alters a parameter value.

- The set_name function does not return a value but instead alters an object of epiworld_model.

- get_name returns the name of the model.

- get_n_viruses returns the number of viruses of the model.

- get_n_tools returns the number of tools of the model.

- get_ndays returns the number of days of the model.

- get_n_replicates returns the number of replicates of the model.

- size.epiworld_model returns the number of agents in the model.

- The 'set_agents_data' function returns an object of class DataFrame.

- 'get_agents_data_ncols' returns the number of columns in the model dataframe.

- 'get_virus' returns a [virus](#).

- get_tool returns a [tool](#).

- inital_states returns the model with an updated initial state.

- clone_model returns a copy of the model.

Examples

```
model_sirconn <- ModelSIRCONN(
name                = "COVID-19",
n                   = 10000,
prevalence          = 0.01,
contact_rate        = 5,
transmission_rate   = 0.4,
recovery_rate       = 0.95
)

# Queuing - If you wish to implement the queuing function, declare whether
# you would like it "on" or "off", if any.
queuing_on(model_sirconn)
queuing_off(model_sirconn)
run(model_sirconn, ndays = 100, seed = 1912)

# Verbose - "on" prints the progress bar on the screen while "off"
# deactivates the progress bar. Declare which function you want to implement,
# if any.
verbose_on(model_sirconn)
verbose_off(model_sirconn)
run(model_sirconn, ndays = 100, seed = 1912)

get_states(model_sirconn) # Returns all unique states found within the model.

get_param(model_sirconn, 'Contact rate') # Returns the value of the selected
                                         # parameter within the model object.
                                         # In order to view the parameters,
                                         # run the model object and find the
                                         # "Model parameters" section.

set_param(model_sirconn, 'Contact rate', 2) # Allows for adjustment of model
                                            # parameters within the model
                                            # object. In this example, the
                                            # Contact rate parameter is
                                            # changed to 2. You can now rerun
                                            # the model to observe any
                                            # differences.

set_name(model_sirconn, 'My Epi-Model') # This function allows for setting
                                        # a name for the model. Running the
                                        # model object, the name of the model
                                        # is now reflected next to "Name of
```

```
                                              # the model".

get_name(model_sirconn) # Returns the set name of the model.

get_n_viruses(model_sirconn) # Returns the number of viruses in the model.
                             # In this case, there is only one virus:
                             # "COVID-19".

get_n_tools(model_sirconn) # Returns the number of tools in the model. In
                           # this case, there are zero tools.

get_ndays(model_sirconn) # Returns the length of the simulation in days. This
                         # will match "ndays" within the "run" function.

get_n_replicates(model_sirconn) # Returns the number of replicates of the
                                # model.

size(model_sirconn) # Returns the population size in the model. In this case,
                    # there are 10,000 agents in the model.
# Set Agents Data
# First, your data matrix must have the same number of rows as agents in the
# model. Below is a generated matrix which will be passed into the
# "set_agents_data" function.
data <- matrix(data=runif(20000, min=0, max=100), nrow=10000, ncol=2)
set_agents_data(model_sirconn, data)
get_agents_data_ncols(model_sirconn) # Returns number of columns

get_virus(model_sirconn, 0) # Returns information about the first virus in
                            # the model (index begins at 0).

add_tool(model_sirconn, tool("Vaccine", .9, .9, .5, 1), proportion = .5)
get_tool(model_sirconn, 0) # Returns information about the first tool in the
                           # model. In this case, there are no tools so an
                           # error message will occur.
```

---

epiworldR-deprecated   *Deprecated functions in epiworldR*

Description

Starting version 0.0-4, epiworld changed how it refered to "actions." Following more traditional ABMs, actions are now called "events."

Usage

```
globalaction_tool(...)

globalaction_tool_logit(...)

globalaction_set_params(...)
```

```
globalaction_fun(...)
```

Arguments

...	Arguments to be passed to the new function.

---

get_agents   *Agents in epiworldR*

Description

These functions provide read-access to the agents of the model. The get_agents function returns an object of class epiworld_agents which contains all the information about the agents in the model. The get_agent function returns the information of a single agent. And the get_state function returns the state of a single agent.

Usage

```
get_agents(model)

## S3 method for class 'epiworld_agents'
x[i]

## S3 method for class 'epiworld_agent'
print(x, compressed = FALSE, ...)

## S3 method for class 'epiworld_agents'
print(x, compressed = TRUE, max_print = 10, ...)

get_state(x)
```

Arguments

model	An object of class epiworld_model.
x	An object of class epiworld_agents
i	Index (id) of the agent (from 0 to n-1)
compressed	Logical scalar. When FALSE, it prints detailed information about the agent.
...	Ignored
max_print	Integer scalar. Maximum number of agents to print.

Value

- The `get_agents` function returns an object of class epiworld_agents.

- The `[` method returns an object of class epiworld_agent.

- The `print` function returns information about each individual agent of class epiworld_agent.

- The `get_state` function returns the state of the epiworld_agents object.

See Also

agents

Examples

```
model_sirconn <- ModelSIRCONN(
name              = "COVID-19",
n                 = 10000,
prevalence        = 0.01,
contact_rate      = 5,
transmission_rate = 0.4,
recovery_rate     = 0.95
)

run(model_sirconn, ndays = 100, seed = 1912)

x <- get_agents(model_sirconn) # Storing all agent information into object of
                               # class epiworld_agents

print(x, compressed = FALSE, max_print = 5) # Displaying detailed information of
                                            # the first 5 agents using
                                            # compressed=F. Using compressed=T
                                            # results in less-detailed
                                            # information about each agent.

x[0] # Print information about the first agent. Substitute the agent of
     # interest's position where '0' is.
```

---

global-actions   *Global Actions*

Description

Global actions are functions that are executed at each time step of the simulation. They are useful for implementing interventions, such as vaccination, isolation, and social distancing by means of tools.

Usage

```
globalevent_tool(tool, prob, name = get_name_tool(tool), day = -99)

globalevent_tool_logit(
  tool,
  vars,
  coefs,
  name = get_name_tool(tool),
  day = -99
)

globalevent_set_params(
  param,
  value,
  name = paste0("Set ", param, " to ", value),
  day = -99
)

globalevent_fun(fun, name = deparse(substitute(fun)), day = -99)

add_globalevent(model, action)
```

Arguments

tool	An object of class [tool](#).
prob	Numeric scalar. A probability between 0 and 1.
name	Character scalar. The name of the action.
day	Integer. The day (step) at which the action is executed (see details).
vars	Integer vector. The position of the variables in the model.
coefs	Numeric vector. The coefficients of the logistic regression.
param	Character scalar. The name of the parameter to be set.
value	Numeric scalar. The value of the parameter.
fun	Function. The function to be executed.
model	An object of class [epiworld_model](#).
action	A global action.

Details

The function `globalevent_tool_logit` allows to specify a logistic regression model for the probability of using a tool. The model is specified by the vector of coefficients `coefs` and the vector of variables `vars`. `vars` is an integer vector indicating the position of the variables in the model.

The function `globalevent_set_param` allows to set a parameter of the model. The parameter is specified by its name `param` and the value by `value`.

The function `globalevent_fun` allows to specify a function to be executed at a given day. The function object must receive an object of class [epiworld_model](#) as only argument.

The function `add_globalevent` adds a global action to a model. The model checks for actions to be executed at each time step. If the added action matches the current time step, the action is executed. When day is negative, the action is executed at each time step. When day is positive, the action is executed at the specified time step.

Value

- The `globalevent_set_params` function returns an object of class epiworld_globalevent_set_param and epiworld_globalevent.

- `globalevent_tool` returns an object of class epiworld_globalevent_tool and epiworld_globalevent.

- `globalevent_tool_logit` returns an object of class epiworld_globalevent_tool_logit and epiworld_globalevent.

- The function `add_globalevent` returns the model with the added action.

See Also

epiworld-model

Examples

```
# Simple model
model_sirconn <- ModelSIRCONN(
  name              = "COVID-19",
  n                 = 10000,
  prevalence        = 0.01,
  contact_rate      = 5,
  transmission_rate = 0.4,
  recovery_rate     = 0.95
)

# Creating a tool
epitool <- tool(
  name = "Vaccine",
  susceptibility_reduction = .9,
  transmission_reduction = .5,
  recovery_enhancer = .5,
  death_reduction = .9
)


# Adding a global action
vaccine_day_20 <- globalevent_tool(epitool, .2, day = 20)
add_globalevent(model_sirconn, vaccine_day_20)

# Running and printing
run(model_sirconn, ndays = 40, seed = 1912)
model_sirconn
plot_incidence(model_sirconn)

# Example 2: Changing the contact rate -------------------------------------
```

```
model_sirconn2 <- ModelSIRCONN(
  name                = "COVID-19",
  n                   = 10000,
  prevalence          = 0.01,
  contact_rate        = 5,
  transmission_rate   = 0.4,
  recovery_rate       = 0.95
)

closure_day_10 <- globalevent_set_params("Contact rate", 0, day = 10)
add_globalevent(model_sirconn2, closure_day_10)

# Running and printing
run(model_sirconn2, ndays = 40, seed = 1912)
model_sirconn2
plot_incidence(model_sirconn2)
# Example using `globalevent_fun` to record the state of the
# agents at each time step.

# We start by creating an SIR connected model
model <- ModelSIRCONN(
  name              = "SIR with Global Saver",
  n                 = 1000,
  prevalence        = 0.01,
  contact_rate      = 5,
  transmission_rate = 0.4,
  recovery_rate     = 0.3
  )

# We create the object where the history of the agents will be stored
agents_history <- NULL

# This function prints the total number of agents in each state
# and stores the history of the agents in the object `agents_history`
hist_saver <- function(m) {

  message("Today's totals are: ", paste(get_today_total(m), collapse = ", "))

  # We use the `<<-` operator to assign the value to the global variable
  # `agents_history` (see ?"<<-")
  agents_history <<- cbind(
    agents_history,
    get_agents_states(m)
    )

}
```

ModelDiffNet   *Network Diffusion Model*

Description

The network diffusion model is a simple model that assumes that the probability of adoption of a behavior is proportional to the number of adopters in the network.

Usage

```
ModelDiffNet(
  name,
  prevalence,
  prob_adopt,
  normalize_exposure = TRUE,
  data = matrix(nrow = 0, ncol = 0),
  data_cols = 1L:ncol(data),
  params = vector("double")
)

## S3 method for class 'epiworld_diffnet'
plot(x, main = get_name(x), ...)
```

Arguments

name	Name of the model.
prevalence	Prevalence of the disease.
prob_adopt	Probability of adoption.
normalize_exposure	
	Normalize exposure.
data	Data.
data_cols	Data columns.
params	Parameters.
x	Object of class epiworld_diffnet.
main	Title of the plot
...	Passed to graphics::plot.

Details

Different from common epidemiological models, the network diffusion model assumes that the probability of adoption of a behavior is proportional to the number of adopters in the network. The model is defined by the following equations:

$$P(adopt) = \text{Logit}^{-1}(prob\_adopt + params * data + exposure)$$

Where exposure is the number of adopters in the agent's network.

Another important difference is that the transmission network is not necesary useful since adoption in this model is not from a particular neighbor.

Value

An object of class epiworld_diffnet and epiworld_model.

See Also

Other Models: `ModelSEIR()`, `ModelSEIRCONN()`, `ModelSEIRD()`, `ModelSEIRDCONN()`, `ModelSIR()`, `ModelSIRCONN()`, `ModelSIRD()`, `ModelSIRDCONN()`, `ModelSIRLogit()`, `ModelSIS()`, `ModelSISD()`, `ModelSURV()`, `epiworld-data`

Examples

```
set.seed(2223)
n <- 10000

# Generating synthetic data on a matrix with 2 columns.
X <- cbind(
 age = sample(1:100, n, replace = TRUE),
 female = sample.int(2, n, replace = TRUE) - 1
)

adopt_chatgpt <- ModelDiffNet(
  "ChatGPT",
  prevalence = .01,
  prob_adopt = .1,
  data       = X,
  params     = c(1, 4)
)

# Simulating a population from smallworld
agents_smallworld(adopt_chatgpt, n, 8, FALSE, .01)

# Running the model for 50 steps
run(adopt_chatgpt, 50)

# Plotting the model
plot(adopt_chatgpt)
```

ModelSEIR   *Susceptible Exposed Infected Recovered model (SEIR)*

Description

Susceptible Exposed Infected Recovered model (SEIR)

Usage

```
ModelSEIR(name, prevalence, transmission_rate, incubation_days, recovery_rate)

## S3 method for class 'epiworld_seir'
plot(x, main = get_name(x), ...)
```

Arguments

`name`	String. Name of the virus.
`prevalence`	Double. Initial proportion of individuals with the virus.
`transmission_rate`	
	Numeric scalar between 0 and 1. Virus's rate of infection.
`incubation_days`	
	Numeric scalar greater than 0. Average number of incubation days.
`recovery_rate`	Numeric scalar between 0 and 1. Rate of recovery_rate from virus.
`x`	Object of class SEIR.
`main`	Title of the plot
`...`	Currently ignore.

Details

The initial_states function allows the user to set the initial state of the model. The user must provide a vector of proportions indicating the following values: (1) Proportion of non-infected agents who are removed, and (2) Proportion of exposed agents to be set as infected.

Value

- The `ModelSEIR`function returns a model of class epiworld_model.

The `plot` function returns a plot of the SEIR model of class epiworld_model.

See Also

epiworld-methods

Other Models: `ModelDiffNet()`, `ModelSEIRCONN()`, `ModelSEIRD()`, `ModelSEIRDCONN()`, `ModelSIR()`, `ModelSIRCONN()`, `ModelSIRD()`, `ModelSIRDCONN()`, `ModelSIRLogit()`, `ModelSIS()`, `ModelSISD()`, `ModelSURV()`, `epiworld-data`

Examples

```
model_seir <- ModelSEIR(name = "COVID-19", prevalence = 0.01,
transmission_rate = 0.9, recovery_rate = 0.1, incubation_days = 4)

# Adding a small world population
agents_smallworld(
  model_seir,
  n = 1000,
  k = 5,
  d = FALSE,
  p = .01
  )

# Running and printing
run(model_seir, ndays = 100, seed = 1912)
model_seir

plot(model_seir, main = "SEIR Model")
```

ModelSEIRCONN   *Susceptible Exposed Infected Removed model (SEIR connected)*

Description

The SEIR connected model implements a model where all agents are connected. This is equivalent to a compartmental model ([wiki](#)).

Usage

```
ModelSEIRCONN(
  name,
  n,
  prevalence,
  contact_rate,
  transmission_rate,
  incubation_days,
  recovery_rate
)

## S3 method for class 'epiworld_seirconn'
plot(x, main = get_name(x), ...)
```

Arguments

name	String. Name of the virus.
n	Number of individuals in the population.
prevalence	Initial proportion of individuals with the virus.
contact_rate	Numeric scalar. Average number of contacts per step.
transmission_rate	
	Numeric scalar between 0 and 1. Probability of transmission.
incubation_days	
	Numeric scalar greater than 0. Average number of incubation days.
recovery_rate	Numeric scalar between 0 and 1. Probability of recovery_rate.
x	Object of class SEIRCONN.
main	Title of the plot.
...	Currently ignore.

Value

- The ModelSEIRCONNfunction returns a model of class [epiworld_model](#).

The plot function returns a plot of the SEIRCONN model of class [epiworld_model](#).

See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRD(), ModelSEIRDCONN(), ModelSIR(),
ModelSIRCONN(), ModelSIRD(), ModelSIRDCONN(), ModelSIRLogit(), ModelSIS(), ModelSISD(),
ModelSURV(), epiworld-data

Examples

```
# An example with COVID-19
model_seirconn <- ModelSEIRCONN(
  name              = "COVID-19",
  prevalence        = 0.01,
  n                 = 10000,
  contact_rate      = 2,
  incubation_days   = 7,
  transmission_rate = 0.5,
  recovery_rate     = 0.3
)

# Running and printing
run(model_seirconn, ndays = 100, seed = 1912)
model_seirconn

plot(model_seirconn)

# Adding the flu
flu <- virus("Flu", .9, 1/7)
add_virus(model_seirconn, flu, .001)

#' # Running and printing
run(model_seirconn, ndays = 100, seed = 1912)
model_seirconn

plot(model_seirconn)
```

ModelSEIRD   *Susceptible-Exposed-Infected-Recovered-Deceased model (SEIRD)*

Description

Susceptible-Exposed-Infected-Recovered-Deceased model (SEIRD)

Usage

```
ModelSEIRD(
  name,
  prevalence,
  transmission_rate,
```

```
  incubation_days,
  recovery_rate,
  death_rate
)

## S3 method for class 'epiworld_seird'
plot(x, main = get_name(x), ...)
```

Arguments

`name`	String. Name of the virus.
`prevalence`	Double. Initial proportion of individuals with the virus.
`transmission_rate`	
	Numeric scalar between 0 and 1. Virus's rate of infection.
`incubation_days`	
	Numeric scalar greater than 0. Average number of incubation days.
`recovery_rate`	Numeric scalar between 0 and 1. Rate of recovery_rate from virus.
`death_rate`	Numeric scalar between 0 and 1. Rate of death from virus.
`x`	Object of class SEIRD.
`main`	Title of the plot
`...`	Currently ignore.

Details

The [initial_states](#) function allows the user to set the initial state of the model. The user must provide a vector of proportions indicating the following values: (1) Proportion of exposed agents who are infected, (2) proportion of non-infected agents already removed, and (3) proportion of non-ifected agents already deceased.

Value

- The `ModelSEIRD`function returns a model of class [epiworld_model](#).

The `plot` function returns a plot of the SEIRD model of class [epiworld_model](#).

See Also

epiworld-methods

Other Models: [ModelDiffNet](#)(), [ModelSEIR](#)(), [ModelSEIRCONN](#)(), [ModelSEIRDCONN](#)(), [ModelSIR](#)(), [ModelSIRCONN](#)(), [ModelSIRD](#)(), [ModelSIRDCONN](#)(), [ModelSIRLogit](#)(), [ModelSIS](#)(), [ModelSISD](#)(), [ModelSURV](#)(), [epiworld-data](#)

Examples

```
model_seird <- ModelSEIRD(name = "COVID-19", prevalence = 0.01,
transmission_rate = 0.9, recovery_rate = 0.1, incubation_days = 4,
death_rate = 0.01)
```

```
# Adding a small world population
agents_smallworld(
  model_seird,
  n = 100000,
  k = 5,
  d = FALSE,
  p = .01
  )

# Running and printing
run(model_seird, ndays = 100, seed = 1912)
model_seird

plot(model_seird, main = "SEIRD Model")
```

ModelSEIRDCONN   *Susceptible Exposed Infected Removed Deceased model (SEIRD con-*
                        nected)

Description

The SEIRD connected model implements a model where all agents are connected. This is equivalent to a compartmental model ([wiki](#)).

Usage

```
ModelSEIRDCONN(
  name,
  n,
  prevalence,
  contact_rate,
  transmission_rate,
  incubation_days,
  recovery_rate,
  death_rate
)

## S3 method for class 'epiworld_seirdconn'
plot(x, main = get_name(x), ...)
```

Arguments

name	String. Name of the virus.
n	Number of individuals in the population.
prevalence	Initial proportion of individuals with the virus.
contact_rate	Numeric scalar. Average number of contacts per step.
transmission_rate	
	Numeric scalar between 0 and 1. Probability of transmission.

incubation_days

            Numeric scalar greater than 0. Average number of incubation days.

recovery_rate   Numeric scalar between 0 and 1. Probability of recovery_rate.

death_rate   Numeric scalar between 0 and 1. Probability of death.

x   Object of class SEIRCONN.

main   Title of the plot.

...   Currently ignore.

Details

The [initial_states](#) function allows the user to set the initial state of the model. The user must provide
a vector of proportions indicating the following values: (1) Proportion of exposed agents who are
infected, (2) proportion of non-infected agents already removed, and (3) proportion of non-ifected
agents already deceased.

Value

- The ModelSEIRDCONNfunction returns a model of class [epiworld_model](#).

The plot function returns a plot of the SEIRDCONN model of class [epiworld_model](#).

See Also

epiworld-methods

Other Models: [ModelDiffNet](#)(), [ModelSEIR](#)(), [ModelSEIRCONN](#)(), [ModelSEIRD](#)(), [ModelSIR](#)(),
[ModelSIRCONN](#)(), [ModelSIRD](#)(), [ModelSIRDCONN](#)(), [ModelSIRLogit](#)(), [ModelSIS](#)(), [ModelSISD](#)(),
[ModelSURV](#)(), [epiworld-data](#)

Examples

```
# An example with COVID-19
model_seirdconn <- ModelSEIRDCONN(
  name              = "COVID-19",
  prevalence        = 0.01,
  n                 = 10000,
  contact_rate      = 2,
  incubation_days   = 7,
  transmission_rate = 0.5,
  recovery_rate     = 0.3,
  death_rate        = 0.01
)

# Running and printing
run(model_seirdconn, ndays = 100, seed = 1912)
model_seirdconn

plot(model_seirdconn)

# Adding the flu
flu <- virus("Flu", prob_infecting = .3, recovery_rate = 1/7, prob_death = 0.001)
```

```
add_virus(model = model_seirdconn, virus = flu, proportion = .001)

#' # Running and printing
run(model_seirdconn, ndays = 100, seed = 1912)
model_seirdconn

plot(model_seirdconn)
```

ModelSIR   *SIR model*

Description

SIR model

Usage

```
ModelSIR(name, prevalence, transmission_rate, recovery_rate)

## S3 method for class 'epiworld_sir'
plot(x, main = get_name(x), ...)
```

Arguments

`name`	String. Name of the virus
`prevalence`	Double. Initial proportion of individuals with the virus.
`transmission_rate`	
	Numeric scalar between 0 and 1. Virus's rate of infection.
`recovery_rate`	Numeric scalar between 0 and 1. Rate of recovery_rate from virus.
`x`	Object of class SIR.
`main`	Title of the plot
`...`	Additional arguments passed to graphics::plot.

Details

The initial_states function allows the user to set the initial state of the model. In particular, the user can specify how many of the non-infected agents have been removed at the beginning of the simulation.

Value

- The `ModelSIR` function returns a model of class epiworld_model.

- The `plot` function returns a plot of the SIR model of class epiworld_model.

See Also

epiworld-methods

Other Models: `ModelDiffNet()`, `ModelSEIR()`, `ModelSEIRCONN()`, `ModelSEIRD()`, `ModelSEIRDCONN()`,
`ModelSIRCONN()`, `ModelSIRD()`, `ModelSIRDCONN()`, `ModelSIRLogit()`, `ModelSIS()`, `ModelSISD()`,
`ModelSURV()`, `epiworld-data`

Examples

```
model_sir <- ModelSIR(name = "COVID-19", prevalence = 0.01,
                      transmission_rate = 0.9, recovery_rate = 0.1)

# Adding a small world population
agents_smallworld(
  model_sir,
  n = 1000,
  k = 5,
  d = FALSE,
  p = .01
  )

# Running and printing
run(model_sir, ndays = 100, seed = 1912)
model_sir

# Plotting
plot(model_sir)
```

ModelSIRCONN   *Susceptible Infected Removed model (SIR connected)*

Description

Susceptible Infected Removed model (SIR connected)

Usage

```
ModelSIRCONN(
  name,
  n,
  prevalence,
  contact_rate,
  transmission_rate,
  recovery_rate
)

## S3 method for class 'epiworld_sirconn'
plot(x, main = get_name(x), ...)
```

Arguments

name	String. Name of the virus
n	Number of individuals in the population.
prevalence	Double. Initial proportion of individuals with the virus.
contact_rate	Numeric scalar. Average number of contacts per step.
transmission_rate	
	Numeric scalar between 0 and 1. Probability of transmission.
recovery_rate	Numeric scalar between 0 and 1. Probability of recovery.
x	Object of class SIRCONN.
main	Title of the plot
...	Currently ignore.

Details

The initial_states function allows the user to set the initial state of the model. In particular, the user can specify how many of the non-infected agents have been removed at the beginning of the simulation.

Value

- The ModelSIRCONNfunction returns a model of class epiworld_model.

The plot function returns a plot of the SIRCONN model of class epiworld_model.

See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSIR(), ModelSIRD(), ModelSIRDCONN(), ModelSIRLogit(), ModelSIS(), ModelSISD(), ModelSURV(), epiworld-data

Examples

```
model_sirconn <- ModelSIRCONN(
  name               = "COVID-19",
  n                  = 10000,
  prevalence         = 0.01,
  contact_rate       = 5,
  transmission_rate  = 0.4,
  recovery_rate      = 0.95
)

# Running and printing
run(model_sirconn, ndays = 100, seed = 1912)
model_sirconn

plot(model_sirconn,  main = "SIRCONN Model")
```

ModelSIRD   *SIRD model*

Description

SIRD model

Usage

```
ModelSIRD(name, prevalence, transmission_rate, recovery_rate, death_rate)

## S3 method for class 'epiworld_sird'
plot(x, main = get_name(x), ...)
```

Arguments

name	String. Name of the virus
prevalence	Double. Initial proportion of individuals with the virus.
transmission_rate	
	Numeric scalar between 0 and 1. Virus's rate of infection.
recovery_rate	Numeric scalar between 0 and 1. Rate of recovery_rate from virus.
death_rate	Numeric scalar between 0 and 1. Rate of death from virus.
x	Object of class SIR.
main	Title of the plot
...	Additional arguments passed to graphics::plot.

Details

The initial_states function allows the user to set the initial state of the model. The user must provide a vector of proportions indicating the following values: (1) proportion of non-infected agents already removed, and (2) proportion of non-ifected agents already deceased.

Value

- The ModelSIRD function returns a model of class epiworld_model.

- The plot function returns a plot of the SIRD model of class epiworld_model.

See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSIR(), ModelSIRCONN(), ModelSIRDCONN(), ModelSIRLogit(), ModelSIS(), ModelSISD(), ModelSURV(), epiworld-data

Examples

```
model_sird <- ModelSIRD(
 name             = "COVID-19",
 prevalence       = 0.01,
 transmission_rate = 0.9,
 recovery_rate    = 0.1,
 death_rate       = 0.01
)

# Adding a small world population
agents_smallworld(
  model_sird,
  n = 1000,
  k = 5,
  d = FALSE,
  p = .01
  )

# Running and printing
run(model_sird, ndays = 100, seed = 1912)
model_sird

# Plotting
plot(model_sird)
```

ModelSIRDCONN   *Susceptible Infected Removed Deceased model (SIRD connected)*

Description

Susceptible Infected Removed Deceased model (SIRD connected)

Usage

```
ModelSIRDCONN(
  name,
  n,
  prevalence,
  contact_rate,
  transmission_rate,
  recovery_rate,
  death_rate
)

## S3 method for class 'epiworld_sirdconn'
plot(x, main = get_name(x), ...)
```

Arguments

`name`	String. Name of the virus
`n`	Number of individuals in the population.
`prevalence`	Double. Initial proportion of individuals with the virus.
`contact_rate`	Numeric scalar. Average number of contacts per step.
`transmission_rate`	
	Numeric scalar between 0 and 1. Probability of transmission.
`recovery_rate`	Numeric scalar between 0 and 1. Probability of recovery.
`death_rate`	Numeric scalar between 0 and 1. Probability of death.
`x`	Object of class SIRDCONN.
`main`	Title of the plot
`...`	Currently ignore.

Details

The [initial_states](#) function allows the user to set the initial state of the model. The user must provide a vector of proportions indicating the following values: (1) proportion of non-infected agents already removed, and (2) proportion of non-ifected agents already deceased.

Value

- The `ModelSIRDCONN`function returns a model of class [epiworld_model](#).

The `plot` function returns a plot of the SIRDCONN model of class [epiworld_model](#).

See Also

epiworld-methods

Other Models: [ModelDiffNet()](#), [ModelSEIR()](#), [ModelSEIRCONN()](#), [ModelSEIRD()](#), [ModelSEIRDCONN()](#), [ModelSIR()](#), [ModelSIRCONN()](#), [ModelSIRD()](#), [ModelSIRLogit()](#), [ModelSIS()](#), [ModelSISD()](#), [ModelSURV()](#), [epiworld-data](#)

Examples

```
model_sirdconn <- ModelSIRDCONN(
  name              = "COVID-19",
  n                 = 100000,
  prevalence        = 0.01,
  contact_rate      = 5,
  transmission_rate = 0.4,
  recovery_rate     = 0.5,
  death_rate        = 0.1
)

# Running and printing
run(model_sirdconn, ndays = 100, seed = 1912)
model_sirdconn

plot(model_sirdconn,  main = "SIRDCONN Model")
```

ModelSIRLogit *SIR Logistic model*

Description

SIR Logistic model

Usage

```
ModelSIRLogit(
  vname,
  data,
  coefs_infect,
  coefs_recover,
  coef_infect_cols,
  coef_recover_cols,
  prob_infection,
  recovery_rate,
  prevalence
)
```

Arguments

vname	Name of the virus.
data	A numeric matrix with n rows.
coefs_infect	Numeric vector. Coefficients associated to infect.
coefs_recover	Numeric vector. Coefficients associated to recover.
coef_infect_cols	
	Integer vector. Columns in the coeficient.
coef_recover_cols	
	Integer vector. Columns in the coeficient.
prob_infection	Numeric scalar. Baseline probability of infection.
recovery_rate	Numeric scalar. Baseline probability of recovery.
prevalence	Numeric scalar. Prevalence (initial state) in proportion.

Value

- The ModelSIRLogit function returns a model of class epiworld_model.

See Also

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSIR(), ModelSIRCONN(), ModelSIRD(), ModelSIRDCONN(), ModelSIS(), ModelSISD(), ModelSURV(), epiworld-data

Examples

```
set.seed(2223)
n <- 100000

# Creating the data to use for the "ModelSIRLogit" function. It contains
# information on the sex of each agent and will be used to determine
# differences in disease progression between males and females. Note that
# the number of rows in these data are identical to n (100000).
X <- cbind(
  Intercept = 1,
  Female    = sample.int(2, n, replace = TRUE) - 1
)

# Declare coefficients for each sex regarding transmission_rate and recovery.
coef_infect  <- c(.1, -2, 2)
coef_recover <- rnorm(2)

# Feed all above information into the "ModelSIRLogit" function.
model_logit <- ModelSIRLogit(
  "covid2",
  data = X,
  coefs_infect     = coef_infect,
  coefs_recover    = coef_recover,
  coef_infect_cols = 1L:ncol(X),
  coef_recover_cols = 1L:ncol(X),
  prob_infection = .8,
  recovery_rate = .3,
  prevalence = .01
)

agents_smallworld(model_logit, n, 8, FALSE, .01)

run(model_logit, 50)

plot(model_logit)

# Females are supposed to be more likely to become infected.
rn <- get_reproductive_number(model_logit)

# Probability of infection for males and females.
(table(
  X[, "Female"],
  (1:n %in% rn$source)
) |> prop.table())[,2]

# Looking into the individual agents.
get_agents(model_logit)
```

ModelSIS   *SIS model*

Description

Susceptible-Infected-Susceptible model (SIS) ([wiki](#))

Usage

```
ModelSIS(name, prevalence, transmission_rate, recovery_rate)

## S3 method for class 'epiworld_sis'
plot(x, main = get_name(x), ...)
```

Arguments

name	String. Name of the virus.
prevalence	Double. Initial proportion of individuals with the virus.
transmission_rate	
	Numeric scalar between 0 and 1. Virus's rate of infection.
recovery_rate	Numeric scalar between 0 and 1. Rate of recovery from virus.
x	Object of class SIS.
main	Title of the plot.
...	Currently ignore.

Value

- The ModelSIS function returns a model of class [epiworld_model](#).

- The plot function returns a plot of the SIS model of class [epiworld_model](#).

See Also

epiworld-methods

Other Models: [ModelDiffNet](#)(), [ModelSEIR](#)(), [ModelSEIRCONN](#)(), [ModelSEIRD](#)(), [ModelSEIRDCONN](#)(),
[ModelSIR](#)(), [ModelSIRCONN](#)(), [ModelSIRD](#)(), [ModelSIRDCONN](#)(), [ModelSIRLogit](#)(), [ModelSISD](#)(),
[ModelSURV](#)(), [epiworld-data](#)

Examples

```
model_sis <- ModelSIS(name = "COVID-19", prevalence = 0.01,
                      transmission_rate = 0.9, recovery_rate = 0.1)

# Adding a small world population
agents_smallworld(
  model_sis,
  n = 1000,
  k = 5,
  d = FALSE,
  p = .01
  )
```

```
# Running and printing
run(model_sis, ndays = 100, seed = 1912)
model_sis

# Plotting
plot(model_sis, main = "SIS Model")
```

ModelSISD   *SISD model*

Description

Susceptible-Infected-Susceptible-Deceased model (SISD) ([wiki](#))

Usage

```
ModelSISD(name, prevalence, transmission_rate, recovery_rate, death_rate)

## S3 method for class 'epiworld_sisd'
plot(x, main = get_name(x), ...)
```

Arguments

name	String. Name of the virus.
prevalence	Double. Initial proportion of individuals with the virus.
transmission_rate	
	Numeric scalar between 0 and 1. Virus's rate of infection.
recovery_rate	Numeric scalar between 0 and 1. Rate of recovery from virus.
death_rate	Numeric scalar between 0 and 1. Rate of death from virus.
x	Object of class SISD.
main	Title of the plot.
...	Currently ignore.

Value

- The ModelSISD function returns a model of class [epiworld_model](#).

- The plot function returns a plot of the SISD model of class [epiworld_model](#).

See Also

epiworld-methods

Other Models: [ModelDiffNet()](#), [ModelSEIR()](#), [ModelSEIRCONN()](#), [ModelSEIRD()](#), [ModelSEIRDCONN()](#), [ModelSIR()](#), [ModelSIRCONN()](#), [ModelSIRD()](#), [ModelSIRDCONN()](#), [ModelSIRLogit()](#), [ModelSIS()](#), [ModelSURV()](#), [epiworld-data](#)

Examples

```
model_sisd <- ModelSISD(
                 name = "COVID-19",
                 prevalence = 0.01,
                 transmission_rate = 0.9,
                 recovery_rate = 0.1,
                 death_rate = 0.01
               )

# Adding a small world population
agents_smallworld(
  model_sisd,
  n = 1000,
  k = 5,
  d = FALSE,
  p = .01
  )

# Running and printing
run(model_sisd, ndays = 100, seed = 1912)
model_sisd

# Plotting
plot(model_sisd, main = "SISD Model")
```

ModelSURV   *SURV model*

Description

SURV model

Usage

```
ModelSURV(
  name,
  prevalence,
  efficacy_vax,
  latent_period,
  infect_period,
  prob_symptoms,
  prop_vaccinated,
  prop_vax_redux_transm,
  prop_vax_redux_infect,
  surveillance_prob,
  transmission_rate,
  prob_death,
  prob_noreinfect
```

```
)

## S3 method for class 'epiworld_surv'
plot(x, main = get_name(x), ...)
```

Arguments

name	String. Name of the virus.
prevalence	Initial number of individuals with the virus.
efficacy_vax	Double. Efficacy of the vaccine. (1 - P(acquire the disease)).
latent_period	Double. Shape parameter of a 'Gamma(latent_period, 1)' distribution. This coincides with the expected number of latent days.
infect_period	Double. Shape parameter of a 'Gamma(infected_period, 1)' distribution. This coincides with the expected number of infectious days.
prob_symptoms	Double. Probability of generating symptoms.
prop_vaccinated	
	Double. Probability of vaccination. Coincides with the initial prevalence of vaccinated individuals.
prop_vax_redux_transm	
	Double. Factor by which the vaccine reduces transmissibility.
prop_vax_redux_infect	
	Double. Factor by which the vaccine reduces the chances of becoming infected.
surveillance_prob	
	Double. Probability of testing an agent.
transmission_rate	
	Double. Raw transmission probability.
prob_death	Double. Raw probability of death for symptomatic individuals.
prob_noreinfect	
	Double. Probability of no re-infection.
x	Object of class SURV.
main	Title of the plot.
...	Currently ignore.

Value

- The ModelSURVfunction returns a model of class epiworld_model.

The plot function returns a plot of the SURV model of class epiworld_model.

See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSIR(), ModelSIRCONN(), ModelSIRD(), ModelSIRDCONN(), ModelSIRLogit(), ModelSIS(), ModelSISD(), epiworld-data

Examples

```
model_surv <- ModelSURV(
  name                 = "COVID-19",
  prevalence           = 20,
  efficacy_vax         = 0.6,
  latent_period        = 4,
  infect_period        = 5,
  prob_symptoms        = 0.5,
  prop_vaccinated      = 0.7,
  prop_vax_redux_transm = 0.8,
  prop_vax_redux_infect = 0.95,
  surveillance_prob    = 0.1,
  transmission_rate    = 0.2,
  prob_death           = 0.001,
  prob_noreinfect      = 0.5
)

# Adding a small world population
agents_smallworld(
  model_surv,
  n = 10000,
  k = 5,
  d = FALSE,
  p = .01
  )

# Running and printing
run(model_surv, ndays = 100, seed = 1912)
model_surv

# Plotting
plot(model_surv, main = "SURV Model")
```

---

run_multiple   *Run multiple simulations at once*

Description

The `run_multiple` function allows running multiple simulations at once. When available, users can take advantage of parallel computing to speed up the process.

Usage

```
run_multiple(
  m,
  ndays,
  nsims,
  seed = sample.int(10000, 1),
```

```
    saver = make_saver(),
    reset = TRUE,
    verbose = TRUE,
    nthreads = 1L
)

run_multiple_get_results(m)

make_saver(..., fn = "")
```

Arguments

`m, ndays, seed`	See [run](#).
`nsims`	Integer. Number of replicats
`saver`	An object of class [epiworld_saver](#).
`reset`	When `TRUE` (default,) resets the simulation.
`verbose`	When `TRUE` (default,) prints a progress bar.
`nthreads`	Integer. Number of threads (parallel computing.)
`...`	List of strings (characters) specifying what to save (see details).
`fn`	A file name pattern.

Details

Currently, the following elements can be saved:

- `total_hist` History of the model (total numbers per time).
- `virus_info` Information about `viruses`.
- `virus_hist` Changes in `viruses`.
- `tool_info` Information about `tools`.
- `tool_hist` Changes in `tools`.
- `transmission` Transmission events.
- `transition` Transition matrices.
- `reproductive` Reproductive number.
- `generation` Estimation of generation time.

Value

- In the case of `make_saver`, an list of class `epiworld_saver`.

- The `run_multiple` function runs a specified number of simulations and returns a model object of class [epiworld_model](#).

- The `run_multiple_get_results` function returns a named list with the data specified by `make_saver`.

Examples

```
model_sir <- ModelSIRCONN(
  name = "COVID-19",
  prevalence = 0.01,
  n = 1000,
  contact_rate = 2,
  transmission_rate = 0.9, recovery_rate = 0.1
  )

# Generating a saver
saver <- make_saver("total_hist", "reproductive")

# Running and printing
run_multiple(model_sir, ndays = 100, nsims = 50, saver = saver, nthreads = 2)

# Retrieving the results
ans <- run_multiple_get_results(model_sir)

head(ans$total_hist)
head(ans$reproductive)

# Plotting
multi_sir <- run_multiple_get_results(model_sir)$total_hist
multi_sir <- multi_sir[multi_sir$date <= 20,]
plot(multi_sir)
```

---

tool   *Tools in epiworld*

Description

Tools are functions that affect how agents react to the virus. They can be used to simulate the effects of vaccination, isolation, and social distancing.

Usage

```
tool(
  name,
  susceptibility_reduction,
  transmission_reduction,
  recovery_enhancer,
  death_reduction
)

set_name_tool(tool, name)

get_name_tool(tool)
```

```
add_tool(model, tool, proportion)

add_tool_n(model, tool, n)

rm_tool(model, tool_pos)

tool_fun_logit(vars, coefs, model)

set_susceptibility_reduction(tool, prob)

set_susceptibility_reduction_ptr(tool, model, param)

set_susceptibility_reduction_fun(tool, model, tfun)

set_transmission_reduction(tool, prob)

set_transmission_reduction_ptr(tool, model, param)

set_transmission_reduction_fun(tool, model, tfun)

set_recovery_enhancer(tool, prob)

set_recovery_enhancer_ptr(tool, model, param)

set_recovery_enhancer_fun(tool, model, tfun)

set_death_reduction(tool, prob)

set_death_reduction_ptr(tool, model, param)

set_death_reduction_fun(tool, model, tfun)

## S3 method for class 'epiworld_agents_tools'
print(x, max_print = 10, ...)
```

Arguments

name	Name of the tool
susceptibility_reduction	
	Numeric. Proportion it reduces susceptibility.
transmission_reduction	
	Numeric. Proportion it reduces transmission.
recovery_enhancer	
	Numeric. Proportion it improves recovery.
death_reduction	
	Numeric. Proportion it reduces probability of death.e
tool	An object of class epiworld_tool

model	Model
proportion	In the case of add_tool, a proportion, otherwise, an integer.
n	A positive integer. Number of agents to initially have the tool.
tool_pos	Positive integer. Index of the tool's position in the model.
vars	Integer vector. Indices (starting from 0) of the positions of the variables used to compute the logit probability.
coefs	Numeric vector. Of the same length of vars, is a vector of coefficients associated to the logit probability.
prob	Numeric scalar. A probability (between zero and one).
param	Character scalar. Name of the parameter featured in model that will be added to the tool (see details).
tfun	An object of class epiworld_tool_fun.
x	An object of class epiworld_agents_tools.
max_print	Numeric scalar. Maximum number of tools to print.
...	Currently ignored.

Details

The name of the epiworld_tool object can be manipulated with the functions [set_name_tool()](#) and [get_name_tool()](#).

The add_tool function adds the specified tool to the model of class [epiworld_model](#) with specified proportion.

In the case of set_susceptibility_reduction_ptr, set_transmission_reduction_ptr, set_recovery_enhancer, and set_death_reduction_ptr, the corresponding parameters are passed as a pointer to the tool. The implication of using pointers is that the values will be read directly from the model object, so changes will be reflected.

Value

- The tool function creates a tool of class [epiworld_tool](#).

- The set_name_tool function assigns a name to the tool of class [epiworld_tool](#) and returns the tool.

- The get_name_tool function returns the name of the tool of class [epiworld_tool](#).

- The add_tool_n function adds the specified tool to the model of class [epiworld_model](#) with specified count n.

- The rm_tool function removes the specified tool from a model.

- The set_susceptibility_reduction function assigns a probability reduction to the specified tool of class [epiworld_tool](#).

- The set_transmission_reduction function assigns a probability reduction to the specified tool of class [epiworld_tool](#).

- The `set_recovery_enhancer` function assigns a probability increase to the specified tool of class [epiworld_tool](.).

- The `set_death_reduction` function assigns a probability decrease to the specified tool of class [epiworld_tool](.).

Examples

```
# Simple model
model_sirconn <- ModelSIRCONN(
  name              = "COVID-19",
  n                 = 10000,
  prevalence        = 0.01,
  contact_rate      = 5,
  transmission_rate = 0.4,
  recovery_rate     = 0.95
)

# Running and printing
run(model_sirconn, ndays = 100, seed = 1912)
plot(model_sirconn)

epitool <- tool(
  name = "Vaccine",
  susceptibility_reduction = .9,
  transmission_reduction = .5,
  recovery_enhancer = .5,
  death_reduction = .9
)

epitool

set_name_tool(epitool, 'Pfizer') # Assigning name to the tool
get_name_tool(epitool) # Returning the name of the tool
add_tool(model_sirconn, epitool, .5)
run(model_sirconn, ndays = 100, seed = 1912)
model_sirconn
plot(model_sirconn)

# To declare a certain number of individuals with the tool
rm_tool(model_sirconn, 0) # Removing epitool from the model
add_tool_n(model_sirconn, epitool, 5500)
run(model_sirconn, ndays = 100, seed = 1912)

# Adjusting probabilities due to tool
set_susceptibility_reduction(epitool, 0.1) # Susceptibility reduction
set_transmission_reduction(epitool, 0.2) # Transmission reduction
set_recovery_enhancer(epitool, 0.15) # Probability increase of recovery
set_death_reduction(epitool, 0.05) # Probability reduction of death
run(model_sirconn, ndays = 100, seed = 1912) # Run model to view changes


# Using the logit function --------------
```

```r
sir <- ModelSIR(
  name = "COVID-19", prevalence = 0.01,
  transmission_rate = 0.9, recovery_rate = 0.1
  )

# Adding a small world population
agents_smallworld(
  sir,
  n = 10000,
  k = 5,
  d = FALSE,
  p = .01
)

# Creating a tool
mask_wearing <- tool(
  name = "Mask",
  susceptibility_reduction = 0.0,
  transmission_reduction   = 0.3, # Only transmission
  recovery_enhancer        = 0.0,
  death_reduction          = 0.0
)

add_tool(sir, mask_wearing, .5)

run(sir, ndays = 50, seed = 11)
hist_0 <- get_hist_total(sir)

# And adding features
dat <- cbind(
  female = sample.int(2, 10000, replace = TRUE) - 1,
  x      = rnorm(10000)
)

set_agents_data(sir, dat)

# Creating the logit function
tfun <- tool_fun_logit(
  vars  = c(0L, 1L),
  coefs = c(-1, 1),
  model = sir
)

# The infection prob is lower
hist(plogis(dat %*% rbind(.5,1)))

tfun # printing


set_susceptibility_reduction_fun(
  tool  = get_tool(sir, 0),
  model = sir,
  tfun  = tfun
```

```
  )

  run(sir, ndays = 50, seed = 11)
  hist_1 <- get_hist_total(sir)

  op <- par(mfrow = c(1, 2))
  plot(hist_0); abline(v = 30)
  plot(hist_1); abline(v = 30)
  par(op)
```

---

virus   *Virus design*

Description

Viruses can be considered to be anything that can be transmitted (e.g., diseases, as well as ideas.)
Most models in epiworldR can feature multiple viruses.

Usage

```
virus(
  name,
  prob_infecting,
  recovery_rate = 0.5,
  prob_death = 0,
  post_immunity = -1,
  incubation = 7
)

set_name_virus(virus, name)

get_name_virus(virus)

add_virus(model, virus, proportion)

add_virus_n(model, virus, n)

virus_set_state(virus, init, end, removed)

rm_virus(model, virus_pos)

virus_fun_logit(vars, coefs, model)

set_prob_infecting(virus, prob)

set_prob_infecting_ptr(virus, model, param)
```

```
set_prob_infecting_fun(virus, model, vfun)

set_prob_recovery(virus, prob)

set_prob_recovery_ptr(virus, model, param)

set_prob_recovery_fun(virus, model, vfun)

set_prob_death(virus, prob)

set_prob_death_ptr(virus, model, param)

set_prob_death_fun(virus, model, vfun)

set_incubation(virus, incubation)

set_incubation_ptr(virus, model, param)

set_incubation_fun(virus, model, vfun)
```

Arguments

`name`	of the virus
`prob_infecting`	Numeric scalar. Probability of infection (transmission).
`recovery_rate`	Numeric scalar. Probability of recovery.
`prob_death`	Numeric scalar. Probability of death.
`post_immunity`	Numeric scalar. Post immunity (prob of re-infection).
`incubation`	Numeric scalar. Incubation period (in days) of the virus.
`virus`	An object of class epiworld_virus
`model`	An object of class epiworld_model.
`proportion`	In the case of add_virus, a proportion, otherwise, an integer.
`n`	A positive integer. Initial count of agents to have the virus.
`init, end, removed`	
	states after acquiring a virus, removing a virus, and removing the agent as a result of the virus, respectively.
`virus_pos`	Positive integer. Index of the virus's position in the model.
`vars`	Integer vector. Indices (starting from 0) of the positions of the variables used to compute the logit probability.
`coefs`	Numeric vector. Of the same length of vars, is a vector of coefficients associated to the logit probability.
`prob`	Numeric scalar. A probability (between zero and one).
`param`	Character scalar. Name of the parameter featured in model that will be added to the virus (see details).
`vfun`	An object of class epiworld_virus_fun.

Details

The `virus()` function can be used to initialize a virus. Virus features can then be modified using the functions set_prob_*.

The function `virus_fun_logit()` creates a "virus function" that can be evaluated for transmission, recovery, and death. As the name sugests, it computes those probabilities using a logit function (see examples).

The name of the epiworld_virus object can be manipulated with the functions `set_name_virus()` and `get_name_virus()`.

In the case of set_prob_infecting_ptr, set_prob_recovery_ptr, and set_prob_death_ptr, the corresponding parameters is passed as a pointer to the virus. The implication of using pointers is that the values will be read directly from the model object, so changes will be reflected.

Value

- The `set_name_virus` function does not return a value, but merely assigns a name to the virus of choice.

- The `get_name_virus` function returns the name of the virus of class epiworld_virus.

- The `add_virus` function does not return a value, instead it adds the virus of choice to the model object of class epiworld_model.

- The `add_virus_n` function does not return a value, but instead adds a specified number of agents with the virus of choice to the model object of class epiworld_model.

- The `virus_set_state` function does not return a value but assigns epidemiological properties to the specified virus of class epiworld_virus.

- The `rm_virus` function does not return a value, but instead removes a specified virus from the model of class epiworld_model.

- The `set_prob_infecting` function does not return a value, but instead assigns a probability to infection for the specified virus of class epiworld_virus.

- The `set_prob_recovery` function does not return a value, but instead assigns a probability to recovery for the specified virus of class epiworld_virus.

- The `set_prob_death` function does not return a value, but instead assigns a probability to death for the specified virus of class epiworld_virus.

- The `set_incubation` function does not return a value, but instead assigns an incubation period to the specified virus of class epiworld_virus.

Examples

```
mseirconn <- ModelSEIRCONN(
  name              = "COVID-19",
  prevalence        = 0.01,
  n                 = 10000,
  contact_rate      = 4,
  incubation_days   = 7,
  transmission_rate = 0.5,
  recovery_rate     = 0.99
)

delta <- virus("Delta Variant", 0, .5, .2, .01)

# Adding virus and setting/getting virus name
add_virus(mseirconn, delta, .3)
set_name_virus(delta, "COVID-19 Strain")
get_name_virus(delta)

run(mseirconn, ndays = 100, seed = 992)
mseirconn

rm_virus(mseirconn, 0) # Removing the first virus from the model object
add_virus_n(mseirconn, delta, 100) # Setting initial count of delta virus
                                   # to n = 100

# Setting parameters for the delta virus manually
set_prob_infecting(delta, 0.5)
set_prob_recovery(delta, 0.9)
set_prob_death(delta, 0.01)
run(mseirconn, ndays = 100, seed = 992) # Run the model to observe changes

# If the states were (for example):
# 1: Infected
# 2: Recovered
# 3: Dead
delta2 <- virus("Delta Variant 2", 0, .5, .2, .01)
virus_set_state(delta2, 1, 2, 3)
# Using the logit function --------------
sir <- ModelSIR(
  name = "COVID-19", prevalence = 0.01,
  transmission_rate = 0.9, recovery = 0.1
  )

# Adding a small world population
agents_smallworld(
  sir,
  n = 10000,
  k = 5,
  d = FALSE,
  p = .01
)
```

```
run(sir, ndays = 50, seed = 11)
plot(sir)

# And adding features
dat <- cbind(
  female = sample.int(2, 10000, replace = TRUE) - 1,
  x      = rnorm(10000)
)

set_agents_data(sir, dat)

# Creating the logit function
vfun <- virus_fun_logit(
  vars  = c(0L, 1L),
  coefs = c(-1, 1),
  model = sir
)

# The infection prob is lower
hist(plogis(dat %*% rbind(-1,1)))

vfun # printing

set_prob_infecting_fun(
  virus = get_virus(sir, 0),
  model = sir,
  vfun  = vfun
  )

run(sir, ndays = 50, seed = 11)
plot(sir)
```

Index