Package 'epiworldR'

May 8, 2026

Type Package

Title Fast Agent-Based Epi Models

Version 0.14.0.0

Depends R (>= 4.1.0)

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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RoxygenNote 7.3.3

Encoding UTF-8

LinkingTo cpp11

Suggests quarto, tinytest, netplot, igraph, data.table, DiagrammeR

Imports utils, parallel, methods

SystemRequirements C++17

VignetteBuilder quarto

NeedsCompilation yes

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Date/Publication 2026-03-28 06:11:20 UTC

Contents

`add_entities_from_dataframe` *Add entities to a model according to a data.frame*

Description

Helper function that facilities creating entities and adding them to models. It is a wrapper of `add_entity()`.

Usage

```
add_entities_from_dataframe(model, entities, col_name, col_number, ...)
```

Arguments

`model`	An epiworld_model object.
`entities`	A `data.frame` with the entities to add. It must contain two columns: entity names (character) and size (proportion or integer).
`col_name`	The name of the column in `entities` that contains the entity names.
`col_number`	The name of the column in `entities` that contains the entity sizes (either as proportions or integers).
`...`	Further arguments passed to `add_entity()`

Value

Inivisible the model with the added entities.

Examples

```
# Start off creating three entities.
# Individuals will be distributed randomly between the three.
entities <- data.frame(
  name = c("Pop 1", "Pop 2", "Pop 3"),
  size = rep(3e3, 3)
)

# Row-stochastic matrix (rowsums 1)
cmatrix <- c(
  c(0.9, 0.05, 0.05),
  c(0.1, 0.8, 0.1),
  c(0.1, 0.2, 0.7)
) |> matrix(byrow = TRUE, nrow = 3)

flu_model <- ModelSIRMixing(
  name              = "Flu",
  n                 = 9e3,
  prevalence        = 1 / 9e3,
```

```
  contact_rate      = 20,
  transmission_rate = 0.1,
  recovery_rate     = 1 / 7,
  contact_matrix    = cmatrix
) |>
  add_entities_from_dataframe(
    entities = entities,
    col_name = "name",
    col_number = "size",
    # This is passed to `add_entity()`
    as_proportion = FALSE
  )
```

---

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_model'
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.
`...`	Ignored
`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.
`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.
```

`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)
```

---

entities *Get entities*

Description

Entities in epiworld are objects that can contain agents.

Usage

```
get_entities(model)

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

entity(name, prevalence, as_proportion, to_unassigned = TRUE)

get_entity_size(entity)

get_entity_name(entity)

entity_add_agent(entity, agent, model = attr(entity, "model"))

rm_entity(model, id)

add_entity(model, entity)

load_agents_entities_ties(model, agents_id, entities_id)

entity_get_agents(entity)

distribute_entity_randomly(prevalence, as_proportion, to_unassigned = TRUE)

distribute_entity_to_set(agents_ids)

set_distribution_entity(entity, distfun)
```

Arguments

model	Model object of class epiworld_model.
x	Object of class epiworld_entities.
i	Integer index.
name	Character scalar. Name of the entity.

prevalence	Numeric scalar. Prevalence of the entity.
as_proportion	Logical scalar. If TRUE, prevalence is interpreted as a proportion.
to_unassigned	Logical scalar. If TRUE, the entity is added to the unassigned pool.
entity	Entity object of class epiworld_entity.
agent	Agent object of class epiworld_agent.
id	Integer scalar. Entity id to remove (starting from zero).
agents_id	Integer vector.
entities_id	Integer vector.
agents_ids	Integer vector. Ids of the agents to distribute.
distfun	Distribution function object of class epiworld_distribution_entity.

Details

Epiworld entities are especially useful for mixing models, particularly ModelSIRMixing and ModelSEIRMixing.

Value

- The function entity creates an entity object.
- The function get_entity_size returns the number of agents in the entity.
- The function get_entity_name returns the name of the entity.
- The function entity_add_agent adds an agent to the entity.
- The function rm_entity removes an entity from the model.
- The function load_agents_entities_ties loads agents into entities.
- The function entity_get_agents returns an integer vector with the agents in the entity (ids).

Examples

```
# Creating a mixing model
mymodel <- ModelSIRMixing(
  name = "My model",
  n = 10000,
  prevalence = .001,
  contact_rate = 10,
  transmission_rate = .1,
  recovery_rate = 1 / 7,
  contact_matrix = matrix(c(.9, .1, .1, .9), 2, 2)
)

ent1 <- entity("First", 5000, FALSE)
ent2 <- entity("Second", 5000, FALSE)

mymodel |>
```

```
  add_entity(ent1) |>
  add_entity(ent2)

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

summary(mymodel)
```

---

epiworld-gentime *Generation time*

Description

Extraction and plotting of generation time by virus over time.

Usage

```
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), or an object of class epiworld_generation_time.
ylab, xlab, main, type	Further parameters passed to graphics::plot()
plot	Logical scalar. If TRUE (default), the function will plot the desired statistic.
...	In the case of plot methods, further arguments passed to graphics::plot.

Value

- 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 Epidemiological metrics: epiworld-repnum

Examples

```
# SEIR Connected model
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
)

set.seed(937)
run(seirconn, 50)

# Get and plot generation time
gent <- plot_generation_time(seirconn)
```

---

epiworld-history *Model history and totals*

Description

Functions to extract simulation history at total, variant, and tool levels, plus snapshot totals and a common plot method for history objects.

Usage

```
get_hist_total(x)

get_today_total(x)

## S3 method for class 'epiworld_hist'
plot(x, y, ...)

get_hist_virus(x)

get_hist_tool(x)
```

Arguments

x	An object of class epiworld_sir, epiworld_seir, etc. (any model).
y	Ignored.
...	In the case of plot methods, further arguments passed to graphics::plot.

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_tool.

Examples

```
# SEIR Connected model
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 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))

# Snapshot of totals at end of simulation
get_today_total(seirconn)
```

---

epiworld-hospitalizations

Hospitalizations by tool

Description

Weighted hospitalization tracking when agents have multiple tools.

Usage

```
get_hospitalizations(x)
```

Arguments

x	An object of class epiworld_sir, epiworld_seir, etc. (any model).

Value

- The function get_hospitalizations returns a data.frame with five columns: date, virus_id, tool_id, hospitalizations, and weight. The weight column is used to keep track of individuals having multiple tools. For example, if an agent has two tools (vaccination and mask-wearing), then it will show up twice under count, but with weights 0.5 for each count. Models with no hospitalization tracking will return the same data.frame with no rows.

See Also

Other Summaries: epiworld-summaries

Examples

```
# See model documentation for examples with hospitalization tracking
```

---

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 = NULL)

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

```
get_states(x)

get_param(x, pname)

add_param(x, pname, pval)

## S3 method for class 'epiworld_model'
add_param(x, pname, pval)

set_param(x, pname, pval)

set_name(x, mname)

get_name(x)

get_n_viruses(x)

get_n_tools(x)

get_ndays(x)

today(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)

draw_mermaid(model, output_file = "", allow_self_transitions = FALSE)
```

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 (passed to set.seed()).
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).
output_file	String. Optional path to a file. If provided, the diagram will be written to the file.
allow_self_transitions	Logical. Whether to allow self-transitions, defaults to FALSE.

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.

draw_mermaid generates a mermaid diagram of the model. The diagram is saved in the specified output file (or printed to the standard output if the filename is empty). See draw_mermaid_from_data().

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.
- add_param returns the model with the added parameter invisibly.
- 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.
- `today` returns the current model day
- `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.
- The `draw_mermaid` returns the mermaid diagram as a string.

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.

today(model_sirconn) # Returns the current day of the simulation. This will
# match "get_ndays()" if run at the end of a simulation, but will differ if run
# during a simulation

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, prevalence = 0.5, as_prop = TRUE))
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.

# Draw a mermaid diagram of the transitions
```

```
draw_mermaid(model_sirconn)
```

---

epiworld-repnum *Reproductive number (Rt)*

Description

Extraction and plotting of the reproductive number (Rt) by virus over time.

Usage

```
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, ...)
```

Arguments

x	An object of class epiworld_sir, epiworld_seir, etc. (any model), or an object of class epiworld_repnum.
y	Ignored.
ylab, xlab, main, type	Further parameters passed to graphics::plot()
plot	Logical scalar. If TRUE (default), the function will plot the desired statistic.
...	In the case of plot methods, further arguments passed to graphics::plot.

Details

The plot_reproductive_number function is a wrapper around get_reproductive_number that plots the result.

Value

- The get_reproductive_number function returns an object of class epiworld_repnum.
- The plot method for epiworld_repnum returns a plot of the reproductive number over time.

See Also

Other Epidemiological metrics: epiworld-gentime

Examples

```
# SEIR Connected model
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
)

set.seed(937)
run(seirconn, 50)

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

---

epiworld-summaries *Summary counts and probabilities*

Description

Functions to extract summary statistics from models, including transition probabilities, active cases, and outbreak sizes.

Usage

```
get_transition_probability(x)

get_active_cases(x)

get_outbreak_size(x)
```

Arguments

x	An object of class epiworld_sir, epiworld_seir, etc. (any model).

Value

- The `get_transition_probability` function returns an object of class `matrix`.
- The function `get_active_cases` returns a data.frame with four columns: date, virus_id, virus, and active_cases indicating the number of active cases (individuals with a virus) at each point in time.
- The function `get_outbreak_size` returns a data.frame with four columns: `date`, `virus_id`, `virus`, and `outbreak_size` indicating the outbreak size per virus at each point in time.

See Also

Other Summaries: epiworld-hospitalizations

Examples

```
# SEIR Connected model
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
)

set.seed(937)
run(seirconn, 50)

# Retrieving the transition probability
get_transition_probability(seirconn)

# Get active cases
head(get_active_cases(seirconn))

# Get outbreak size
head(get_outbreak_size(seirconn))
```

---

epiworld-transition *Transition dynamics and incidence*

Description

Functions to extract and visualize state transition counts, daily incidence, and conversion to array format.

Usage

```
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,
  ...
)
```

Arguments

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

Details

The plot_incidence function is a wrapper between get_hist_transition_matrix and its 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

- 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 method for epiworld_hist_transition returns a plot of the daily incidence.

Examples

```
# SEIR Connected model
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
)

set.seed(937)
run(seirconn, 50)

# Get the transition history
t_hist <- get_hist_transition_matrix(seirconn)
head(t_hist)

# Convert to array
as.array(t_hist)[, , 1:3]

# Plot incidence
inci <- plot_incidence(seirconn)
```

---

epiworld-transmissions

Transmission network

Description

Transmission edges, including seeded infections (`source = -1`).

Usage

```
get_transmissions(x)
```

Arguments

`x`	An object of class `epiworld_sir`, `epiworld_seir`, etc. (any model).

Details

The function `get_transmissions` includes the seeded infections, with the `source` column coded as `-1`.

Value

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

Examples

```
# SEIR Connected model
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
)

set.seed(937)
run(seirconn, 50)

# Get transmission data
head(get_transmissions(seirconn))
```

---

global-events *Global Events*

Description

Global events 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, event, action = NULL)

rm_globalevent(model, event)
```

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.
event	The event to be added or removed. If it is to add, then it should be an object of class epiworld_globalevent. If it is to remove, it should be the name of the event (character).
action	(Deprecated) use event instead.

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 event
- The function `rm_globalevent` returns the model with the removed event.

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",
  prevalence = 0,
  as_proportion = FALSE,
  susceptibility_reduction = .9,
  transmission_reduction = .5,
  recovery_enhancer = .5,
  death_reduction = .9
)


# Adding a global event
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)
  )

}

# We create the global event that will execute the function `hist_saver`
# at each time step
hist_saver_event <- globalevent_fun(hist_saver, "Agent History Saver")

# We add the global event to the model
model <- add_globalevent(model, hist_saver_event)
```

globalaction_tool *Deprecated and removed 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."

Starting version 0.11.0.0, the measles models have been removed from `epiworldR` and now are part of the `measles` R package: https://github.com/UofUEpiBio/measles. The models previously available in `epiworldR` were: `ModelMeaslesSchool` and `ModelMeaslesMixing`.

Usage

```
globalaction_tool(...)

globalaction_tool_logit(...)

globalaction_set_params(...)

globalaction_fun(...)

add_tool_n(model, tool, n)

add_virus_n(model, virus, n)
```

Arguments

`...`	Arguments to be passed to the new function.
`model`	Model object of class `epiworld_model`.
`tool`	Tool object of class `epiworld_tool`.
`n`	Deprecated.
`virus`	Virus object of class `epiworld_virus`.

LFMCMC *Likelihood-Free Markhov Chain Monte Carlo (LFMCMC)*

Description

Likelihood-Free Markhov Chain Monte Carlo (LFMCMC)

Usage

```
LFMCMC(model = NULL)

run_lfmcmc(lfmcmc, params_init, n_samples, epsilon, seed = NULL)

set_observed_data(lfmcmc, observed_data)

set_proposal_fun(lfmcmc, fun)

use_proposal_norm_reflective(lfmcmc)

set_simulation_fun(lfmcmc, fun)

set_summary_fun(lfmcmc, fun)

set_kernel_fun(lfmcmc, fun)

use_kernel_fun_gaussian(lfmcmc)

get_mean_params(lfmcmc)

get_mean_stats(lfmcmc)

get_initial_params(lfmcmc)

get_current_proposed_params(lfmcmc)

get_current_accepted_params(lfmcmc)

get_current_proposed_stats(lfmcmc)

get_current_accepted_stats(lfmcmc)

get_observed_stats(lfmcmc)

get_all_sample_params(lfmcmc)

get_all_sample_stats(lfmcmc)

get_all_sample_acceptance(lfmcmc)

get_all_sample_drawn_prob(lfmcmc)

get_all_sample_kernel_scores(lfmcmc)

get_all_accepted_params(lfmcmc)

get_all_accepted_stats(lfmcmc)
```

```
get_all_accepted_kernel_scores(lfmcmc)

get_n_samples(lfmcmc)

get_n_stats(lfmcmc)

get_n_params(lfmcmc)

## S3 method for class 'epiworld_lfmcmc'
verbose_off(x)

set_params_names(lfmcmc, names)

set_stats_names(lfmcmc, names)

## S3 method for class 'epiworld_lfmcmc'
print(x, burnin = 0, ...)
```

Arguments

`model`	A model of class epiworld_model or `NULL` (see details).
`lfmcmc`	LFMCMC model
`params_init`	Initial model parameters, treated as double
`n_samples`	Number of samples, treated as integer
`epsilon`	Epsilon parameter, treated as double
`seed`	Random engine seed
`observed_data`	Observed data, treated as double.
`fun`	A function (see details).
`x`	LFMCMC model to print
`names`	Character vector of names.
`burnin`	Integer. Number of samples to discard as burnin before computing the summary.
`...`	Ignored

Details

Performs a Likelihood-Free Markhov Chain Monte Carlo simulation. When `model` is not `NULL`, the model uses the same random-number generator engine as the model. Otherwise, when `model` is `NULL`, a new random-number generator engine is created.

The functions passed to the LFMCMC object have different arguments depending on the object:

- `set_proposal_fun`: A vector of parameters and the model.
- `set_simulation_fun`: A vector of parameters and the model.
- `set_summary_fun`: A vector of simulated data and the model.
- `set_kernel_fun`: A vector of simulated statistics, observed statistics, epsilon, and the model.

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

Value

The LFMCMC function returns a model of class epiworld_lfmcmc.

The simulated model of class epiworld_lfmcmc.

- use_kernel_fun_gaussian: The LFMCMC model with kernel function set to gaussian.
- get_mean_params: The param means for the given lfmcmc model.
- get_mean_stats: The stats means for the given lfmcmc model.
- The function get_initial_params returns the initial parameters for the given LFMCMC model.
- The function get_current_proposed_params returns the proposed parameters for the next LFMCMC sample.
- The function get_current_accepted_params returns the most recently accepted parameters (the current state of the LFMCMC)
- The function get_current_proposed_stats returns the statistics from the simulation run with the proposed parameters
- The function get_current_accepted_stats returns the statistics from the most recently accepted parameters
- The function get_observed_stats returns the statistics for the observed data
- The function get_all_sample_params returns a matrix of sample parameters for the given LFMCMC model. with the number of rows equal to the number of samples and the number of columns equal to the number of parameters.
- The function get_all_sample_stats returns a matrix of statistics for the given LFMCMC model. with the number of rows equal to the number of samples and the number of columns equal to the number of statistics.
- The function get_all_sample_acceptance returns a vector of boolean flags which indicate whether a given sample was accepted
- The function get_all_sample_drawn_prob returns a vector of drawn probabilities for each sample
- The function get_all_sample_kernel_scores returns a vector of kernel scores for each sample
- The function get_all_accepted_params returns a matrix of accepted parameters for the given LFMCMC model. with the number of rows equal to the number of samples and the number of columns equal to the number of parameters.

- The function `get_all_accepted_stats` returns a matrix of accepted statistics for the given LFMCMC model. with the number of rows equal to the number of samples and the number of columns equal to the number of statistics.
- The function `get_all_accepted_kernel_scores` returns a vector of kernel scores for each accepted sample
- The functions `get_n_samples`, `get_n_stats`, and `get_n_params` return the number of samples, statistics, and parameters for the given LFMCMC model, respectively.
- The `verbose_on` and `verbose_off` functions return the same model, however `verbose_off` returns the model with no progress bar.
- `set_params_names`: The lfmcmc model with the parameter names added.
- `set_stats_names`: The lfmcmc model with the stats names added.

Examples

```
## Setup an SIR model to use in the simulation
model_seed <- 122
model_sir <- ModelSIR(name = "COVID-19", prevalence = .1,
  transmission_rate = .9, recovery_rate = .3)
agents_smallworld(
  model_sir,
  n = 1000,
  k = 5,
  d = FALSE,
  p = 0.01
)
verbose_off(model_sir)
run(model_sir, ndays = 50, seed = model_seed)

## Setup LFMCMC
# Extract the observed data from the model
obs_data <- get_today_total(model_sir)

# Define the simulation function
simfun <- function(params, lfmcmc_obj) {
  set_param(model_sir, "Recovery rate", params[1])
  set_param(model_sir, "Transmission rate", params[2])
  run(model_sir, ndays = 50)
  res <- get_today_total(model_sir)
  return(res)
}

# Define the summary function
sumfun <- function(dat, lfmcmc_obj) {
  return(dat)
}

# Create the LFMCMC model
lfmcmc_model <- LFMCMC(model_sir) |>
```

```
  set_simulation_fun(simfun) |>
  set_summary_fun(sumfun) |>
  use_proposal_norm_reflective() |>
  use_kernel_fun_gaussian() |>
  set_observed_data(obs_data)

## Run LFMCMC simulation
# Set initial parameters
par0 <- c(0.1, 0.5)
n_samp <- 2000
epsil <- 1.0

# Run the LFMCMC simulation
verbose_off(lfmcmc_model)
run_lfmcmc(
  lfmcmc = lfmcmc_model,
  params_init = par0,
  n_samples = n_samp,
  epsilon = epsil,
  seed = model_seed
)

# Print the results
set_stats_names(lfmcmc_model, get_states(model_sir))
set_params_names(lfmcmc_model, c("Immune recovery", "Infectiousness"))

print(lfmcmc_model)

get_mean_stats(lfmcmc_model)
get_mean_params(lfmcmc_model)
```

`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")
)
```

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.

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()`, `ModelSEIRMixing()`, `ModelSEIRMixingQuarantine()`, `ModelSIR()`, `ModelSIRCONN()`, `ModelSIRD()`, `ModelSIRDCONN()`, `ModelSIRLogit()`, `ModelSIRMixing()`, `ModelSIS()`, `ModelSISD()`, `ModelSURV()`

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)
```

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.

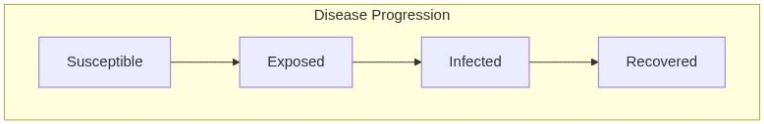
Details

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.

Model diagram



See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSEIRMixing(), ModelSEIRMixingQuarantine(), ModelSIR(), ModelSIRCONN(), ModelSIRD(), ModelSIRDCONN(), ModelSIRLogit(), ModelSIRMixing(), ModelSIS(), ModelSISD(), ModelSURV()

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
)
```

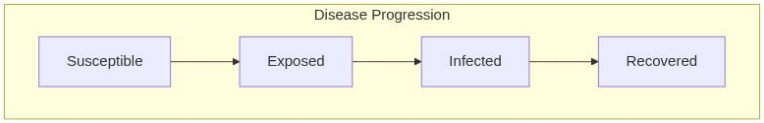
Arguments

`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.

Value

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

Model diagram



See Also

epiworld-methods

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

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, prevalence = 0.001, as_proportion = TRUE)
add_virus(model_seirconn, flu)

#' # 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
)
```

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.

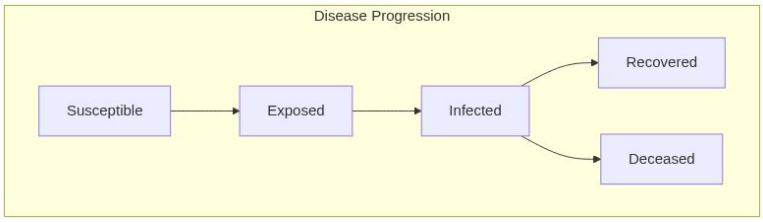
Details

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.

Model diagram



See Also

epiworld-methods

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

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 connected)*

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
)
```

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.

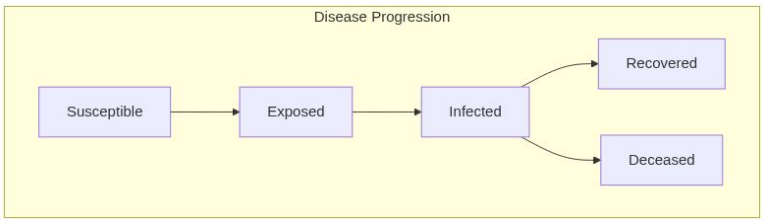
Details

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 `ModelSEIRDCONN`function returns a model of class epiworld_model.

Model diagram



See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRMixing(), ModelSEIRMixingQuarantine(), ModelSIR(), ModelSIRCONN(), ModelSIRD(), ModelSIRDCONN(), ModelSIRLogit(), ModelSIRMixing(), ModelSIS(), ModelSISD(), ModelSURV()

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,
  prevalence = 0.001, as_proportion = TRUE
)
add_virus(model = model_seirdconn, virus = flu)

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

plot(model_seirdconn)
```

ModelSEIRMixing *Susceptible Exposed Infected Removed model (SEIR) with mixing*

Description

Susceptible Exposed Infected Removed model (SEIR) with mixing

Usage

```
ModelSEIRMixing(
  name,
  n,
  prevalence,
  contact_rate,
  transmission_rate,
  incubation_days,
  recovery_rate,
  contact_matrix
)
```

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.
`incubation_days`	Numeric scalar. Average number of days in the incubation period.
`recovery_rate`	Numeric scalar between 0 and 1. Probability of recovery.
`contact_matrix`	Matrix of contact rates between individuals.

Details

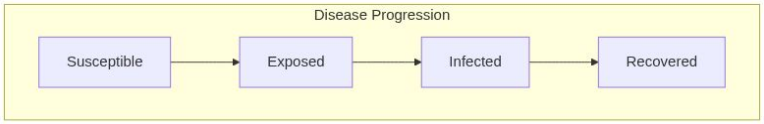
The `contact_matrix` is a matrix of contact rates between entities. The matrix should be of size `n x n`, where `n` is the number of entities. This is a row-stochastic matrix, i.e., the sum of each row should be 1.

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 `ModelSEIRMixing`function returns a model of class epiworld_model.

Model diagram



See Also

epiworld-methods

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

Examples

```
# Start off creating three entities.
# Individuals will be distribured randomly between the three.
e1 <- entity("Population 1", 3e3, as_proportion = FALSE)
e2 <- entity("Population 2", 3e3, as_proportion = FALSE)
e3 <- entity("Population 3", 3e3, as_proportion = FALSE)

# Row-stochastic matrix (rowsums 1)
cmatrix <- c(
  c(0.9, 0.05, 0.05),
  c(0.1, 0.8, 0.1),
  c(0.1, 0.2, 0.7)
) |> matrix(byrow = TRUE, nrow = 3)

N <- 9e3

flu_model <- ModelSEIRMixing(
  name              = "Flu",
  n                 = N,
  prevalence        = 1 / N,
  contact_rate      = 20,
  transmission_rate = 0.1,
  recovery_rate     = 1 / 7,
  incubation_days   = 7,
  contact_matrix    = cmatrix
)

# Adding the entities to the model
flu_model |>
  add_entity(e1) |>
  add_entity(e2) |>
  add_entity(e3)

set.seed(331)
run(flu_model, ndays = 100)
summary(flu_model)
plot_incidence(flu_model)
```

`ModelSEIRMixingQuarantine` *Susceptible Exposed Infected Removed model (SEIR) with mixing and quarantine*

Description

`ModelSEIRMixingQuarantine` creates a model of the SEIR type with mixing and a quarantine mechanism. Agents who are infected can be quarantined or isolated. Isolation happens after the agent has been detected as infected, and agents who have been in contact with the detected person will me moved to quarantined status.

Usage

```
ModelSEIRMixingQuarantine(
  name,
  n,
  prevalence,
  contact_rate,
  transmission_rate,
  incubation_days,
  recovery_rate,
  contact_matrix,
  hospitalization_rate,
  hospitalization_period,
  days_undetected,
  quarantine_period,
  quarantine_willingness,
  isolation_willingness,
  isolation_period,
  contact_tracing_success_rate,
  contact_tracing_days_prior
)
```

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.
`incubation_days`	Numeric scalar. Average number of days in the incubation period.
`recovery_rate`	Numeric scalar between 0 and 1. Probability of recovery.
`contact_matrix`	Matrix of contact rates between individuals.
`hospitalization_rate`	Double. Rate of hospitalization.
`hospitalization_period`	Double. Period of hospitalization.
`days_undetected`	Double. Number of days an infection goes undetected.

`quarantine_period`
: Integer. Number of days for quarantine.

`quarantine_willingness`
: Double. Proportion of agents willing to quarantine.

`isolation_willingness`
: Double. Proportion of agents willing to isolate.

`isolation_period`
: Integer. Number of days for isolation.

`contact_tracing_success_rate`
: Double. Probability of successful contact tracing.

`contact_tracing_days_prior`
: Integer. Number of days prior to the onset of the infection for which contact tracing is effective.

Details

The `contact_matrix` is a matrix of contact rates between entities. The matrix should be of size `n x n`, where `n` is the number of entities. This is a row-stochastic matrix, i.e., the sum of each row should be 1.

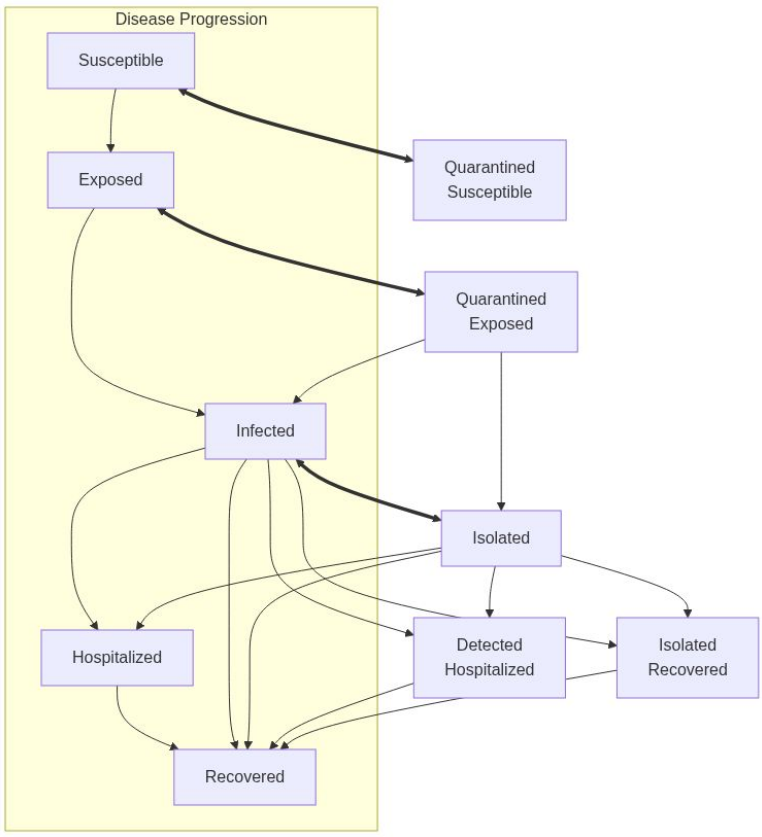
The quarantine and isolation processes can be turned off by specifying `quarantine_period < 0` and `isolation_period < 0` respectively. In other words, any negative value for these parameters will suppress the corresponding process.

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 `ModelSEIRMixingQuarantine` function returns a model of class epiworld_model.

Model diagram



See Also

epiworld-methods

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

Examples

```
# Start off creating three entities.
# Individuals will be distributed randomly between the three.
e1 <- entity("Population 1", 3e3, as_proportion = FALSE)
e2 <- entity("Population 2", 3e3, as_proportion = FALSE)
e3 <- entity("Population 3", 3e3, as_proportion = FALSE)

# Row-stochastic matrix (rowsums 1)
cmatrix <- c(
  c(0.9, 0.05, 0.05),
  c(0.1, 0.8, 0.1),
  c(0.1, 0.2, 0.7)
```

```
) |> matrix(byrow = TRUE, nrow = 3)

N <- 9e3

flu_model <- ModelSEIRMixingQuarantine(
  name                  = "Flu",
  n                     = N,
  prevalence            = 1 / N,
  contact_rate          = 20,
  transmission_rate     = 0.1,
  recovery_rate         = 1 / 7,
  incubation_days       = 7,
  contact_matrix        = cmatrix,
  hospitalization_rate  = 0.05,
  hospitalization_period = 7,
  days_undetected       = 3,
  quarantine_period     = 14,
  quarantine_willingness = 0.8,
  isolation_period      = 7,
  isolation_willingness = 0.5,
  contact_tracing_success_rate = 0.7,
  contact_tracing_days_prior = 3
)

# Adding the entities to the model
flu_model |>
  add_entity(e1) |>
  add_entity(e2) |>
  add_entity(e3)

set.seed(331)
run(flu_model, ndays = 100)
summary(flu_model)
```

`ModelSIR` *SIR model*

Description

SIR model

Usage

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

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.

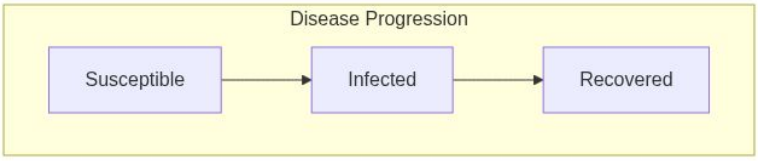
Details

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.

Model diagram



See Also

epiworld-methods

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

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
)
```

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.

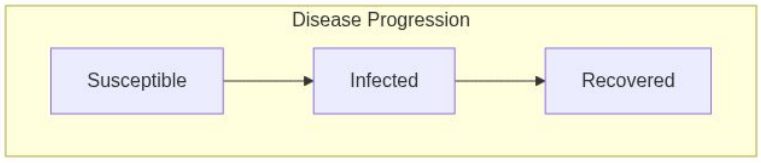
Details

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 `ModelSIRCONN`function returns a model of class epiworld_model.

Model diagram



See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSEIRMixing(), ModelSEIRMixingQuarantine(), ModelSIR(), ModelSIRD(), ModelSIRDCONN(), ModelSIRLogit(), ModelSIRMixing(), ModelSIS(), ModelSISD(), ModelSURV()

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)
```

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.

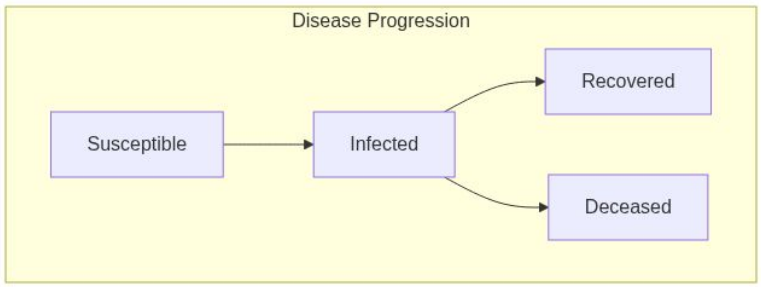
Details

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.

Model diagram



See Also

epiworld-methods

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

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
)
```

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.

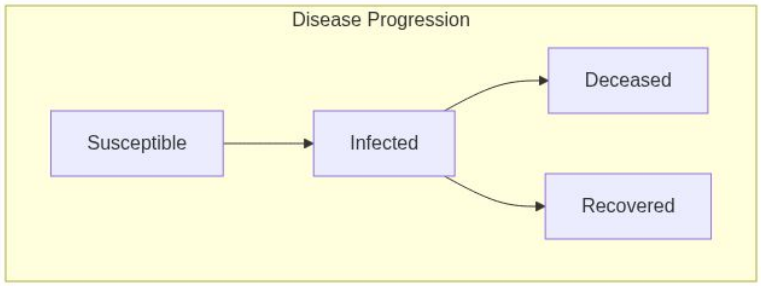
Details

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.

Model diagram



See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSEIRMixing(), ModelSEIRMixingQuarantine(), ModelSIR(), ModelSIRCONN(), ModelSIRD(), ModelSIRLogit(), ModelSIRMixing(), ModelSIS(), ModelSISD(), ModelSURV()

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
)
```

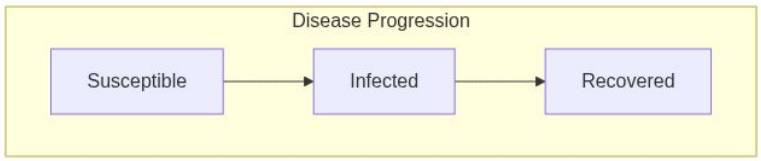
Arguments

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.

Model diagram



See Also

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSEIRMixing(), ModelSEIRMixingQuarantine(), ModelSIR(), ModelSIRCONN(), ModelSIRD(), ModelSIRDCONN(), ModelSIRMixing(), ModelSIS(), ModelSISD(), ModelSURV()

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)
```

`ModelSIRMixing` *Susceptible Infected Removed model (SIR) with mixing*

Description

Susceptible Infected Removed model (SIR) with mixing

Usage

```
ModelSIRMixing(
  name,
  n,
  prevalence,
  contact_rate,
  transmission_rate,
  recovery_rate,
  contact_matrix
)
```

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.
`contact_matrix`	Matrix of contact rates between individuals.

Details

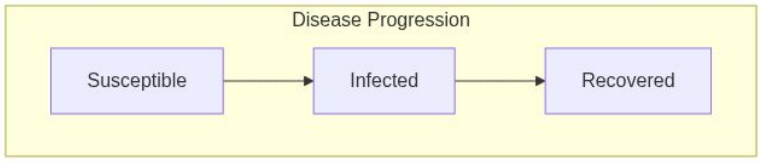
The `contact_matrix` is a matrix of contact rates between entities. The matrix should be of size `n x n`, where `n` is the number of entities. This is a row-stochastic matrix, i.e., the sum of each row should be 1.

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 `ModelSIRMixing`function returns a model of class epiworld_model.

Model diagram



See Also

epiworld-methods

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

Examples

```
# From the vignette

# Start off creating three entities.
# Individuals will be distribured randomly between the three.
e1 <- entity("Population 1", 3e3, as_proportion = FALSE)
e2 <- entity("Population 2", 3e3, as_proportion = FALSE)
e3 <- entity("Population 3", 3e3, as_proportion = FALSE)

# Row-stochastic matrix (rowsums 1)
cmatrix <- c(
  c(0.9, 0.05, 0.05),
  c(0.1, 0.8, 0.1),
  c(0.1, 0.2, 0.7)
) |> matrix(byrow = TRUE, nrow = 3)

N <- 9e3

flu_model <- ModelSIRMixing(
  name              = "Flu",
  n                 = N,
  prevalence        = 1 / N,
  contact_rate      = 20,
  transmission_rate = 0.1,
  recovery_rate     = 1 / 7,
  contact_matrix    = cmatrix
)

# Adding the entities to the model
flu_model |>
  add_entity(e1) |>
  add_entity(e2) |>
  add_entity(e3)

set.seed(331)
run(flu_model, ndays = 100)
summary(flu_model)
plot_incidence(flu_model)
```

ModelSIS *SIS model*

Description

Susceptible-Infected-Susceptible model (SIS) (wiki)

Usage

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

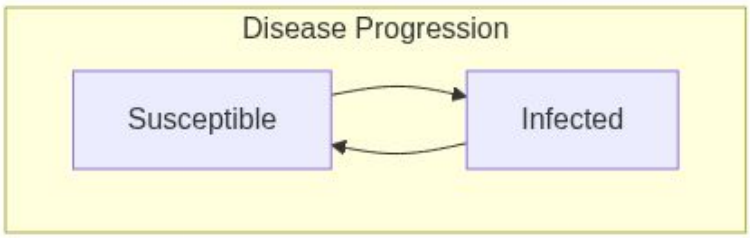
Arguments

`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.

Value

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

Model diagram



See Also

epiworld-methods

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

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)
```

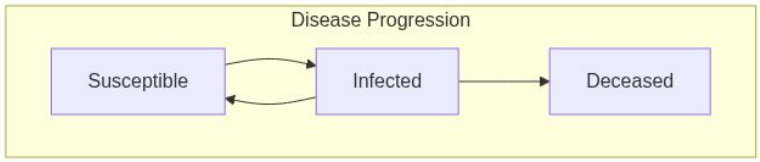
Arguments

`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.

Value

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

Model diagram



See Also

epiworld-methods

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

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
)
```

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.

Value

- The ModelSURVfunction returns a model of class epiworld_model.

See Also

epiworld-methods

Other Models: ModelDiffNet(), ModelSEIR(), ModelSEIRCONN(), ModelSEIRD(), ModelSEIRDCONN(), ModelSEIRMixing(), ModelSEIRMixingQuarantine(), ModelSIR(), ModelSIRCONN(), ModelSIRD(), ModelSIRDCONN(), ModelSIRLogit(), ModelSIRMixing(), ModelSIS(), ModelSISD()

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")
```

`print.epiworld_diagram` *Model Diagram*

Description

Functions described here are helper functions for drawing diagrams from model data. These generate mermaid diagrams from transition probability matrices which can then be rendered using other packages.

Usage

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

## S3 method for class 'epiworld_diagram'
plot(x, ...)

draw_mermaid_from_data(
  states,
  transition_probs,
  output_file = "",
  allow_self_transitions = FALSE
)
```

```
draw_mermaid_from_matrix(
  transition_matrix,
  output_file = "",
  allow_self_transitions = FALSE
)

draw_mermaid_from_file(
  transitions_file,
  output_file = "",
  allow_self_transitions = FALSE
)

draw_mermaid_from_files(
  transitions_files,
  output_file = "",
  allow_self_transitions = FALSE
)
```

Arguments

x	An epiworld_diagram object.
...	Additional arguments passed to DiagrammeR::mermaid().
states	String vector. List of model states.
transition_probs	Numeric vector. Transition probability matrix
output_file	String. Optional path to a file. If provided, the diagram will be written to the file.
allow_self_transitions	Logical. Whether to allow self-transitions, defaults to FALSE.
transition_matrix	Square matrix. Contains states and transition probabilities.
transitions_file	String. Path to file containing the transition probabilities matrix.
transitions_files	String vector. List of files containing transition probabilities matrices from multiple model runs.

Value

- The draw_mermaid_from_data function returns the mermaid diagram as a string.
- The draw_mermaid_from_matrix function returns the mermaid diagram as a string.
- The draw_mermaid_from_file function returns the mermaid diagram as a string.
- The draw_mermaid_from_files function returns the mermaid diagram as a string.

Examples

```
# Create and run a model
model <- ModelSIRCONN(
  name = "A Virus",
  n = 10000,
  prevalence = .01,
  contact_rate = 4.0,
  transmission_rate = .5,
  recovery_rate = 1.0 / 7.0
)

verbose_off(model)
run(model, ndays = 50, seed = 1912)

# Draw mermaid diagrams from model data
diagram <- draw_mermaid_from_data(
  states = get_states(model),
  transition_probs = c(get_transition_probability(model))
)

## Not run:
# If DiagrammeR is installed, we can plot the diagram
plot(diagram)

## End(Not run)
```

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

run_multiple_get_results(
```

```
  m,
  nthreads = min(2L, parallel::detectCores()),
  freader = NULL,
  ...
)

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 (passed to parallel::makeCluster()).
freader	A function to read the files. If NULL (default,) uses utils::read.table.
...	Additional arguments passed to freader.
fn	A file name pattern.

Details

Currently, the following elements can be saved:

Keyword	Description	Function
total_hist	History of the model (total numbers per time).	get_hist_total()
virus_info	Information about viruses.	
virus_hist	Changes in viruses.	get_hist_virus()
tool_info	Information about tools.	
tool_hist	Changes in tools.	get_hist_tool()
transmission	Transmission events.	get_transmissions()
transition	Transition matrices.	get_hist_transition_matrix()
reproductive	Reproductive number.	get_reproductive_number()
generation	Estimation of generation time.	get_generation_time()
active_cases	Number of active cases per virus.	get_active_cases()
outbreak_size	Size of outbreaks per virus.	get_outbreak_size()
hospitalizations	Number of hospitalizations per virus/tool.	get_hospitalizations()

An alternative to using the default utils::read.table function is to use data.table::fread from the data.table package. This can be done by specifying freader = data.table::fread and passing additional arguments (e.g., nThread = 2L) via .... This can significantly speed up the reading process, especially for large datasets.

If the model does not have, for example, tools, then the corresponding data frame will be empty (0 rows). A warning will be issued in this case when trying to retrieve or plot the results.

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`. Each entry will be a data.frame (default), or the output of `freader`.

Data structures

The datasets generated by `run_multiple_get_results` have the following columns:

- `total_hist`: `date` (integer), `nviruses` (integer), `state` (character), `counts` (integer).
- `virus_info`: `virus_id` (integer), `virus` (character), `virus_sequence` (character), `date_recorded` (integer), `parent` (integer)
- `virus_hist`: `date` (integer), `virus_id` (integer), `virus` (character), `n` (integer).
- `tool_info`: `id` (integer), `tool_name` (character), `tool_sequence` (character), `date_recorded` (integer).
- `tool_hist`: `date` (integer), `id` (integer), `state` (character), `n` (integer).
- `transmission`: `date` (integer), `virus_id` (integer), `virus` (character), `source_exposure_date` (integer), `source` (integer), `target` (integer).
- `transition`: `date` (integer), `from` (character), `to` (character), `counts` (integer).
- `reproductive`: `virus_id` (integer), `virus` (character), `source` (integer), `source_exposure_date` (integer), `rt` (integer).
- `generation`: `virus` (integer), `source` (integer), `source_exposure_date` (integer), `generation_time` (integer).
- `active_cases`: `date` (integer), `virus_id` (integer), `virus` (character), `active_cases` (integer).
- `outbreak_size`: `date` (integer), `virus_id` (integer), `virus` (character), `outbreak_size` (integer).
- `hospitalizations`: `date` (integer), `virus_id` (integer), `tool_id` (integer), `counts` (integer), and `weight` (numeric).

An **important difference** from the function `get_reproductive_number()` is that the returned reproductive number here includes a `-1` in the column `source`. This is the reproductive number of the model as an agent, a number that matches the initial number of infected agents at the start of the model.

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, nthreads = 2)

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

# Plotting
multi_sir <- ans$total_hist
multi_sir <- multi_sir[multi_sir$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,
  prevalence,
  as_proportion,
  susceptibility_reduction,
  transmission_reduction,
  recovery_enhancer,
  death_reduction
)

set_name_tool(tool, name)

get_name_tool(tool)

add_tool(model, tool, proportion)

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, ...)

set_distribution_tool(tool, distfun)

distribute_tool_randomly(prevalence, as_proportion, agents_ids = integer(0))

distribute_tool_to_set(agents_ids)

distribute_tool_to_entities(prevalence, as_proportion)
```

Arguments

`name`	Name of the tool
`prevalence`	Numeric scalar. Prevalence of the tool. In the case of `distribute_tool_to_entities`, it is a vector of prevalences, one per entity.
`as_proportion`	Logical scalar. If `TRUE`, `prevalence` is interpreted as a proportion of the total number of agents in the model.
`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
: Deprecated.

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.

distfun
: An object of class epiworld_tool_distfun.

agents_ids
: Integer vector. Indices of the agents to which the tool will be assigned.

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.

The set_distribution_tool function assigns a distribution function to the specified tool of class epiworld_tool. The distribution function can be created using the functions distribute_tool_randomly() and distribute_tool_to_set().

The distribute_tool_randomly function creates a distribution function that randomly assigns the tool to a proportion of the population.

The distribute_tool_to_set function creates a distribution function that assigns the tool to a set of agents.

The distribute_tool_to_entities function creates a distribution function that assigns the tool to a number of agents based on prevalence at the entity level. This is only useful for the mixing models.

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 `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.
- The `distribute_tool_randomly` function returns a distribution function of class `epiworld_tool_distfun`. When `agents_ids` is not empty, it will distribute the tool randomly within that set. Otherwise it uses all the agents in the model.
- The `distribute_tool_to_set` function returns a distribution function of class `epiworld_tool_distfun`.

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",
  prevalence = 0.5,
  as_proportion = TRUE,
  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)
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
# Setting prevalence to 0.1
set_distribution_tool(epitool, distribute_tool_randomly(0.1, TRUE))
add_tool(model_sirconn, epitool)
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

rm_tool(model_sirconn, 0)
add_tool(model_sirconn, epitool)
run(model_sirconn, ndays = 100, seed = 1912) # Run model to view changes


# Using the logit function ---------------
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",
  prevalence               = 0.5,
  as_proportion            = TRUE,
  susceptibility_reduction = 0.0,
  transmission_reduction   = 0.3, # Only transmission
  recovery_enhancer        = 0.0,
  death_reduction          = 0.0
```

```
)

add_tool(sir, mask_wearing)

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,
  prevalence,
  as_proportion,
  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)

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)

set_distribution_virus(virus, distfun)

distribute_virus_randomly(prevalence, as_proportion, agents_ids = integer(0))

distribute_virus_to_set(agents_ids)

distribute_virus_set(agents_ids)

distribute_virus_to_entities(prevalence, as_proportion)
```

Arguments

name	of the virus
prevalence	Numeric scalar. Prevalence of the virus. In the case of distribute_virus_to_entities, it is a vector of prevalences, one per entity.
as_proportion	Logical scalar. If TRUE, the prevalence is set as a proportion of the total number of agents in the model.
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	Deprecated.
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.
distfun	An object of class epiworld_distribution_virus.
agents_ids	Integer vector. Indices of the agents that will receive the virus.

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.

The distribute_virus_randomly function is a factory function used to randomly distribute the virus in the model. The prevalence can be set as a proportion or as a number of agents. The resulting function can then be passed to set_distribution_virus.

The distribute_virus_to_entities function is a factory function used to distribute the virus to a number of agents based on a prevalence at the entity level.

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 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.
- The distribute_virus_randomly function returns a function that can be used to distribute the virus in the model. When agents_ids is not empty, it will distribute the virus randomly within that set. Otherwise it uses all the agents in the model.

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, prevalence = 0.3, as_proportion = TRUE
)

# Adding virus and setting/getting virus name
add_virus(mseirconn, delta)
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
set_distribution_virus(delta, distribute_virus_randomly(100, as_proportion = FALSE))
add_virus(mseirconn, delta)

# 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, prevalence = 0, as_proportion = TRUE
)
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)
```

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