

Package ‘epiworldR’

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Type Package

Title Fast Agent-Based Epi Models

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Description A flexible framework for Agent-Based Models (ABM), the 'epiworldR' package provides methods for prototyping disease outbreaks and transmission models using a 'C++' back-end, 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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`add_entities_from_dataframe`
Add entities to a model according to a data.frame

Description

Helper function that facilitates 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

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

Value

Invisible 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

<code>model</code>	An object of class <code>epiworld_model</code> .
<code>...</code>	Ignored
<code>x</code>	An object of class <code>epiworld_agents</code>

<code>i</code>	Index (id) of the agent (from 0 to n-1)
<code>compressed</code>	Logical scalar. When FALSE, it prints detailed information about the agent.
<code>max_print</code>	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

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

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
e1 <- 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 <code>epiworld_model</code> .
x	Object of class <code>epiworld_entities</code> .
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 <code>epiworld_entity</code> .
agent	Agent object of class <code>epiworld_agent</code> .
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 <code>epiworld_distribution_entity</code> .

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	<i>Generation time</i>
------------------	------------------------

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

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

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
```

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 <code>epiworld_model</code> .
model	Model object.
ndays	Number of days (steps) of the simulation.
seed	Seed to set for initializing random number generator (passed to <code>set.seed()</code>).
object	Object of class <code>epiworld_model</code> .
...	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 <code>FALSE</code> .

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](#).
- `initial_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 <code>epiworld_sir</code> , <code>epiworld_seir</code> , etc. (any model), or an object of class <code>epiworld_repnum</code> .
y	Ignored.
ylab, xlab, main, type	Further parameters passed to <code>graphics::plot()</code>
plot	Logical scalar. If TRUE (default), the function will plot the desired statistic.
...	In the case of plot methods, further arguments passed to <code>graphics::plot</code> .

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 <code>graphics::plot</code> .
ylab, xlab, main, type	Further parameters passed to <code>graphics::plot()</code>
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 <code>epiworld_model</code> .
event	The event to be added or removed. If it is to add, then it should be an object of class <code>epiworld_globalevent</code> . 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 referred 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 <code>epiworld_model</code> .
tool	Tool object of class <code>epiworld_tool</code> .
n	Deprecated.
virus	Virus object of class <code>epiworld_virus</code> .

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 Markov 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	<i>Network Diffusion Model</i>
--------------	--------------------------------

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:

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

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

Another important difference is that the transmission network is not necessary 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.

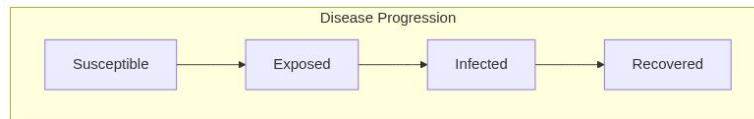
Details

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
)
```

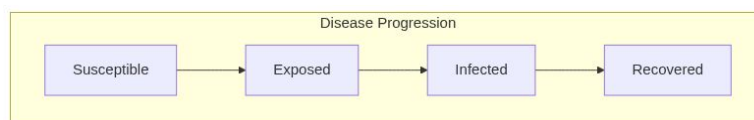
Arguments

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 ModelSEIRCONNfunction 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 <- ModelSEIRDCONN(
  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.

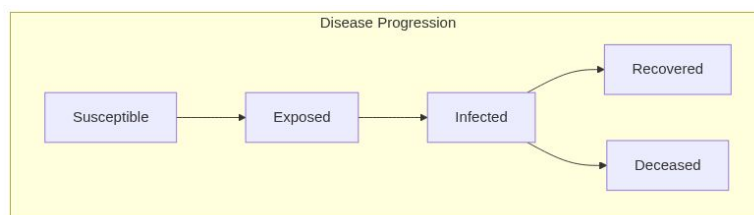
Details

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-infected agents already deceased.

Value

- The ModelSEIRDfunction 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	<i>Susceptible Exposed Infected Removed Deceased model (SEIRD connected)</i>
----------------	--

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.

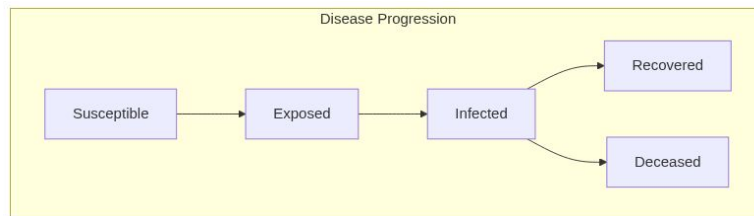
Details

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-infected 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

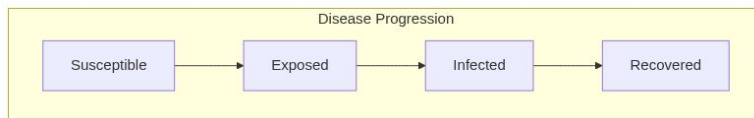
The `contact_matrix` is a matrix of contact rates between entities. The matrix should be of size $n \times n$, where n is the number of entities. This is a row-stochastic matrix, i.e., the sum of each row should be 1.

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 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 <- 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 be 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 $n \times n$, where n is the number of entities. This is a row-stochastic matrix, i.e., the sum of each row should be 1.

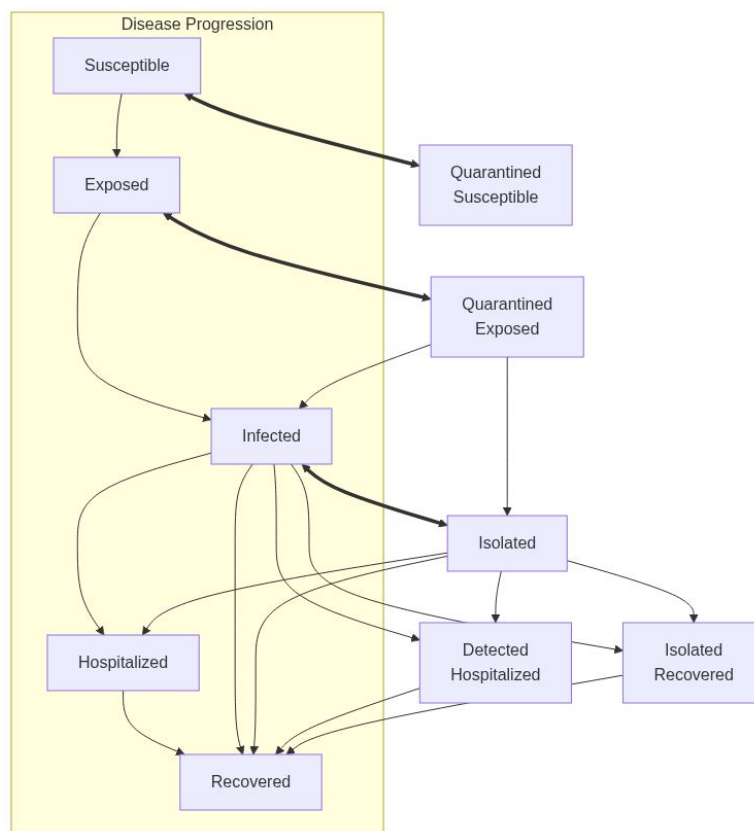
The quarantine and isolation processes can be turned off by specifying `quarantine_period < 0` and `isolation_period < 0` respectively. In other words, any negative value for these parameters will suppress the corresponding process.

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.

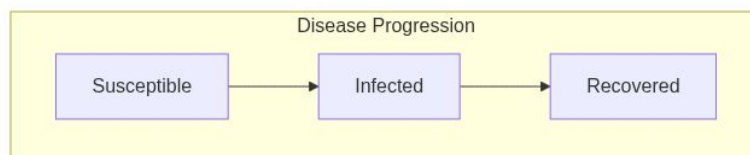
Details

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

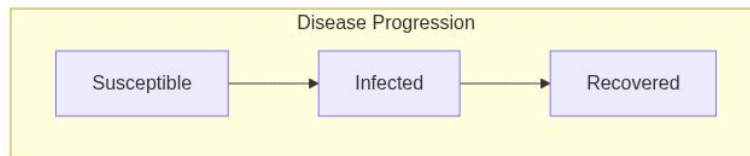
name	String. Name of the virus
n	Number of individuals in the population.
prevalence	Double. Initial proportion of individuals with the virus.
contact_rate	Numeric scalar. Average number of contacts per step.
transmission_rate	Numeric scalar between 0 and 1. Probability of transmission.
recovery_rate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

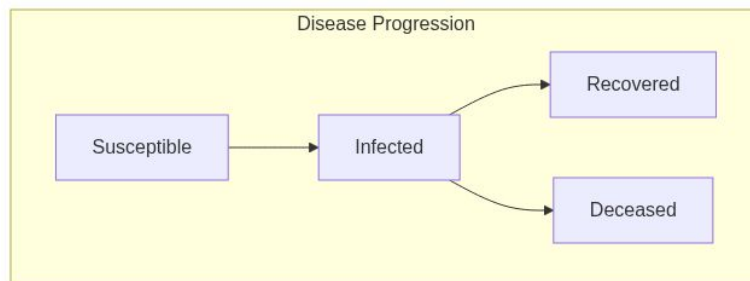
name	String. Name of the virus
prevalence	Double. Initial proportion of individuals with the virus.
transmission_rate	Numeric scalar between 0 and 1. Virus's rate of infection.
recovery_rate	Numeric scalar between 0 and 1. Rate of recovery_rate from virus.
death_rate	Numeric scalar between 0 and 1. Rate 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-infected 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.

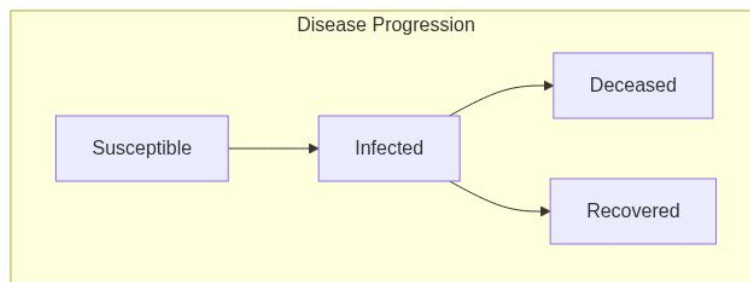
Details

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-infected 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
)

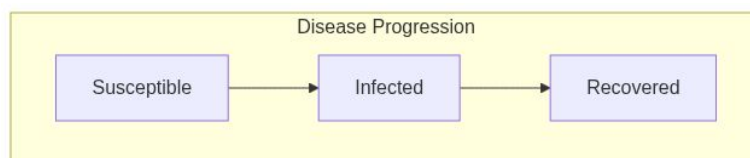
```

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 coefficient.
coef_recover_cols	Integer vector. Columns in the coefficient.
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	<i>Susceptible Infected Removed model (SIR) with mixing</i>
----------------	---

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.

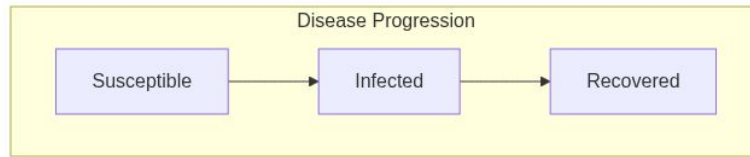
Details

The `contact_matrix` is a matrix of contact rates between entities. The matrix should be of size $n \times n$, 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 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 <- 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)
```

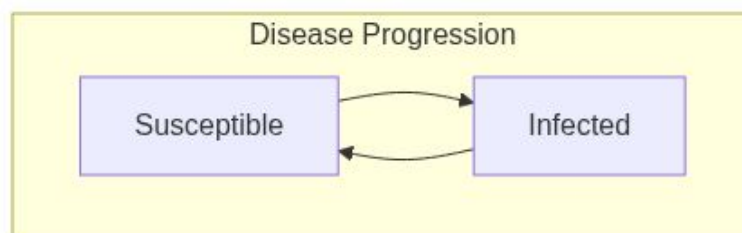
Arguments

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

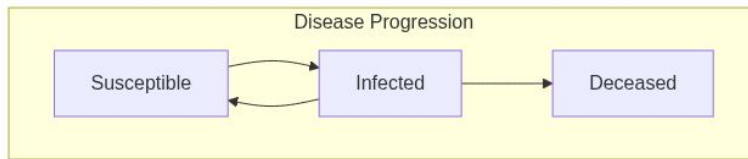
```
ModelSISD(name, prevalence, transmission_rate, recovery_rate, death_rate)
```

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")
```

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(infect_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

<code>x</code>	An <code>epiworld_diagram</code> object.
<code>...</code>	Additional arguments passed to <code>DiagrammeR::mermaid()</code> .
<code>states</code>	String vector. List of model states.
<code>transition_probs</code>	Numeric vector. Transition probability matrix
<code>output_file</code>	String. Optional path to a file. If provided, the diagram will be written to the file.
<code>allow_self_transitions</code>	Logical. Whether to allow self-transitions, defaults to <code>FALSE</code> .
<code>transition_matrix</code>	Square matrix. Contains states and transition probabilities.
<code>transitions_file</code>	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 = sample.int(10000, 1),
  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.	<code>get_generation_time()</code>
active_cases	Number of active cases per virus.	<code>get_active_cases()</code>
outbreak_size	Size of outbreaks per virus.	<code>get_outbreak_size()</code>
hospitalizations	Number of hospitalizations per virus/tool.	<code>get_hospitalizations()</code>

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 <code>distribute_tool_to_entities</code> , 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.
tool	An object of class <code>epiworld_tool</code>
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 <code>vars</code> , 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 <code>model</code> that will be added to the tool (see details).
tfun	An object of class <code>epiworld_tool_fun</code> .
x	An object of class <code>epiworld_agents_tools</code> .
max_print	Numeric scalar. Maximum number of tools to print.
...	Currently ignored.
distfun	An object of class <code>epiworld_tool_distfun</code> .
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 <code>distribute_virus_to_entities</code> , 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.

<code>virus</code>	An object of class <code>epiworld_virus</code>
<code>model</code>	An object of class <code>epiworld_model</code> .
<code>proportion</code>	Deprecated.
<code>init, end, removed</code>	states after acquiring a virus, removing a virus, and removing the agent as a result of the virus, respectively.
<code>virus_pos</code>	Positive integer. Index of the virus's position in the model.
<code>vars</code>	Integer vector. Indices (starting from 0) of the positions of the variables used to compute the logit probability.
<code>coefs</code>	Numeric vector. Of the same length of <code>vars</code> , is a vector of coefficients associated to the logit probability.
<code>prob</code>	Numeric scalar. A probability (between zero and one).
<code>param</code>	Character scalar. Name of the parameter featured in <code>model</code> that will be added to the virus (see details).
<code>vfun</code>	An object of class <code>epiworld_virus_fun</code> .
<code>distfun</code>	An object of class <code>epiworld_distribution_virus</code> .
<code>agents_ids</code>	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 suggests, 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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