

Package ‘epiworldR’

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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/>

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Description

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

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See Also

Useful links:

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

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

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

Details

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

Value

- The `'agents_smallworld'` function returns a model with the agents loaded.
- The `agents_from_edgelist` function returns an empty model of class [epiworld_model](#).
- The `get_network` function returns a data frame with two columns (source and target) describing the edgelist of the network.
- `get_agents_states` returns an character vector with the states of the agents by the end of the simulation.
- The function `add_virus_agent` adds a virus to an agent and returns the agent invisibly.
- The function `add_tool_agent` adds a tool to an agent and returns the agent invisibly.

- The functions `has_virus` and `has_tool` return a logical scalar indicating whether the agent has the virus/tool or not.
- `get_agents_tools` returns a list of class `epiworld_agents_tools` with `epiworld_tools` (list of lists).

Examples

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

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

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

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

# Running the simulation
run(sir, 50)

plot(sir)
```

Description

Entities in epiworld are objects that can contain agents.

Usage

```
get_entities(model)

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

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

get_entity_size(entity)

get_entity_name(entity)

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

rm_entity(model, id)

add_entity(model, entity)

load_agents_entities_ties(model, agents_id, entities_id)

entity_get_agents(entity)

distribute_entity_randomly(prevalence, as_proportion, to_unassigned = TRUE)

distribute_entity_to_set(agents_ids)

set_distribution_entity(entity, distfun)
```

Arguments

model	Model object of class epiworld_model.
x	Object of class epiworld_entities.
i	Integer index.
name	Character scalar. Name of the entity.
prevalence	Numeric scalar. Prevalence of the entity.
as_proportion	Logical scalar. If TRUE, prevalence is interpreted as a proportion.
to_unassigned	Logical scalar. If TRUE, the entity is added to the unassigned pool.
entity	Entity object of class epiworld_entity.
agent	Agent object of class epiworld_agent.
id	Integer scalar. Entity id to remove (starting from zero).
agents_id	Integer vector.

entities_id	Integer vector.
agents_ids	Integer vector. Ids of the agents to distribute.
distfun	Distribution function object of class <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)
```

Description

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

Usage

```

get_hist_total(x)

get_today_total(x)

get_hist_virus(x)

get_hist_tool(x)

get_transition_probability(x)

get_reproductive_number(x)

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

plot_reproductive_number(x, ...)

get_hist_transition_matrix(x, skip_zeros = FALSE)

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

plot_incidence(x, ...)

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

```

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

get_transmissions(x)

get_generation_time(x)

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

plot_generation_time(x, ...)
```

Arguments

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

Details

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

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

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

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

Value

- The `get_hist_total` function returns an object of class `epiworld_hist_total`.
- The `get_today_total` function returns a named vector with the total number of individuals in each state at the end of the simulation.
- The `get_hist_virus` function returns an object of class `epiworld_hist_virus`.
- The `get_hist_tool` function returns an object of `epiworld_hist_virus`.
- The `get_transition_probability` function returns an object of class `matrix`.
- The `get_reproductive_number` function returns an object of class `epiworld_repnum`.
- The `plot` function returns a plot of the reproductive number over time.
- `get_hist_transition_matrix` returns a `data.frame` with four columns: "state_from", "state_to", "date", and "counts."
- The `as.array` method for `epiworld_hist_transition` objects turns the `data.frame` returned by `get_hist_transition_matrix` into an array of `nstates x nstates x (ndays + 1)` entries, where the first entry is the initial state.
- The `plot_incidence` function returns a plot originating from the object `get_hist_transition_matrix`.
- The `plot` function returns a plot which originates from the `epiworld_hist_transition` object.
- The function `get_transmissions` returns a `data.frame` with the following columns: `date`, `source`, `target`, `virus_id`, `virus`, and `source_exposure_date`.
- The function `get_generation_time` returns a `data.frame` with the following columns: "agent", "virus_id", "virus", "date", and "gentime".
- The function `plot_generation_time` is a wrapper for `plot` and `get_generation_time`.

See Also

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

Examples

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

```
    recovery_rate      = 0.3
  )

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

# Retrieving the transition probability
get_transition_probability(seirconn)

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

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

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

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

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

head(t_hist)

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

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

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

<code>x</code>	An object of class <code>epiworld_model</code> .
<code>model</code>	Model object.
<code>ndays</code>	Number of days (steps) of the simulation.
<code>seed</code>	Seed to set for initializing random number generator (passed to <code>set.seed()</code>).
<code>object</code>	Object of class <code>epiworld_model</code> .
<code>...</code>	Additional arguments.
<code>pname</code>	String. Name of the parameter.
<code>pval</code>	Numeric. Value of the parameter.
<code>mname</code>	String. Name of the model.
<code>data</code>	A numeric matrix.
<code>virus_pos</code>	Integer. Relative location (starting from 0) of the virus in the model
<code>tool_pos</code>	Integer. Relative location (starting from 0) of the tool in the model
<code>proportions</code>	Numeric vector. Proportions in which agents will be distributed (see details).
<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 FALSE.

Details

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

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

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

Value

- The `verbose_on` and `verbose_off` functions return the same model, however `verbose_off` returns the model with no progress bar.
- The `run` function returns the simulated model of class `epiworld_model`.
- The `summary` function prints a more detailed view of the model, and returns the same model invisibly.
- The `get_states` function returns the unique states found in a model.

- The `get_param` function returns a selected parameter from the model object of class `epiworld_model`.
- `add_param` returns the model with the added parameter invisibly.
- The `set_param` function does not return a value but instead alters a parameter value.
- The `set_name` function does not return a value but instead alters an object of `epiworld_model`.
- `get_name` returns the name of the model.
- `get_n_viruses` returns the number of viruses of the model.
- `get_n_tools` returns the number of tools of the model.
- `get_ndays` returns the number of days of the model.
- `today` returns the current model day
- `get_n_replicates` returns the number of replicates of the model.
- `size.epiworld_model` returns the number of agents in the model.
- The `'set_agents_data'` function returns an object of class `DataFrame`.
- `'get_agents_data_ncols'` returns the number of columns in the model dataframe.
- `'get_virus'` returns a [virus](#).
- `get_tool` returns a [tool](#).
- `inital_states` returns the model with an updated initial state.
- `clone_model` returns a copy of the model.
- The `draw_mermaid` returns the mermaid diagram as a string.

Examples

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

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

```

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

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

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

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

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

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

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

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

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

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

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

size(model_sirconn) # Returns the population size in the model. In this case,
# there are 10,000 agents in the model.
# Set Agents Data
# First, your data matrix must have the same number of rows as agents in the
# model. Below is a generated matrix which will be passed into the

```

```
# "set_agents_data" function.
data <- matrix(data = runif(20000, min = 0, max = 100), nrow = 10000, ncol = 2)
set_agents_data(model_sirconn, data)
get_agents_data_ncols(model_sirconn) # Returns number of columns

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

add_tool(model_sirconn, tool("Vaccine", .9, .9, .5, 1, prevalence = 0.5, as_prop = TRUE))
get_tool(model_sirconn, 0) # Returns information about the first tool in the
# model. In this case, there are no tools so an
# error message will occur.

# Draw a mermaid diagram of the transitions
draw_mermaid(model_sirconn)
```

epiworld-model-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

```
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>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 FALSE.
<code>transition_matrix</code>	Square matrix. Contains states and transition probabilities.
<code>transitions_file</code>	String. Path to file containing the transition probabilities matrix.
<code>transitions_files</code>	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
draw_mermaid_from_data(
  states = get_states(model),

```

```

    transition_probs = c(get_transition_probability(model))
  )

```

epiworldR-deprecated *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."

Usage

```

add_tool_n(model, tool, n)

add_virus_n(model, virus, n)

globalaction_tool(...)

globalaction_tool_logit(...)

globalaction_set_params(...)

globalaction_fun(...)

```

Arguments

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

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

<code>tool</code>	An object of class tool .
<code>prob</code>	Numeric scalar. A probability between 0 and 1.
<code>name</code>	Character scalar. The name of the action.
<code>day</code>	Integer. The day (step) at which the action is executed (see details).
<code>vars</code>	Integer vector. The position of the variables in the model.
<code>coefs</code>	Numeric vector. The coefficients of the logistic regression.
<code>param</code>	Character scalar. The name of the parameter to be set.
<code>value</code>	Numeric scalar. The value of the parameter.
<code>fun</code>	Function. The function to be executed.
<code>model</code>	An object of class epiworld_model .
<code>event</code>	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 an integer with the position of the event in the model (starting from zero).
<code>action</code>	(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_globlevent(model, hist_saver_event)

```

LFMCMC

Likelihood-Free Markhov Chain Monte Carlo (LFMCMC)

Description

Likelihood-Free Markhov Chain Monte Carlo (LFMCMC)

Usage

```

LFMCMC(model = NULL)

run_lfmcnc(lfmcnc, params_init, n_samples, epsilon, seed = NULL)

set_observed_data(lfmcnc, observed_data)

set_proposal_fun(lfmcnc, fun)

use_proposal_norm_reflective(lfmcnc)

set_simulation_fun(lfmcnc, fun)

set_summary_fun(lfmcnc, fun)

set_kernel_fun(lfmcnc, fun)

use_kernel_fun_gaussian(lfmcnc)

get_mean_params(lfmcnc)

get_mean_stats(lfmcnc)

get_initial_params(lfmcnc)

get_current_proposed_params(lfmcnc)

get_current_accepted_params(lfmcnc)

get_current_proposed_stats(lfmcnc)

```

```

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

<code>model</code>	A model of class epiworld_model or NULL (see details).
<code>lfmcmc</code>	LFMCMC model
<code>params_init</code>	Initial model parameters, treated as double
<code>n_samples</code>	Number of samples, treated as integer
<code>epsilon</code>	Epsilon parameter, treated as double
<code>seed</code>	Random engine seed
<code>observed_data</code>	Observed data, treated as double.
<code>fun</code>	A function (see details).

x	LFMCMC model to print
names	Character vector of names.
burnin	Integer. Number of samples to discard as burnin before computing the summary.
...	Ignored

Details

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

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

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

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

Value

The LFMCMC function returns a model of class `epiworld_lfmcmc`.

The simulated model of class `epiworld_lfmcmc`.

- `use_kernel_fun_gaussian`: The LFMCMC model with kernel function set to gaussian.
- `get_mean_params`: The param means for the given lfmcmc model.
- `get_mean_stats`: The stats means for the given lfmcmc model.
- The function `get_initial_params` returns the initial parameters for the given LFMCMC model.
- The function `get_current_proposed_params` returns the proposed parameters for the next LFMCMC sample.
- The function `get_current_accepted_params` returns the most recently accepted parameters (the current state of the LFMCMC)
- The function `get_current_proposed_stats` returns the statistics from the simulation run with the proposed parameters
- The function `get_current_accepted_stats` returns the statistics from the most recently accepted parameters
- The function `get_observed_stats` returns the statistics for the observed data

- The function `get_all_sample_params` returns a matrix of sample parameters for the given LFMCMC model. with the number of rows equal to the number of samples and the number of columns equal to the number of parameters.
- The function `get_all_sample_stats` returns a matrix of statistics for the given LFMCMC model. with the number of rows equal to the number of samples and the number of columns equal to the number of statistics.
- The function `get_all_sample_acceptance` returns a vector of boolean flags which indicate whether a given sample was accepted
- The function `get_all_sample_drawn_prob` returns a vector of drawn probabilities for each sample
- The function `get_all_sample_kernel_scores` returns a vector of kernel scores for each sample
- The function `get_all_accepted_params` returns a matrix of accepted parameters for the given LFMCMC model. with the number of rows equal to the number of samples and the number of columns equal to the number of parameters.
- The function `get_all_accepted_stats` returns a matrix of accepted statistics for the given LFMCMC model. with the number of rows equal to the number of samples and the number of columns equal to the number of statistics.
- The function `get_all_accepted_kernel_scores` returns a vector of kernel scores for each accepted sample
- The functions `get_n_samples`, `get_n_stats`, and `get_n_params` return the number of samples, statistics, and parameters for the given LFMCMC model, respectively.
- The `verbose_on` and `verbose_off` functions return the same model, however `verbose_off` returns the model with no progress bar.
- `set_params_names`: The `lfmcmc` model with the parameter names added.
- `set_stats_names`: The `lfmcmc` model with the stats names added.

Examples

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

```

run(model_sir, ndays = 50, seed = model_seed)

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

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

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

# Create the LFMCMC model
lfmcmc_model <- LFMCMC(model_sir) |>
  set_simulation_fun(simfun) |>
  set_summary_fun(sumfun) |>
  use_proposal_norm_reflective() |>
  use_kernel_fun_gaussian() |>
  set_observed_data(obs_data)

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

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

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

print(lfmcmc_model)

get_mean_stats(lfmcmc_model)
get_mean_params(lfmcmc_model)

```

ModelDiffNet	<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:

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

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

Another important difference is that the transmission network is not 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: [ModelMeaslesQuarantine\(\)](#), [ModelSEIR\(\)](#), [ModelSEIRCONN\(\)](#), [ModelSEIRD\(\)](#), [ModelSEIRDCONN\(\)](#), [ModelSEIRMixing\(\)](#), [ModelSIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIRD\(\)](#), [ModelSIRDCONN\(\)](#), [ModelSIRLogit\(\)](#), [ModelSIRMixing\(\)](#), [ModelSIS\(\)](#), [ModelSISD\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

Examples

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

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

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

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

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

# Plotting the model
plot(adopt_chatgpt)
```

ModelMeaslesQuarantine

Measles model with quarantine

Description

Implements a Susceptible-Exposed-Infectious-Hospitalized-Recovered (SEIHR) model for Measles within a school. The model includes isolation of detected cases and optional quarantine of unvaccinated individuals.

Usage

```
ModelMeaslesQuarantine(
  n,
  prevalence = 1,
  contact_rate = 15/transmission_rate/prodromal_period,
```

```

    transmission_rate = 0.9,
    vax_efficacy = 0.99,
    vax_improved_recovery = 0.5,
    incubation_period = 12,
    prodromal_period = 4,
    rash_period = 3,
    days_undetected = 2,
    hospitalization_rate = 0.2,
    hospitalization_period = 7,
    prop_vaccinated = 1 - 1/15,
    quarantine_period = 21,
    quarantine_willingness = 1,
    isolation_period = 4
)

```

Arguments

n	Number of agents in the model.
prevalence	Initial number of agents with the virus.
contact_rate	Average number of contacts per step. Default is set to match the basic reproductive number (R0) of 15 (see details).
transmission_rate	Probability of transmission.
vax_efficacy	Probability of vaccine efficacy.
vax_improved_recovery	Increase in recovery rate due to vaccination.
incubation_period	Average number of incubation days.
prodromal_period	Average number of prodromal days.
rash_period	Average number of rash days.
days_undetected	Average number of days undetected. Detected cases are moved to isolation and trigger the quarantine process.
hospitalization_rate	Probability of hospitalization.
hospitalization_period	Average number of days in hospital.
prop_vaccinated	Proportion of the population vaccinated.
quarantine_period	Total duration of quarantine.
quarantine_willingness	Probability of accepting quarantine (see details).
isolation_period	Total duration of isolation.

Details

This model can be described as a SEIHR model with isolation and quarantine. The infectious state is divided into prodromal and rash phases. Furthermore, the quarantine state includes exposed, susceptible, prodromal, and recovered states.

The model is a perfect mixing model, meaning that all agents are in contact with each other. The model is designed to simulate the spread of Measles within a school setting, where the population is assumed to be homogeneous.

The quarantine process is triggered any time that an agent with rash is detected. The agent is then isolated and all agents who are unvaccinated are quarantined (if willing). Isolated agents then may be moved out of the isolation in `isolation_period` days. The quarantine willingness parameter sets the probability of accepting quarantine. If a quarantined agent develops rash, they are moved to isolation, which triggers a new quarantine process.

The basic reproductive number in Measles is estimated to be about 15. By default, the contact rate of the model is set so that the R_0 matches 15.

When `quarantine_period` is set to -1, the model assumes there is no quarantine process. The same happens with `isolation_period`. Since the quarantine process is triggered by an isolation, then `isolation_period = -1` automatically sets `quarantine_period = -1`.

Value

- The `ModelMeaslesQuarantine` function returns a model of classes `epiworld_model` and `epiworld_measlesquarantine`.

Author(s)

This model was built as a response to the US Measles outbreak in 2025. This is a collaboration between the University of Utah (ForeSITE center grant) and the Utah Department of Health and Human Services.

References

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Liu, Fengchen, Wayne T A Enanoria, Jennifer Zipprich, Seth Blumberg, Kathleen Harriman, Sarah F Ackley, William D Wheaton, Justine L Allpress, and Travis C Porco. 2015. "The Role of Vaccination Coverage, Individual Behaviors, and the Public Health Response in the Control of Measles Epidemics: An Agent-Based Simulation for California." *BMC Public Health* 15 (1): 447. doi:10.1186/s1288901517666.

"Measles Disease Plan." 2019. Utah Department of Health and Human Services. <https://epi.utah.gov/wp-content/uploads/Measles-disease-plan.pdf>.

See Also

`epiworld-methods`

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

Examples

```
# An in a school with low vaccination
model_measles <- ModelMeaslesQuarantine(
  n = 500,
  prevalence = 1,
  prop_vaccinated = 0.70
)

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

plot(model_measles)
```

ModelSEIR	<i>Susceptible Exposed Infected Recovered model (SEIR)</i>
-----------	--

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 ModelSEIRfunction returns a model of class [epiworld_model](#).

See Also

epiworld-methods

Other Models: [ModelDiffNet\(\)](#), [ModelMeaslesQuarantine\(\)](#), [ModelSEIRCONN\(\)](#), [ModelSEIRD\(\)](#), [ModelSEIRDCONN\(\)](#), [ModelSEIRMixing\(\)](#), [ModelSIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIRD\(\)](#), [ModelSIRDCONN\(\)](#), [ModelSIRLogit\(\)](#), [ModelSIRMixing\(\)](#), [ModelSIS\(\)](#), [ModelSISD\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

Examples

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

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

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

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

ModelSEIRCONN

Susceptible Exposed Infected Removed model (SEIR connected)

Description

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

Usage

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

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](#).

See Also

[epiworld-methods](#)

Other Models: [ModelDiffNet\(\)](#), [ModelMeaslesQuarantine\(\)](#), [ModelSEIR\(\)](#), [ModelSEIRD\(\)](#), [ModelSEIRDCONN\(\)](#), [ModelSEIRMixing\(\)](#), [ModelSIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIRD\(\)](#), [ModelSIRDCONN\(\)](#), [ModelSIRLogit\(\)](#), [ModelSIRMixing\(\)](#), [ModelSIS\(\)](#), [ModelSISD\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

Examples

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

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

plot(model_seirconn)

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

See Also

[epiworld-methods](#)

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

Examples

```

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

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

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

plot(model_seird, main = "SEIRD Model")

```

ModelSEIRDCONN	<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](#).

See Also

[epiworld-methods](#)

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

Examples

```

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

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

plot(model_seirdconn)

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

```

```

    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	<i>Susceptible Exposed Infected Removed model (SEIR) with mixing</i>
-----------------	--

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`.

See Also

`epiworld-methods`

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

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)

```

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](#).

See Also

epiworld-methods

Other Models: [ModelDiffNet\(\)](#), [ModelMeaslesQuarantine\(\)](#), [ModelSEIR\(\)](#), [ModelSEIRCONN\(\)](#), [ModelSEIRD\(\)](#), [ModelSEIRDCONN\(\)](#), [ModelSEIRMixing\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIRD\(\)](#), [ModelSIRDCONN\(\)](#), [ModelSIRLogit\(\)](#), [ModelSIRMixing\(\)](#), [ModelSIS\(\)](#), [ModelSISD\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

Examples

```

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

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

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

# Plotting
plot(model_sir)

```

ModelSIRCONN

Susceptible Infected Removed model (SIR connected)

Description

Susceptible Infected Removed model (SIR connected)

Usage

```

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

```

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](#).

See Also

[epiworld-methods](#)

Other Models: [ModelDiffNet\(\)](#), [ModelMeaslesQuarantine\(\)](#), [ModelSEIR\(\)](#), [ModelSEIRCONN\(\)](#), [ModelSEIRD\(\)](#), [ModelSEIRDCONN\(\)](#), [ModelSEIRMixing\(\)](#), [ModelSIR\(\)](#), [ModelSIRD\(\)](#), [ModelSIRDCONN\(\)](#), [ModelSIRLogit\(\)](#), [ModelSIRMixing\(\)](#), [ModelSIS\(\)](#), [ModelSISD\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

Examples

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

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

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

ModelSIRD

SIRD model

Description

SIRD model

Usage

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

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](#).

See Also

[epiworld-methods](#)

Other Models: [ModelDiffNet\(\)](#), [ModelMeaslesQuarantine\(\)](#), [ModelSEIR\(\)](#), [ModelSEIRCONN\(\)](#), [ModelSEIRD\(\)](#), [ModelSEIRDCONN\(\)](#), [ModelSEIRMixing\(\)](#), [ModelSIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIRDCONN\(\)](#), [ModelSIRLogit\(\)](#), [ModelSIRMixing\(\)](#), [ModelSIS\(\)](#), [ModelSISD\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

Examples

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

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

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

# Plotting
plot(model_sird)
```

ModelSIRDCONN	<i>Susceptible Infected Removed Deceased model (SIRD connected)</i>
---------------	---

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](#).

See Also

[epiworld-methods](#)

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

Examples

```

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

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

plot(model_sirdconn, main = "SIRDCONN Model")

```

ModelSIRLogit

SIR Logistic model

Description

SIR Logistic model

Usage

```

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

```

Arguments

vname	Name of the virus.
data	A numeric matrix with n rows.
coefs_infect	Numeric vector. Coefficients associated to infect.
coefs_recover	Numeric vector. Coefficients associated to recover.
coef_infect_cols	Integer vector. Columns in the 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`.

See Also

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

Examples

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

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

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

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

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

run(model_logit, 50)
```

```

plot(model_logit)

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

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

# Looking into the individual agents.
get_agents(model_logit)

```

ModelSIRMixing

Susceptible Infected Removed model (SIR) with mixing

Description

Susceptible Infected Removed model (SIR) with mixing

Usage

```

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

```

Arguments

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

Details

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

See Also

`epiworld-methods`

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

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](#).

See Also

[epiworld-methods](#)

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

Examples

```

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

# Adding a small world population
agents_smallworld(
  model_sis,

```

```

    n = 1000,
    k = 5,
    d = FALSE,
    p = .01
  )

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

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

```

ModelSISD

SISD model

Description

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

Usage

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

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](#).

See Also

[epiworld-methods](#)

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

Examples

```

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

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

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

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

```

ModelSURV

SURV model

Description

SURV model

Usage

```

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

```

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\(\)](#), [ModelMeaslesQuarantine\(\)](#), [ModelSEIR\(\)](#), [ModelSEIRCONN\(\)](#), [ModelSEIRD\(\)](#), [ModelSEIRDCONN\(\)](#), [ModelSEIRMixing\(\)](#), [ModelSIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIRD\(\)](#), [ModelSIRDCONN\(\)](#), [ModelSIRLogit\(\)](#), [ModelSIRMixing\(\)](#), [ModelSIS\(\)](#), [ModelSISD\(\)](#), [epiworld-data](#)

Examples

```
model_surv <- ModelSURV(
  name           = "COVID-19",
  prevalence     = 20,
  efficacy_vax   = 0.6,
  latent_period  = 4,
  infect_period  = 5,
  prob_symptoms  = 0.5,
  prop_vaccinated = 0.7,
  prop_vax_redux_transm = 0.8,
```

```

    prop_vax_redux_infect = 0.95,
    surveillance_prob      = 0.1,
    transmission_rate     = 0.2,
    prob_death             = 0.001,
    prob_noreinfect       = 0.5
  )

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

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

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

```

run_multiple

Run multiple simulations at once

Description

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

Usage

```

run_multiple(
  m,
  ndays,
  nsims,
  seed = sample.int(10000, 1),
  saver = make_saver(),
  reset = TRUE,
  verbose = TRUE,
  nthreads = 1L
)

run_multiple_get_results(m, nthreads = parallel::detectCores() - 1L)

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()).
...	List of strings (characters) specifying what to save (see details).
fn	A file name pattern.

Details

Currently, the following elements can be saved:

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

Value

- In the case of `make_saver`, an list of class `epiworld_saver`.
- The `run_multiple` function runs a specified number of simulations and returns a model object of class [epiworld_model](#).
- The `run_multiple_get_results` function returns a named list with the data specified by `make_saver`.

Examples

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

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

```

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

# Retrieving the results
ans <- run_multiple_get_results(model_sir, 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)

```

Arguments

name	Name of the tool
prevalence	Numeric scalar. Prevalence of the tool.
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 epiworld_tool
model	Model

proportion	Deprecated.
tool_pos	Positive integer. Index of the tool's position in the model.
vars	Integer vector. Indices (starting from 0) of the positions of the variables used to compute the logit probability.
coefs	Numeric vector. Of the same length of vars, is a vector of coefficients associated to the logit probability.
prob	Numeric scalar. A probability (between zero and one).
param	Character scalar. Name of the parameter featured in model that will be added to the tool (see details).
tfun	An object of class <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.

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)
```

Arguments

name	of the virus
prevalence	Numeric scalar. Prevalence of the virus.
as_proportion	Logical scalar. If TRUE, the prevalence is set as a proportion of the total number of agents in the model.
prob_infecting	Numeric scalar. Probability of infection (transmission).
recovery_rate	Numeric scalar. Probability of recovery.
prob_death	Numeric scalar. Probability of death.
post_immunity	Numeric scalar. Post immunity (prob of re-infection).
incubation	Numeric scalar. Incubation period (in days) of the virus.
virus	An object of class <code>epiworld_virus</code>
model	An object of class <code>epiworld_model</code> .
proportion	Deprecated.
init, end, removed	states after acquiring a virus, removing a virus, and removing the agent as a result of the virus, respectively.
virus_pos	Positive integer. Index of the virus's position in the model.
vars	Integer vector. Indices (starting from 0) of the positions of the variables used to compute the logit probability.
coefs	Numeric vector. Of the same length of vars, is a vector of coefficients associated to the logit probability.
prob	Numeric scalar. A probability (between zero and one).
param	Character scalar. Name of the parameter featured in model that will be added to the virus (see details).
vfun	An object of class <code>epiworld_virus_fun</code> .
distfun	An object of class <code>epiworld_distribution_virus</code> .
agents_ids	Integer vector. Indices of the agents that will receive the virus.

Details

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

The function `virus_fun_logit()` creates a "virus function" that can be evaluated for transmission, recovery, and death. As the name 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`.

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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