

Package ‘epiworldR’

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Title Fast Epi Simulations in R

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Description Epidemiological simulations using the epiworld C++ template library.
It provides a fast way to prototype models involving social networks, multiple diseases,
and arbitrary policy strategies.

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epiworldR-package	<i>epiworldR</i>
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Description

Epidemiological simulations using the epiworld C++ template library. It provides a fast way to prototype models involving social networks, multiple diseases, and arbitrary policy strategies.

Author(s)

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epiworld-data	<i>Accessing the database of epiworld</i>
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Description

Accessing the database of epiworld

Usage

queuing_on(x)

queuing_off(x)

get_hist_total(x)

get_transition_probability(x)

get_status(x)

get_reproductive_number(x)

Arguments

x	An object of class <code>epiworld_sir</code> , <code>epiworld_seir</code> , etc. any model.
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See Also

Other Models: [ModelSEIRCONN\(\)](#), [ModelSEIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIR\(\)](#), [ModelSIS\(\)](#), [ModelSURV\(\)](#)

Description

Common methods for predefined models of Epiworld

Usage

```
init(m, days, seed)

agents_smallworld(m, n, k, d, p)

run(m)
```

Arguments

m, days, seed, n, k, d, p
to be explained

Description

Susceptible Infected Susceptible model (SEIR)

Usage

```
ModelSEIR(name, prevalence, infectiousness, incubation_days, recovery)

## S3 method for class 'epiworld_seir'
init(m, days, seed)

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

## S3 method for class 'epiworld_seir'
agents_smallworld(m, n, k, d, p)

## S3 method for class 'epiworld_seir'
run(m)

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

Arguments

name	Name of the virus
prevalence	a number
infectiousness	a number
incubation_days	a number
recovery	a number
m	to be documented
days	to be documented
seed	to be documented
x	to be documented
...	to be documented
n	to be documented
k	to be documented
d	to be documented
p	to be documented

See Also

Other Models: [ModelSEIRCONN\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIR\(\)](#), [ModelSIS\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

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.

Usage

```
ModelSEIRCONN(
  name,
  n,
  prevalence,
  reproductive_number,
  prob_transmission,
  incubation_days,
  prob_recovery
)

## S3 method for class 'epiworld_seirconn'
init(m, days, seed)

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

## S3 method for class 'epiworld_seirconn'
run(m)
```

Arguments

name	Name of the virus
n	Integer greater than zero. Population size.
prevalence	Initial proportion of individuals with the virus
reproductive_number	Numeric scalar. Reproductive number.
prob_transmission	Numeric scalar between 0 and 1. Probability of transmission.
incubation_days	Numeric scalar greater than 0. Average number of incubation days.
prob_recovery	a Numeric scalar between 0 and 1. Probability of recovery.
m	to be documented
days	to be documented
seed	to be documented
x	to be documented
...	to be documented

See Also

Other Models: [ModelSEIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIR\(\)](#), [ModelSIS\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

ModelSIR	<i>SIR model</i>
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Description

SIR model

Usage

```
ModelSIR(name, prevalence, infectiousness, recovery)
```

```
## S3 method for class 'epiworld_sir'
init(m, days, seed)
```

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

```
## S3 method for class 'epiworld_sir'
agents_smallworld(m, n, k, d, p)
```

```
## S3 method for class 'epiworld_sir'
run(m)
```

Arguments

name	Name of the virus
prevalence	a number
infectiousness	a number
recovery	a number
m, days, seed, x, ..., n, k, d, p	to be documented

See Also

Other Models: [ModelSEIRCONN\(\)](#), [ModelSEIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIS\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

ModelSIRCONN

*Susceptible Infected Removed model (SIR connected)***Description**

Susceptible Infected Removed model (SIR connected)

Usage

```
ModelSIRCONN(
  name,
  n,
  prevalence,
  reproductive_number,
  prob_transmission,
  prob_recovery
)

## S3 method for class 'epiworld_sirconn'
init(m, days, seed)

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

## S3 method for class 'epiworld_sirconn'
run(m)
```

Arguments

name	Name of the virus
n, m, days, seed, x, ...	to be documented
prevalence	a number
reproductive_number	a number
prob_transmission	a number
prob_recovery	a number

See Also

Other Models: [ModelSEIRCONN\(\)](#), [ModelSEIR\(\)](#), [ModelSIR\(\)](#), [ModelSIS\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

ModelSIS	<i>Susceptible Infected Susceptible model (SIS)</i>
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Description

Susceptible Infected Susceptible model (SIS)

Usage

```
ModelSIS(name, prevalence, infectiousness, recovery)
```

```
## S3 method for class 'epiworld_sis'
init(m, days, seed)
```

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

```
## S3 method for class 'epiworld_sis'
agents_smallworld(m, n, k, d, p)
```

```
## S3 method for class 'epiworld_sis'
run(m)
```

Arguments

name	Name of the virus
prevalence	a number
infectiousness	a number
recovery	a number
m, days, seed, x, ..., n, k, d, p	to be documented

See Also

Other Models: [ModelSEIRCONN\(\)](#), [ModelSEIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIR\(\)](#), [ModelSURV\(\)](#), [epiworld-data](#)

ModelSURV

Susceptible Infected Susceptible model (SURV)

Description

Susceptible Infected Susceptible model (SURV)

Usage

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

## S3 method for class 'epiworld_surv'
init(m, days, seed)

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

## S3 method for class 'epiworld_surv'
agents_smallworld(m, n, k, d, p)

## S3 method for class 'epiworld_surv'
run(m)
```

Arguments

name	Name of the virus
prevalence	a number
efficacy_vax	to be explained
latent_period	to be explained
prob_symptoms	to be explained
prop_vaccinated	
	to be explained
prop_vax_redux_transm	
	to be explained
infect_period	to be explained

prop_vax_redux_infect
to be explained
surveillance_prob
to be explained
prob_transmission
to be explained
prob_death to be explained
prob_noreinfect
to be explained
m, days, seed, x, ..., n, k, d, p
to be explained

See Also

Other Models: [ModelSEIRCONN\(\)](#), [ModelSEIR\(\)](#), [ModelSIRCONN\(\)](#), [ModelSIR\(\)](#), [ModelSIS\(\)](#),
[epiworld-data](#)

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