

Package ‘epiworldRShiny’

July 22, 2025

Type Package

Title A 'shiny' Wrapper of the R Package 'epiworldR'

Version 0.2.3

Date 2025-04-30

Description R 'shiny' web apps for epidemiological Agent-Based Models. It provides a user-friendly interface to the Agent-Based Modeling (ABM) R package 'epiworldR' (Meyer et al., 2023) <[DOI:10.21105/joss.05781](https://doi.org/10.21105/joss.05781)>. Some of the main features of the package include the Susceptible-Infected-Susceptible (SIS), Susceptible-Infected-Recovered (SIR), and Susceptible-Exposed-Infected-Recovered (SEIR) models. 'epiworldR-Shiny' provides a web-based user interface for running various epidemiological ABMs, simulating interventions, and visualizing results interactively.

URL <https://github.com/UofUEpiBio/epiworldRShiny/>,
<https://uofuepibio.github.io/epiworldRShiny/>,

BugReports <https://github.com/UofUEpiBio/epiworldRShiny/issues/>

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RoxygenNote 7.3.2

Encoding UTF-8

Suggests knitr

Imports utils, DT, ggplot2, epiworldR, plotly, bslib

Depends R (>= 4.1.0), shiny

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-05-14 14:50:02 UTC

Contents

epiworldRenv	2
epiworldRShiny	3
epiworldrshiny-ui	3
find_scale	5
interventions_add_all	6
npi_add_masking	6
npi_add_school_closure	7
pi_add_vaccine	8
plot_epi	9
plot_reproductive_epi	10
pop_generator	10
Index	12

epiworldRenv	<i>Access to the epiworldR environment.</i>
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Description

This function is for internal use only.

Usage

epiworldRenv()

Value

Returns the epiworldR_env environment.

`epiworldRShiny`*epiworldRShiny App Launcher*

Description

Fires up the R Shiny App. You can find more examples and documentation at the package's website: <https://UofUEpiBio.github.io/epiworldRShiny/>.

`run_app` is a wrapper for the `epiworldRShiny` function. It is a convenience function to run the app.

Usage

```
epiworldRShiny(custom_models_path = NULL, ...)
```

```
run_app(custom_models_path = NULL, ...)
```

Arguments

<code>custom_models_path</code>	Optional path to custom model files (see details).
<code>...</code>	Currently ignored.

Details

When `custom_models_path` is specified, the function will look for valid model files at the specified path. These will be added to the list of available models. The function expects R files named `shiny_<model_name>.R` which contain the model. The function will also look for optional Markdown files named `shiny_<model_name>.md` which contain the model description.

Value

Loads and opens the R shiny app for the `epiworldR` package

`epiworldrshiny-ui`*epiworldRShiny UI builder functions*

Description

All functions in this section are for internal use only. They are used to build the UI for the `epiworldRShiny` app.

Usage

```
text_input_disease_name(model_name)

slider_prevalence(model_name)

numeric_input_ndays(model_name)

slider_input_rate(model_name, rate_name, value, maxval = 1, input_label = NULL)

network_input(model_name)

npis_input(model_name)

seed_input(model_name)

models_setup(custom_models_path = NULL)

population_input(model_name)

simulate_button(model_name)
```

Arguments

model_name	Name of the epiworldR model.
rate_name	Name of the rate.
value	Initial value for the slider.
maxval	Maximum value for the slider.
input_label	Aids in creating the appropriate slider name.
custom_models_path	Optional path to custom model files (see details).

Details

When `custom_models_path` is specified, the function will look for valid model files at the specified path. These will be added to the list of available models. The function expects R files named `shiny_<model_name>.R` which contain the model.

Value

- Unless otherwise specified, returns an object of class `shiny.tag`.
- `network_input` returns an object of class `shiny::tagList` (`shiny.tag.list`).
- `npis_input` returns an object of class `shiny::tagList` (`shiny.tag.list`).
- `models_setup` returns an object of class `list`.
- `population_input` returns an object of class `shiny.tag.list`.

Examples

```

text_input_disease_name("SEIRD")
slider_prevalence("SEIRD")
numeric_input_ndays("SEIRD")
slider_input_rate("SEIRD", "transmission", value = 0.3, maxval = 1,
input_label = NULL)
network_input("SEIRD")
npis_input("SEIRD")
seed_input("SEIRD")
# Setup with default models only:
models_setup()
# Setup with default and custom models:
## Not run: models_setup(custom_models_path = "path/to/custom/models")
population_input("SEIRD")
simulate_button("SEIRD")

```

find_scale

Find the right plotting-scale

Description

This function determines the scale of the y-axis for plot_epi.

Usage

```
find_scale(x)
```

Arguments

x The maximum value found in the model state counts

Value

An integer representing the scale for the y-axis. A max counts value of 10000 will return a scale of 1, 100000 will return a scale of 1000, 1000000 will return a scale of 10000.

See Also

Other Server side functions: [plot_epi\(\)](#), [plot_reproductive_epi\(\)](#), [pop_generator\(\)](#)

Examples

```
find_scale(100000)
```

interventions_add_all *NPI adding function*

Description

NPI adding function

Usage

```
interventions_add_all(model, modelname, input)
```

Arguments

model	epiworldR model.
modelname	Specified model.
input	User epiworldR model selection.

Value

Returns an object of class epiworld_model, where model is substituted with the model name.

See Also

Other interventions: [npi_add_masking\(\)](#), [npi_add_school_closure\(\)](#), [pi_add_vaccine\(\)](#)

npi_add_masking *Masking intervention (non-pharmaceutical intervention)*

Description

Masking intervention (non-pharmaceutical intervention)

Usage

```
npi_add_masking(model, preval, transmission_reduction)
```

Arguments

model	epiworldR model.
preval	Prevalence of masking within the population.
transmission_reduction	Reduction in transmission probability due to masking

Value

Returns an object of class epiworld_model, where model is substituted with the model name.

See Also

Other interventions: [interventions_add_all\(\)](#), [npi_add_school_closure\(\)](#), [pi_add_vaccine\(\)](#)

Examples

```
library(epiworldR) # for ModelSEIRCONN function
model <- ModelSEIRCONN("COVID-19", n = 1000, prevalence = 0.05,
                        contact_rate = 4, transmission_rate = 0.1,
                        incubation_days = 7, recovery_rate = 0.14)
run(model, ndays = 100, seed = 123)
npi_add_masking(model, preval = .8, transmission_reduction = .7)
```

npi_add_school_closure

School closure intervention (non-pharmaceutical intervention)

Description

School closure intervention (non-pharmaceutical intervention)

Usage

```
npi_add_school_closure(model, preval, day, transmission_reduction)
```

Arguments

model	epiworldR model.
preval	Prevalence of school closure within the population.
day	Day in the simulation where school closure goes into effect.
transmission_reduction	Reduction in transmission probability due to school closure.

Value

Returns an object of class `epiworld_model`, where `model` is substituted with the model name.

See Also

Other interventions: [interventions_add_all\(\)](#), [npi_add_masking\(\)](#), [pi_add_vaccine\(\)](#)

Examples

```
library(epiworldR) # for ModelSEIRCONN function
model <- ModelSEIRCONN("COVID-19", n = 1000, prevalence = 0.05,
                        contact_rate = 4, transmission_rate = 0.1,
                        incubation_days = 7, recovery_rate = 0.14)
run(model, ndays = 100, seed = 123)
npi_add_school_closure(model, preval = .8, transmission_reduction = .3, day = 10)
```

pi_add_vaccine	<i>Vaccination (pharmaceutical intervention)</i>
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Description

Vaccination (pharmaceutical intervention)

Usage

```
pi_add_vaccine(
  model,
  preval,
  susceptibility_reduction,
  transmission_reduction,
  recovery_enhancer,
  death_reduction
)
```

Arguments

model	epiworldR model.
preval	Initial prevalence of the vaccine.
susceptibility_reduction	Reduction in susceptibility probability due to vaccine.
transmission_reduction	Reduction in transmission probability due to vaccine.
recovery_enhancer	Probability increase in recovery due to vaccine.
death_reduction	Reduction in death probability due to vaccine.

Value

Returns an object of class epiworld_model, where model is substituted with the model name.

See Also

Other interventions: [interventions_add_all\(\)](#), [npi_add_masking\(\)](#), [npi_add_school_closure\(\)](#)

Examples

```
library(epiworldR) # for ModelSEIRCONN function
model <- ModelSEIRCONN("COVID-19", n = 1000, prevalence = 0.05,
  contact_rate = 4, transmission_rate = 0.1,
  incubation_days = 7, recovery_rate = 0.14)
run(model, ndays = 100, seed = 123)
pi_add_vaccine(model, preval = .8, susceptibility_reduction = .9,
```



```
transmission_reduction = .5, recovery_enhancer = .5,  
death_reduction = .9)
```

plot_epi

Plot daily incidence

Description

This function generates a plot of the model states over time

Usage

```
plot_epi(model, mark_max)
```

Arguments

model	The number of individuals in the population.
mark_max	The state which will have a mark at the peak

Value

A plot displaying each state from the model over the course of the simulation

See Also

Other Server side functions: [find_scale\(\)](#), [plot_reproductive_epi\(\)](#), [pop_generator\(\)](#)

Examples

```
library(epiworldR) # for ModelSEIRCONN function  
model <- ModelSEIRCONN("COVID-19", n = 1000, prevalence = 0.05,  
  contact_rate = 4, transmission_rate = 0.1,  
  incubation_days = 7, recovery_rate = 0.14)  
run(model, ndays = 100, seed = 123)  
plot_epi(model, mark_max = "Infected")
```

plot_reproductive_epi *Plot Rt*

Description

This function generates a plot of the reproductive number over time

Usage

```
plot_reproductive_epi(model)
```

Arguments

model The model object

Value

A plot displaying the reproductive number for the model over the course of the simulation

See Also

Other Server side functions: [find_scale\(\)](#), [plot_epi\(\)](#), [pop_generator\(\)](#)

Examples

```
library(epiworldR) # for ModelSEIRCONN function
model <- ModelSEIRCONN("COVID-19", n = 1000, prevalence = 0.05,
                       contact_rate = 4, transmission_rate = 0.1,
                       incubation_days = 7, recovery_rate = 0.14)
run(model, ndays = 100, seed = 123)
plot_reproductive_epi(model)
```

pop_generator *Population generator*

Description

This function generates a population matrix with specified characteristics.

Usage

```
pop_generator(
  n,
  prop_hispanic = 0.5,
  prop_female = 0.5,
  prop_19_59_60plus = c(0.3, 0.6)
)
```

Arguments

<code>n</code>	The number of individuals in the population.
<code>prop_hispanic</code>	The proportion of individuals who are Hispanic. Default is 0.5.
<code>prop_female</code>	The proportion of individuals who are female. Default is 0.5.
<code>prop_19_59_60plus</code>	A vector of length 3 representing the proportions of individuals in the age groups 0-19, 20-59, and 60+. Default is <code>c(0.5, 0.3, 0.2)</code> .

Value

A matrix representing the generated population, with columns for age groups (0-19, 20-59, 60+), NotHispanic, and Female.

See Also

Other Server side functions: [find_scale\(\)](#), [plot_epi\(\)](#), [plot_reproductive_epi\(\)](#)

Examples

```
pop_generator(n = 1000, prop_hispanic = .5, prop_female = .5,  
             prop_19_59_60plus = c(.3, .6))
```

Index

* Server side functions

- find_scale, [5](#)
- plot_epi, [9](#)
- plot_reproductive_epi, [10](#)
- pop_generator, [10](#)

* interventions

- interventions_add_all, [6](#)
- npi_add_masking, [6](#)
- npi_add_school_closure, [7](#)
- pi_add_vaccine, [8](#)

* npis

- npi_add_masking, [6](#)

epiworldRenv, [2](#)

epiworldRShiny, [3](#)

epiworldrshiny-ui, [3](#)

find_scale, [5](#), [9–11](#)

interventions_add_all, [6](#), [7](#), [8](#)

models_setup (epiworldrshiny-ui), [3](#)

network_input (epiworldrshiny-ui), [3](#)

npi_add_masking, [6](#), [6](#), [7](#), [8](#)

npi_add_school_closure, [6](#), [7](#), [7](#), [8](#)

npis_input (epiworldrshiny-ui), [3](#)

numeric_input_ndays
(epiworldrshiny-ui), [3](#)

pi_add_vaccine, [6](#), [7](#), [8](#)

plot_epi, [5](#), [9](#), [10](#), [11](#)

plot_reproductive_epi, [5](#), [9](#), [10](#), [11](#)

pop_generator, [5](#), [9](#), [10](#), [10](#)

population_input (epiworldrshiny-ui), [3](#)

run_app (epiworldRShiny), [3](#)

seed_input (epiworldrshiny-ui), [3](#)

shiny::tagList, [4](#)

simulate_button (epiworldrshiny-ui), [3](#)

slider_input_rate (epiworldrshiny-ui), [3](#)

slider_prevalence (epiworldrshiny-ui), [3](#)

text_input_disease_name
(epiworldrshiny-ui), [3](#)