

Package: epiworldRShiny (via r-universe)

November 19, 2024

Type Package

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

Version 0.1-0

Date 2024-05-31

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>. 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. 'epiworldRShiny' 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 7.3.1

Encoding UTF-8

Roxygen list(markdown = TRUE)

Suggests knitr

Imports shinyjs, utils, shinydashboard, DT, ggplot2, epiworldR,
shinycssloaders, plotly

Depends shiny

Config/pak/sysreqs make libicu-dev libssl-dev zlib1g-dev

Repository <https://epiverse-connect.r-universe.dev>

RemoteUrl <https://github.com/UofUEpiBio/epiworldRShiny>

RemoteRef HEAD

RemoteSha a4da9edd91446860663e46a380d2bb3337aa7e1c

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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	<i>epiworldRShiny App Launcher</i>
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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(...)
```

```
run_app(...)
```

Arguments

... Currently ignored.

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()
```

```
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.

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")
models_setup()
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

<code>model</code>	epiworldR model.
<code>preval</code>	Prevalence of school closure within the population.
<code>day</code>	Day in the simulation where school closure goes into effect.
<code>transmission_reduction</code>	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

`n` The number of individuals in the population.

`prop_hispanic` The proportion of individuals who are Hispanic. Default is 0.5.

`prop_female` The proportion of individuals who are female. Default is 0.5.

`prop_19_59_60plus` A vector of length 3 representing the proportions of individuals in the age groups 0-19, 20-59, and 60+. Default is `c(0.5, 0.3, 0.2)`.

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))
```

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