# Package: measles (via r-universe)

May 6, 2026

**Type** Package

**Title** Measles Epidemiological Models

**Version** 0.3.1-0

**Depends** R (>= 4.1.0), epiworldR (>= 0.14.99.99)

**Description** A specialized collection of measles epidemiological models built on the 'epiworldR' framework. This package is a spinoff from 'epiworldR' focusing specifically on measles transmission dynamics. It includes models for school settings with quarantine and isolation policies, mixing models with population groups, and risk-based quarantine strategies. The models use Agent-Based Models (ABM) with a fast 'C++' backend from the 'epiworld' library. Ideal for studying measles outbreaks, vaccination strategies, and intervention policies.

**URL** `https://github.com/UofUEpiBio/measles`

**BugReports** `https://github.com/UofUEpiBio/measles/issues`

**License** MIT + file LICENSE

**RoxygenNote** 7.3.3

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**LinkingTo** cpp11, epiworldR (>= 0.14.99.99)

**SystemRequirements** C++17

**Imports** utils, stats

**Suggests** tinytest, data.table, quarto, multigroup.vaccine

**VignetteBuilder** quarto

**LazyData** true

**Remotes** UofUEpiBio/epiworldR

**Repository** https://uofuepibio.r-universe.dev

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**RemoteUrl** https://github.com/UofUEpiBio/measles

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# Contents

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## `calibrate_mixing_model` *Calibrate a mixing model to a target reproduction number*

---

### Description

Uses the `epiworldR::compute_reproduction_number()` function to optimize the scaling factor of the contact matrix to match a target reproduction number.

### Usage

```
calibrate_mixing_model(
  contact_matrix,
  target_rep_number,
  infectious_period_days,
  transmission_prob,
  ...
)
```

### Arguments

| | |
|---|---|
| `contact_matrix` | A contact matrix to be calibrated. |
| `target_rep_number` | The target reproduction number to calibrate to. |
| `infectious_period_days` | The average number of days an individual is infectious. |
| `transmission_prob` | The probability of transmission per contact. |
| `...` | Additional arguments to pass to `stats::optimize()`. |

### Value

The scaling factor for the contact matrix that achieves the target reproduction number.

### Examples

```
data(short_creek_matrix, package = "measles")

# Calibrating for a measles model with R0 of 10
# assuming agents are infectious during prodomal stage
# (isolated during rash stage)
calibrate_mixing_model(
  contact_matrix = short_creek_matrix,
  target_rep_number = 10,
  infectious_period_days = 4,
  transmission_prob = 0.2
)

# You can then use the scaling factor in a mixing
# model. Instead of using the original contact matrix,
# you would use:
#   contact_matrix * scaling_factor
```

---

## `contact_matrix` *Get and Set Contact Matrix*

---

### Description

These functions allow getting and setting the contact matrix for measles mixing models. The contact matrix specifies the mixing patterns between different population groups.

### Usage

```
get_contact_matrix(model)

## Default S3 method:
get_contact_matrix(model)

## S3 method for class 'epiworld_measlesmixing'
get_contact_matrix(model)

## S3 method for class 'epiworld_measlesmixingriskquarantine'
get_contact_matrix(model)

set_contact_matrix(model, value)

## Default S3 method:
set_contact_matrix(model, value)

## S3 method for class 'epiworld_measlesmixing'
set_contact_matrix(model, value)

## S3 method for class 'epiworld_measlesmixingriskquarantine'
set_contact_matrix(model, value)
```

## Arguments

| | |
|---|---|
| `model` | An epiworld model object of class `epiworld_measlesmixing` or `epiworld_measlesmixingriskquaran` |
| `value` | A numeric square matrix representing contact rates between population groups. The matrix should have one row and one column per entity in the model. |

## Details

Entry `[i, j]` of the contact matrix represents the expected number of contacts that an individual in group `i` has with individuals in group `j` during a time step.

These functions are currently only available for:

- ModelMeaslesMixing
- ModelMeaslesMixingRiskQuarantine

Other mixing models in epiworld will have these methods available in the near future.

## Value

- `get_contact_matrix()` returns a numeric matrix representing the contact rates between population groups.
- `set_contact_matrix()` returns the model object invisibly (called for its side effects).

## Examples

```r
# Create entities for three population groups
e1 <- entity("Population 1", 1000, as_proportion = FALSE)
e2 <- entity("Population 2", 1000, as_proportion = FALSE)
e3 <- entity("Population 3", 1000, as_proportion = FALSE)

# Create an identity contact matrix (no mixing between groups)
cmatrix <- diag(3) * 15

N <- 3000

# Create a measles mixing model
model <- ModelMeaslesMixing(
  n                         = N,
  prevalence                = 1 / N,
  transmission_rate         = 0.9,
  vax_efficacy              = 0.97,
  vax_reduction_recovery_rate = 0.8,
  incubation_period         = 10,
  prodromal_period          = 3,
  rash_period               = 7,
  contact_matrix            = cmatrix,
  hospitalization_rate      = 0.1,
  hospitalization_period    = 10,
  days_undetected           = 2,
  quarantine_period         = 14,
  quarantine_willingness    = 0.9,
```

```
  isolation_willingness    = 0.8,
  isolation_period         = 10,
  prop_vaccinated          = 0.95,
  contact_tracing_success_rate = 0.8,
  contact_tracing_days_window = 4
)

# Add entities to the model
model |>
  add_entity(e1) |>
  add_entity(e2) |>
  add_entity(e3)

# Get the contact matrix (note: requires running the model first)
set.seed(123)
run(model, ndays = 10)
original_matrix <- get_contact_matrix(model)
print(original_matrix)

# Create a new contact matrix
new_matrix <- matrix(
  c(12, 1.5, 1.5,
    2, 11, 2,
    2.25, 2.25, 10.5),
  nrow = 3, byrow = TRUE
)

# Set the new contact matrix
set_contact_matrix(model, new_matrix)

# Verify the change
updated_matrix <- get_contact_matrix(model)
print(updated_matrix)
```

---

`InterventionMeaslesPEP`

## *Create a measles post-exposure prophylaxis (PEP) intervention*

---

### Description

Create a measles post-exposure prophylaxis (PEP) intervention

### Usage

```
InterventionMeaslesPEP(
  name,
  mmr_efficacy,
  ig_efficacy,
  ig_half_life_mean,
```

```
  ig_half_life_sd,
  mmr_willingness,
  ig_willingness,
  mmr_window,
  ig_window,
  target_states,
  states_if_pep_effective,
  states_if_pep_ineffective
)
```

## Arguments

| | |
|---|---|
| `name` | Name of the intervention. |
| `mmr_efficacy` | Probability of MMR vaccine efficacy. |
| `ig_efficacy` | Probability of immunoglobulin (IG) efficacy. |
| `ig_half_life_mean` | Mean of the half-life of immunoglobulin (IG) in days. |
| `ig_half_life_sd` | Standard deviation of the half-life of immunoglobulin (IG) in days. |
| `mmr_willingness` | Probability that an individual will accept MMR vaccine. |
| `ig_willingness` | Probability that an individual will accept immunoglobulin (IG). |
| `mmr_window` | Time window for MMR vaccine administration. |
| `ig_window` | Time window for immunoglobulin (IG) administration. |
| `target_states`, `states_if_pep_effective`, `states_if_pep_ineffective` | Integer vectors of target and destination states (see details). |

## Details

This functions creates a global event that represents a post-exposure prophylaxis (PEP) intervention for measles. The intervention includes the administration of MMR vaccine and immunoglobulin (IG) to individuals after exposure to the virus, with the goal of reducing the probability of infection and preventing the spread of the disease.

The process involves both PEP Measles-Mumps-Rubella (MMR) vaccine and immunoglobulin (IG). The system decides which agent gets MMR or IG based on the time since exposure and the willingness to accept PEP. The flow is the following:

1. Agents in `target_states` are eligible for PEP if they are willing to accept it (based on `pep_willingness`).
2. If the agent is already infected (for example, in a latent state) for at most `mmr_window` days, they are offered MMR vaccine. Otherwise, they are offered IG.
3. Susceptible agents are offered the MMR vaccine, and if they accept, they are automatically moved out of the quarantine process.
4. Agents who were already infected and got either MMR or IG may move out of the quarantine process if the PEP is effective (based on `mmr_efficacy` or `ig_efficacy`). The destination state depends on whether the PEP was effective or not, and is determined by `states_if_pep_effective` and `states_if_pep_ineffective`, respectively.

Since IG winds down over time, the IG "tool" may be removed from the agent as a function of the half-life of IG (based on `ig_half_life_mean` and `ig_half_life_sd`). Particularly, after applied, the IG "tool" will have a random duration based on a normal distribution with mean `ig_half_life_mean` and standard deviation `ig_half_life_sd`. Once the duration is over, the IG "tool" is removed from the agent, and they are again eligible for PEP if they are exposed again.

### Value

An object of class `epiworld_globalevent` representing the measles PEP intervention.

### See Also

epiworldR::global-events

---

## `ModelMeaslesMixing` *Measles model with mixing*

### Description

`ModelMeaslesMixing` creates a measles epidemiological model with mixing between different population groups. The model includes vaccination, quarantine, isolation, and contact tracing mechanisms.

### Usage

```
ModelMeaslesMixing(
  n,
  prevalence,
  contact_matrix,
  vax_reduction_recovery_rate = 0.5,
  transmission_rate = 0.9,
  prop_vaccinated,
  vax_efficacy = 0.97,
  quarantine_period = 21,
  quarantine_willingness = 1,
  isolation_willingness = 1,
  isolation_period = 4,
  incubation_period = 12,
  prodromal_period = 4,
  rash_period = 3,
  hospitalization_rate = 0.2,
  hospitalization_period = 7,
  days_undetected = 2,
  contact_tracing_success_rate = 1,
  contact_tracing_days_window = 4
)
```

## Arguments

| | |
|---|---|
| `n` | Number of individuals in the population. |
| `prevalence` | Double. Initial proportion of individuals with the virus. |
| `contact_matrix` | A numeric square matrix with the expected number of contacts per time step between population groups. |
| `vax_reduction_recovery_rate` | Double. Vaccine reduction in recovery rate (default: 0.5). |
| `transmission_rate` | Numeric scalar between 0 and 1. Probability of transmission (default: 0.9). |
| `prop_vaccinated` | Double. Proportion of population that is vaccinated. |
| `vax_efficacy` | Double. Vaccine efficacy rate (default: 0.99). |
| `quarantine_period` | Integer. Number of days for quarantine (default: 21). |
| `quarantine_willingness` | Double. Proportion of agents willing to quarantine (default: 1). |
| `isolation_willingness` | Double. Proportion of agents willing to isolate (default: 1). |
| `isolation_period` | Integer. Number of days for isolation (default: 4). |
| `incubation_period` | Double. Duration of incubation period (default: 12). |
| `prodromal_period` | Double. Duration of prodromal period (default: 4). |
| `rash_period` | Double. Duration of rash period (default: 3). |
| `hospitalization_rate` | Double. Rate of hospitalization (default: 0.2). |
| `hospitalization_period` | Double. Period of hospitalization (default: 7). |
| `days_undetected` | Double. Number of days an infection goes undetected (default: 2). |
| `contact_tracing_success_rate` | Double. Probability of successful contact tracing (default: 1.0). |
| `contact_tracing_days_window` | Integer. Number of days before rash onset that will be considered for contact tracing (default: 4). |

## Details

The `contact_matrix` is a square matrix of contact rates between entities. Entry `[i, j]` gives the expected number of contacts that an agent in entity `i` has with agents in entity `j` during a time step. The matrix should have one row and one column per entity in the model.

The model includes three distinct phases of measles infection: incubation, prodromal, and rash periods. Vaccination provides protection against infection and may reduce recovery time.

The epiworldR::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 `ModelMeaslesMixing` function returns a model of classes epiworldR::epiworld_model and epiworld_measlesmixing.

### Hospitalization Probability

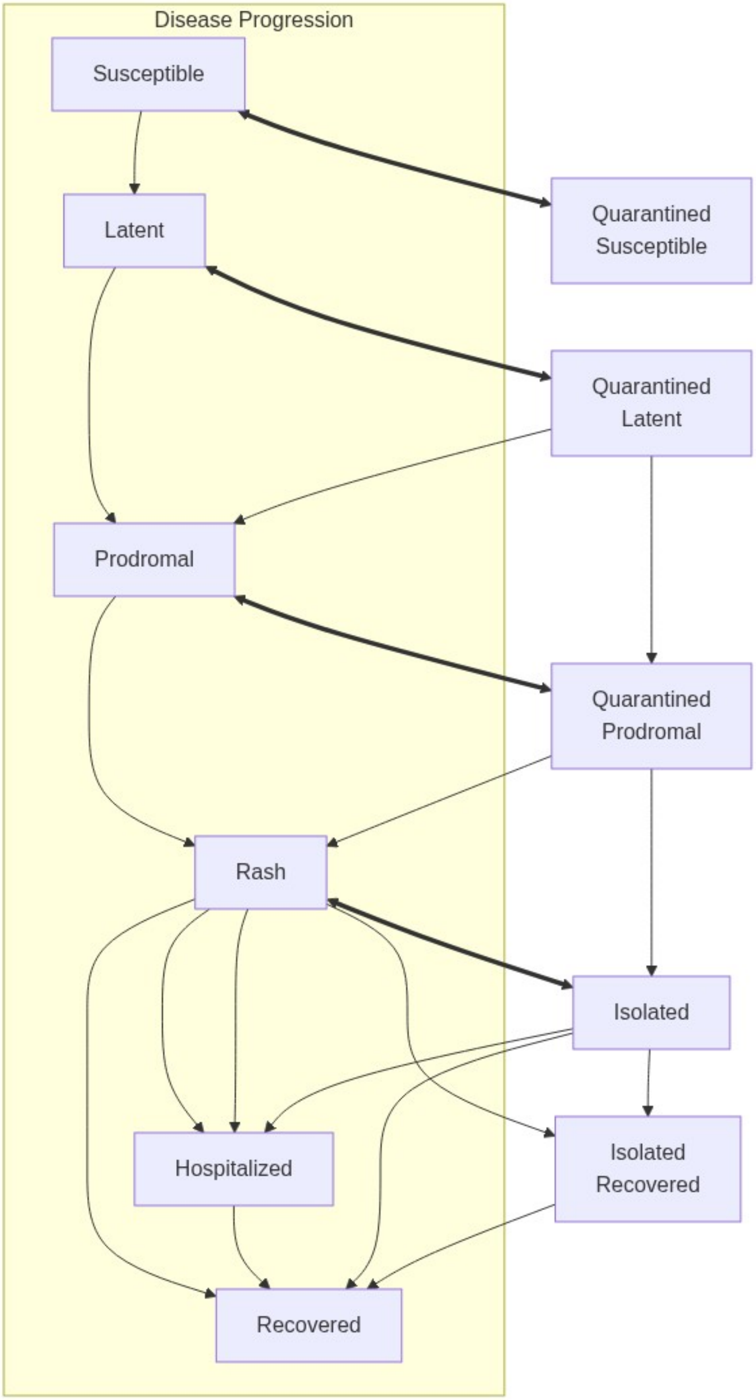
Instead of hospitalization probability, the model uses hospitalization rate. The following equation describes the hospitalization probability as a function of the hospitalization rate and recovery rate (from rash):

$$P(\text{hospitalization}) = \frac{\text{hospitalization}_{\text{rate}}}{\text{hospitalization}_{\text{rate}} + \text{recovery}_{\text{rate}}}$$

Where the $\text{recovery}_{\text{rate}}$ is given by the rash period (1/duration of it). In other words, to match a desired hospitalization probability, the user needs to use the following:

```
h_rate <- p_hosp * (1/rash_days) / (1 - p_hosp)
```

**Model diagram**



## See Also

epiworld-methods

Other Models: `ModelMeaslesMixingRiskQuarantine()`, `ModelMeaslesSchool()`

Other measles models: `ModelMeaslesMixingRiskQuarantine()`, `ModelMeaslesSchool()`

## 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)

# Contact matrix including within- and between-group contact rates
cmatrix <- (c(
  c(0.9, 0.05, 0.05),
  c(0.1, 0.8, 0.1),
  c(0.1, 0.2, 0.7)
) * 15) |> matrix(byrow = TRUE, nrow = 3)

N <- 9e3

measles_model <- ModelMeaslesMixing(
  n                         = N,
  prevalence                = 1 / N,
  transmission_rate         = 0.9,
  vax_efficacy              = 0.97,
  vax_reduction_recovery_rate = 0.8,
  incubation_period         = 10,
  prodromal_period          = 3,
  rash_period               = 7,
  contact_matrix            = cmatrix,
  hospitalization_rate      = 0.1,
  hospitalization_period    = 10,
  days_undetected           = 2,
  quarantine_period         = 14,
  quarantine_willingness    = 0.9,
  isolation_willingness     = 0.8,
  isolation_period          = 10,
  prop_vaccinated           = 0.95,
  contact_tracing_success_rate = 0.8,
  contact_tracing_days_window = 4
)

# Adding the entities to the model
measles_model |>
  add_entity(e1) |>
  add_entity(e2) |>
  add_entity(e3)

set.seed(331)
```

```
run(measles_model, ndays = 100)
summary(measles_model)
```

---

## `ModelMeaslesMixingRiskQuarantine` *Measles model with mixing and risk-based quarantine*

### Description

`ModelMeaslesMixingRiskQuarantine` creates a measles epidemiological model with mixing between different population groups and risk-based quarantine strategies. The model includes vaccination, quarantine with three risk levels (high, medium, low), isolation, and contact tracing mechanisms.

### Usage

```
ModelMeaslesMixingRiskQuarantine(
  n,
  prevalence,
  contact_matrix,
  transmission_rate = 0.9,
  prop_vaccinated,
  vax_efficacy = 0.97,
  quarantine_period_high = 21,
  quarantine_period_medium = 14,
  quarantine_period_low = 7,
  quarantine_willingness = 1,
  isolation_willingness = 1,
  isolation_period = 4,
  incubation_period = 12,
  prodromal_period = 4,
  rash_period = 3,
  hospitalization_rate = 0.2,
  hospitalization_period = 7,
  days_undetected = 2,
  detection_rate_quarantine = 0.5,
  contact_tracing_success_rate = 1,
  contact_tracing_days_window = 4
)
```

### Arguments

| | |
|---|---|
| `n` | Number of individuals in the population. |
| `prevalence` | Double. Initial proportion of individuals with the virus. |
| `contact_matrix` | A numeric square matrix with the expected number of contacts per time step between population groups. |

| | |
|---|---|
| `transmission_rate` | Numeric scalar between 0 and 1. Probability of transmission (default: 0.9). |
| `prop_vaccinated` | Double. Proportion of population that is vaccinated. |
| `vax_efficacy` | Double. Vaccine efficacy rate (default: 0.99). |
| `quarantine_period_high` | Integer. Number of days for quarantine for high-risk contacts (default: 21). |
| `quarantine_period_medium` | Integer. Number of days for quarantine for medium-risk contacts (default: 14). |
| `quarantine_period_low` | Integer. Number of days for quarantine for low-risk contacts (default: 7). |
| `quarantine_willingness` | Double. Proportion of agents willing to quarantine (default: 1). |
| `isolation_willingness` | Double. Proportion of agents willing to isolate (default: 1). |
| `isolation_period` | Integer. Number of days for isolation (default: 4). |
| `incubation_period` | Double. Duration of incubation period (default: 12). |
| `prodromal_period` | Double. Duration of prodromal period (default: 4). |
| `rash_period` | Double. Duration of rash period (default: 3). |
| `hospitalization_rate` | Double. Rate of hospitalization (default: 0.2). |
| `hospitalization_period` | Double. Period of hospitalization (default: 7). |
| `days_undetected` | Double. Number of days rash goes undetected (default: 2). |
| `detection_rate_quarantine` | Double. Detection rate of prodromal agents during active quarantine periods (default: 0.5). |
| `contact_tracing_success_rate` | Double. Probability of successful contact tracing (default: 1.0). |
| `contact_tracing_days_window` | Integer. Number of days before and after the onset of symptoms for which contact tracing is effective (default: 4). |

## Details

The `contact_matrix` is a square matrix of contact rates between entities. Entry `[i, j]` gives the expected number of contacts that an agent in entity `i` has with agents in entity `j` during a time step. The matrix should have one row and one column per entity in the model.

The model includes three distinct phases of measles infection: latent (incubation), prodromal, and rash periods. Vaccination provides protection against transmission.

Risk-based quarantine strategies assign different quarantine durations based on exposure risk:

- **High Risk**: Unvaccinated agents who share entity membership with the case
- **Medium Risk**: Unvaccinated agents who contacted an infected individual but don't share entity membership
- **Low Risk**: Other unvaccinated agents

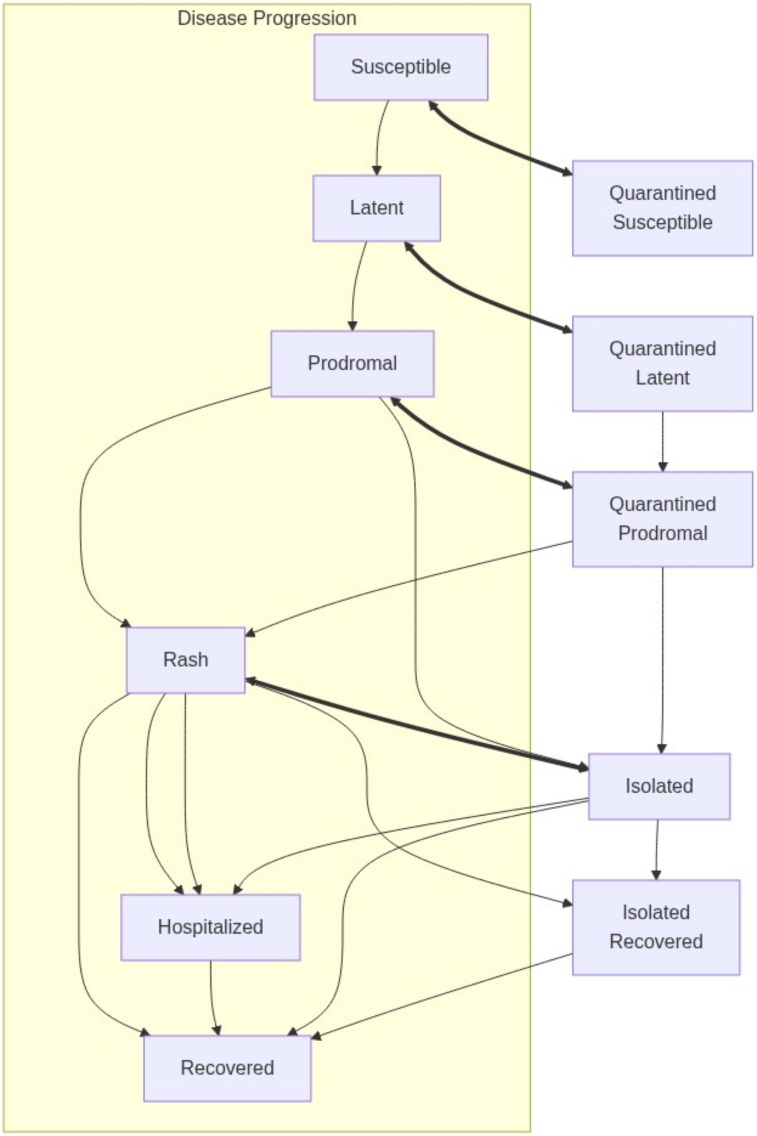
The epiworldR::initial_states function allows the user to set the initial state of the model. In particular, the user can specify how many of the non-infected agents have been removed at the beginning of the simulation.

The model uses hospitalization rates instead of probabilities. To learn more about this, see the documentation in `ModelMeaslesMixing()`.

## Value

- The `ModelMeaslesMixingRiskQuarantine` function returns a model of classes epiworldR::epiworld_model and epiworld_measlesmixingriskquarantine.

### Model diagram



### See Also

epiworld-methods

Other Models: `ModelMeaslesMixing()`, `ModelMeaslesSchool()`

Other measles models: `ModelMeaslesMixing()`, `ModelMeaslesSchool()`

### 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)

# Contact matrix including within- and between-group contact rates
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) * 15

N <- 9e3

measles_model <- ModelMeaslesMixingRiskQuarantine(
  n                         = N,
  prevalence                = 1 / N,
  transmission_rate         = 0.9,
  vax_efficacy              = 0.97,
  incubation_period         = 10,
  prodromal_period          = 3,
  rash_period               = 7,
  contact_matrix            = cmatrix,
  hospitalization_rate      = 0.1,
  hospitalization_period    = 10,
  days_undetected           = 2,
  quarantine_period_high    = 21,
  quarantine_period_medium  = 14,
  quarantine_period_low     = 7,
  quarantine_willingness    = 0.9,
  isolation_willingness     = 0.8,
  isolation_period          = 10,
  prop_vaccinated           = 0.95,
  detection_rate_quarantine = 0.5,
  contact_tracing_success_rate = 0.8,
  contact_tracing_days_window = 4
)

# Adding the entities to the model
measles_model |>
  add_entity(e1) |>
  add_entity(e2) |>
  add_entity(e3)

set.seed(331)
run(measles_model, ndays = 100)
summary(measles_model)
```

---

## `ModelMeaslesSchool` *Measles model with quarantine*

## Description

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

## Usage

```
ModelMeaslesSchool(
  n,
  prevalence = 1,
  contact_rate = 15/transmission_rate/prodromal_period,
  transmission_rate = 0.9,
  vax_efficacy = 0.97,
  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,
  ...
)

ModelMeaslesQuarantine(...)
```

## 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. |
| `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` | Number of days an agent is in quarantine. |
| `quarantine_willingness` | Probability of accepting quarantine ( see details). |
| `isolation_period` | Number of days an agent is in isolation. |
| `...` | Further arguments (not used). |

## Details

This model can be described as a SLIHR model with isolation and quarantine. The infectious state is divided into prodromal and rash phases. Furthermore, the quarantine state includes latent, 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 R0 matches 15.

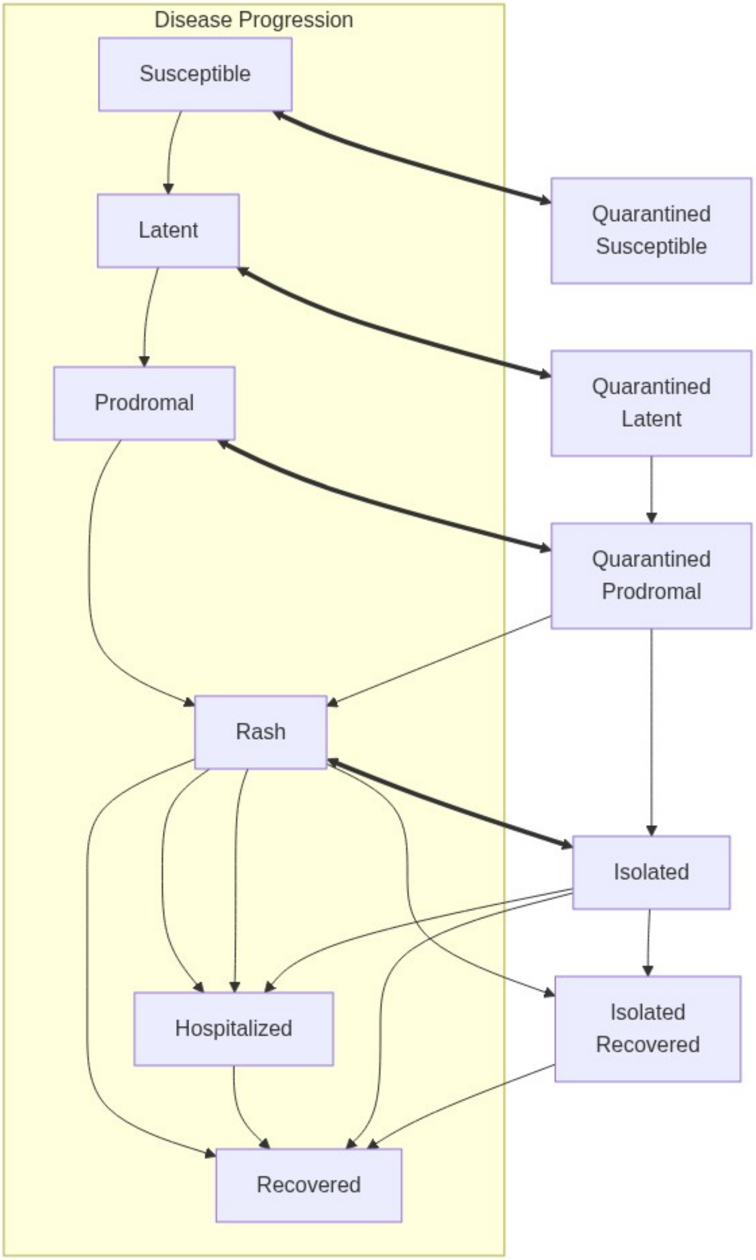
When `quarantine_period` is set to -1, the model assumes there is no quarantine process. The same happens with `isolation_period`. Since the quarantine process is triggered by an isolation, then `isolation_period = -1` automatically sets `quarantine_period = -1`.

The model uses hospitalization rates instead of probabilities. To learn more about this, see the documentation in `ModelMeaslesMixing()`.

## Value

- The `ModelMeaslesSchool` function returns a model of classes epiworldR::epiworld_model and `epiworld_measlesschool`.

### Model diagram



### Note

As of version 0.10.0, the parameter `vax_improved_recovery` has been removed and is no longer used (it never had a side effect). Future versions may not accept it.

### 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

Jones, Trahern W, and Katherine Baranowski. 2019. "Measles and Mumps: Old Diseases, New Outbreaks."

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: `ModelMeaslesMixing()`, `ModelMeaslesMixingRiskQuarantine()`

Other measles models: `ModelMeaslesMixing()`, `ModelMeaslesMixingRiskQuarantine()`

### Examples

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

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

plot(model_measles)
```

---

## `short_creek` *Short Creek Population Data by Age Group*

### Description

A dataset containing population information for the Short Creek area (Hildale city, Utah, Colorado City town, Arizona, and Centennial Park, Arizona) organized by age groups.

## Usage

```
short_creek
```

## Format

A data frame with 15 rows and 4 columns:

**age_labels** character. Labels describing the age groups.

**agepops** numeric. Population counts for each age group.

**agelims** numeric. Age limit boundaries for each group.

**vacc_rate** numeric. Vaccination rate for each age group.

## Details

This dataset provides demographic information for the Short Creek area (Hildale city, Utah, Colorado City town, Arizona, and Centenial Park, Arizona), with population data disaggregated by 15 age categories. This dataset matches the short_creek_matrix matrix.

This data uses real vaccination rates from publicly available school records, and population age structure and composition from the latest US census. Vaccination rates for the non-school-aged population were imputed based on assumptions and do not reflect the actual vaccination information for those age groups.

## Source

The data was generated using the `multigroup.vaccine` R package: Toth D (2025). *multigroup.vaccine: Multigroup Vaccine Model*. R package version 0.1.0, commit 3047ebf568c9b2028336dc14af587a282de9e225, `https://github.com/EpiForeSITE/multigroup-vaccine`. The source code is available at `https://github.com/UofUEpiBio/measles`

## Examples

```
data(short_creek)
head(short_creek)
```

---

# `short_creek_matrix` *Short Creek Mixing Matrix*

## Description

A matrix containing spatial data for the Short Creek area (Hildale city, Utah, Colorado City town, Arizona, and Centenial Park, Arizona). The matrix provides an estimate of the mixing rates between schools and the rest of the population in the area.

## Usage

```
short_creek_matrix
```

## Format

A row-stochastic matrix (rows add up to one) with 15 rows and 15 columns with the

## Source

The data was generated using the `multigroup.vaccine` R package: Toth D (2025). *multigroup.vaccine: Multigroup Vaccine Model*. R package version 0.1.0, commit 3047ebf568c9b2028336dc14af587a282de9e225, `https://github.com/EpiForeSITE/multigroup-vaccine`. The source code is available at `https://github.com/UofUEpiBio/measles`

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