

# Package ‘measles’

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**Type** Package

**Title** Measles Epidemiological Models

**Version** 0.2.0

**Depends** R (>= 4.1.0), epiworldR (>= 0.14.0.0)

**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

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**LinkingTo** cpp11, epiworldR

**SystemRequirements** C++17

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**Author** George Vega Yon [aut, cre] (ORCID:

<<https://orcid.org/0000-0002-3171-0844>>),

Damon Toth [ctb] (ORCID: <<https://orcid.org/0000-0001-7393-4814>>),

Jake Wagoner [ctb] (ORCID: <<https://orcid.org/0009-0000-5053-2281>>),

Olivia Banks [ctb] (ORCID: <<https://orcid.org/0009-0008-7611-6030>>),

Centers for Disease Control and Prevention [fnd] (Award number

1U01CK000585; 75D30121F00003)

**Maintainer** George Vega Yon <g.vegayon@gmail.com>

**Repository** CRAN

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## Contents

contact_matrix . . . . .	2
ModelMeaslesMixing . . . . .	4
ModelMeaslesMixingRiskQuarantine . . . . .	8
ModelMeaslesSchool . . . . .	12
short_creek . . . . .	16
short_creek_matrix . . . . .	17

**Index** **19**

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contact_matrix	<i>Get and Set Contact Matrix</i>
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## 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 <code>epiworld_measlesmixing</code> or <code>epiworld_measlesmixingriskquaran</code>
value	A row-stochastic matrix representing contact rates between population groups. The matrix should be square with dimensions matching the number of entities (population groups) in the model, and each row should sum to 1.

**Details**

The contact matrix is a row-stochastic matrix where entry  $[i, j]$  represents the probability that an individual in group  $i$  will make contact with someone in group  $j$ , given that they make a contact. Each row must sum to 1.

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**

```
# 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)

N <- 3000

# Create a measles mixing model
model <- ModelMeaslesMixing(
  n = N,
  prevalence = 1 / N,
  contact_rate = 15,
  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_prior = 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 random row-stochastic matrix
new_matrix <- matrix(
  c(0.8, 0.1, 0.1,
    0.1, 0.7, 0.2,
    0.15, 0.15, 0.7),
  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)

```

---

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,
contact_rate = 15/transmission_rate/prodromal_period,
prop_vaccinated,
vax_efficacy = 0.99,
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_prior = 4
)

```

### Arguments

n	Number of individuals in the population.
prevalence	Double. Initial proportion of individuals with the virus.
contact_matrix	A row-stochastic matrix of mixing proportions 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).
contact_rate	Numeric scalar. Average number of contacts per step.
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_prior	Integer. Number of days prior to the onset of the infection for which contact tracing is effective (default: 4).

### 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 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.

The default value for the contact rate is an approximation to the disease's basic reproduction number ( $R_0$ ), but it is not 100% accurate. A more accurate way to set the contact rate is available, and will be distributed in the future.

### Value

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

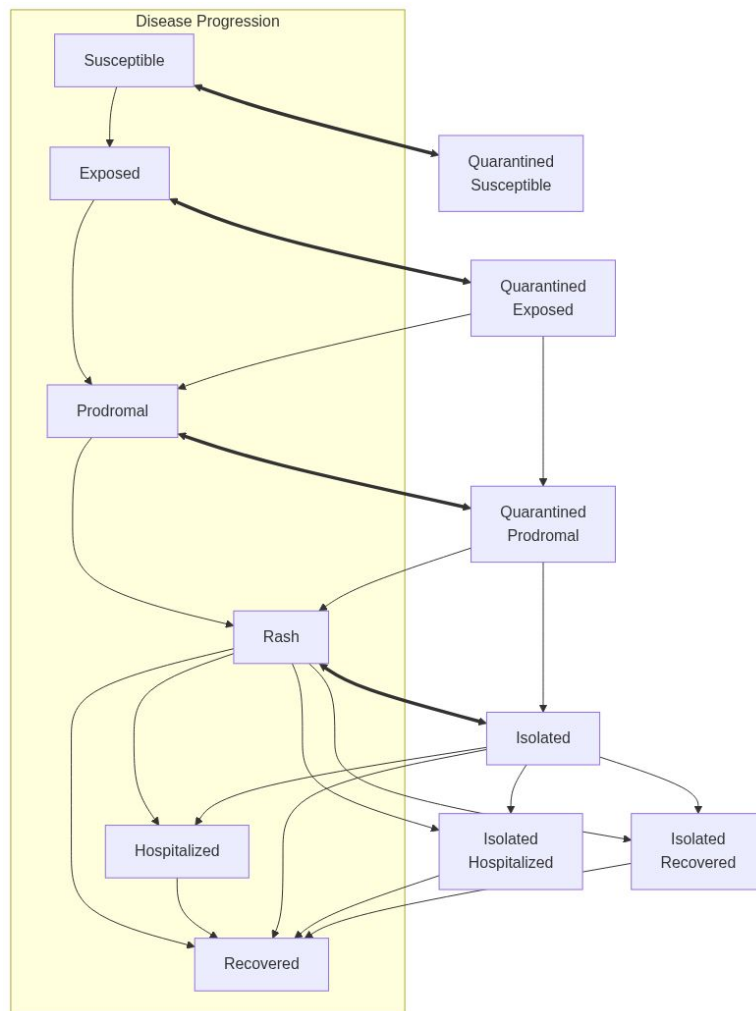
### Hospitalization Probability

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 ( $1/\text{duration}$  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)
  
```

```

# 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

measles_model <- ModelMeaslesMixing(
  n = N,
  prevalence = 1 / N,
  contact_rate = 15,
  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_prior = 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 vacci-



nation, quarantine with three risk levels (high, medium, low), isolation, and contact tracing mechanisms.

### Usage

```
ModelMeaslesMixingRiskQuarantine(
  n,
  prevalence,
  contact_matrix,
  transmission_rate = 0.9,
  contact_rate = 15/transmission_rate/prodromal_period,
  prop_vaccinated,
  vax_efficacy = 0.99,
  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_prior = 4
)
```

### Arguments

n	Number of individuals in the population.
prevalence	Double. Initial proportion of individuals with the virus.
contact_matrix	A row-stochastic matrix of mixing proportions between population groups.
transmission_rate	Numeric scalar between 0 and 1. Probability of transmission (default: 0.9).
contact_rate	Numeric scalar. Average number of contacts per step.
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_prior	Integer. Number of days prior to the onset of the infection for which contact tracing is effective (default: 4).

## 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 model includes three distinct phases of measles infection: incubation (exposed), 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.

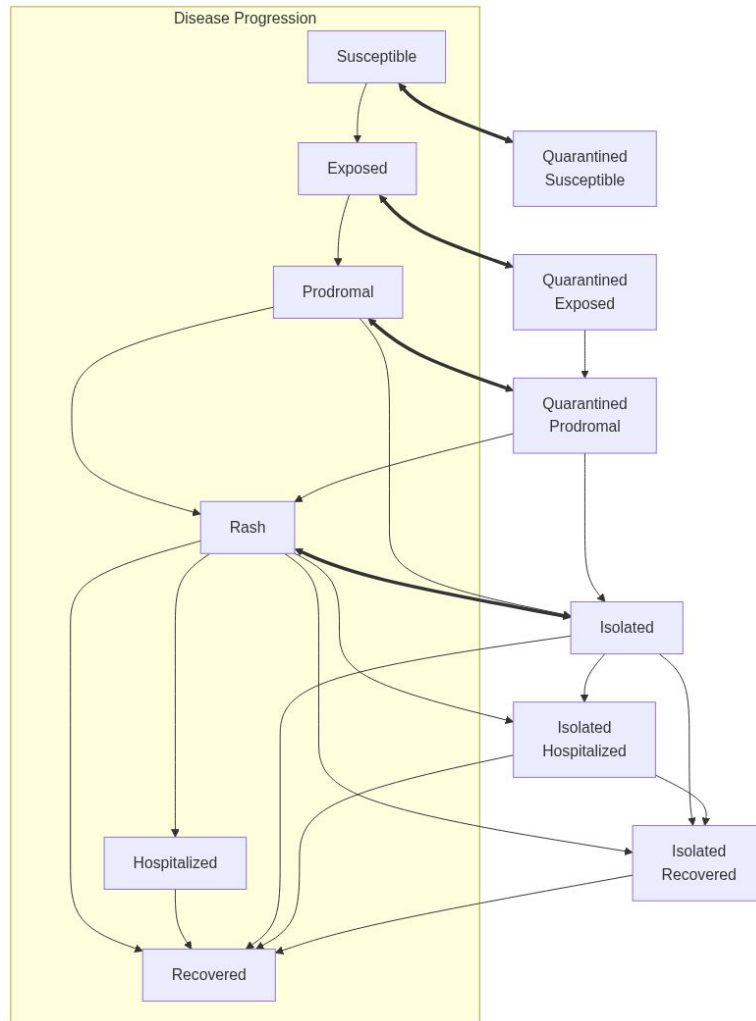
The default value for the contact rate is an approximation to the disease's basic reproduction number ( $R_0$ ), but it is not 100% accurate. A more accurate way to set the contact rate is available, and will be distributed in the future.

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)

# 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

measles_model <- ModelMeaslesMixingRiskQuarantine(
  n = N,
  prevalence = 1 / N,
  contact_rate = 15,
  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_prior = 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)

```

**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**

```
ModelMeaslesSchool(
  n,
  prevalence = 1,
  contact_rate = 15/transmission_rate/prodromal_period,
  transmission_rate = 0.9,
  vax_efficacy = 0.99,
  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**

<code>n</code>	Number of agents in the model.
<code>prevalence</code>	Initial number of agents with the virus.
<code>contact_rate</code>	Average number of contacts per step. Default is set to match the basic reproductive number (R0) of 15 (see details).
<code>transmission_rate</code>	Probability of transmission.
<code>vax_efficacy</code>	Probability of vaccine efficacy.
<code>incubation_period</code>	Average number of incubation days.
<code>prodromal_period</code>	Average number of prodromal days.
<code>rash_period</code>	Average number of rash days.
<code>days_undetected</code>	Average number of days undetected. Detected cases are moved to isolation and trigger the quarantine process.
<code>hospitalization_rate</code>	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 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.

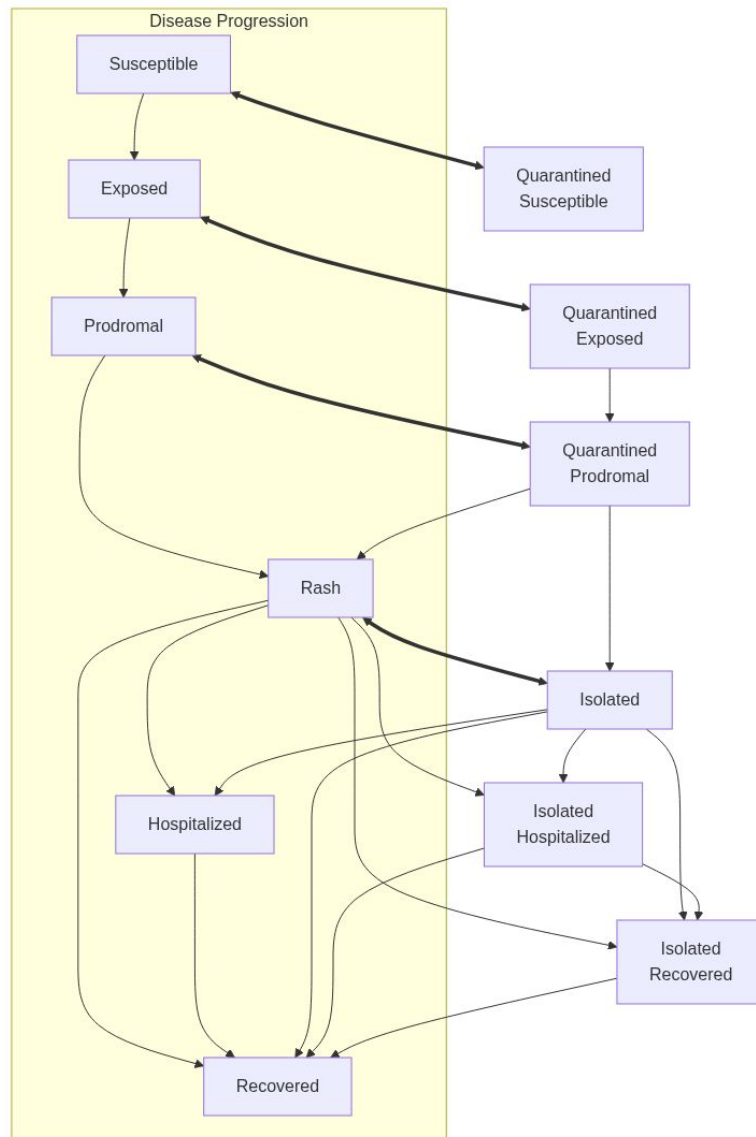
When `quarantine_period` is set to -1, the model assumes there is no quarantine process. The same happens with `isolation_period`. Since the quarantine process is triggered by an isolation, then `isolation_period = -1` automatically sets `quarantine_period = -1`.

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

## Value

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

**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 <- ModelMeaslesQuarantine(
  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 Centennial 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	<i>Short Creek Mixing Matrix</i>
--------------------	----------------------------------

---

## Description

A matrix containing spatial data for the Short Creek area (Hildale city, Utah, Colorado City town, Arizona, and Centennial 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>

# Index

## \* **Models**

ModelMeaslesMixing, [4](#)  
ModelMeaslesMixingRiskQuarantine,  
[8](#)  
ModelMeaslesSchool, [13](#)

## \* **datasets**

short\_creek, [16](#)  
short\_creek\_matrix, [17](#)

## \* **measles models**

ModelMeaslesMixing, [4](#)  
ModelMeaslesMixingRiskQuarantine,  
[8](#)  
ModelMeaslesSchool, [13](#)

## \* **measles-models**

ModelMeaslesMixing, [4](#)  
ModelMeaslesMixingRiskQuarantine,  
[8](#)  
ModelMeaslesSchool, [13](#)

contact\_matrix, [2](#)

epiworld\_measlesmixing, [6](#)

epiworld\_measlesmixing  
(ModelMeaslesMixing), [4](#)

epiworld\_measlesmixingriskquarantine,  
[11](#)

epiworld\_measlesmixingriskquarantine  
(ModelMeaslesMixingRiskQuarantine),  
[8](#)

epiworld\_measlesquarantine  
(ModelMeaslesSchool), [13](#)

epiworldR::epiworld\_model, [6](#), [11](#), [14](#)

epiworldR::initial\_states, [6](#), [10](#)

get\_contact\_matrix(contact\_matrix), [2](#)

ModelMeaslesMixing, [3](#), [4](#), [11](#), [16](#)

ModelMeaslesMixing(), [10](#), [14](#)

ModelMeaslesMixingRiskQuarantine, [3](#), [7](#),  
[8](#), [16](#)

ModelMeaslesQuarantine  
(ModelMeaslesSchool), [13](#)

ModelMeaslesSchool, [7](#), [11](#), [12](#)

set\_contact\_matrix(contact\_matrix), [2](#)

short\_creek, [16](#)

short\_creek\_matrix, [17](#), [17](#)