epiworld

0.8.2

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Chapter 1

Example: 00-hello-world

Output from the program:

```
Running the model...
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
________________________________________________________________________________
SIMULATION STUDY
Name of the model   : (none)
Population size     : 10000
Agents' data        : (none)
Number of entities  : 0
Days (duration)     : 100 (of 100)
Number of viruses   : 1
Last run elapsed t  : 17.00ms
Last run speed      : 56.33 million agents x day / second
Rewiring            : off
Global events:
 (none)
Virus(es):
 - covid 19
Tool(s):
 - vaccine
Model parameters:
 (none)
Distribution of the population at time 100:
  - (0) Susceptible :  9950 -> 0
  - (1) Exposed     :    50 -> 0
  - (2) Recovered   :     0 -> 9399
  - (3) Removed     :     0 -> 601
Transition Probabilities:
 - Susceptible  0.92  0.08     -     -
 - Exposed         -  0.85  0.14  0.01
 - Recovered       -     -  1.00     -
 - Removed         -     -     -  1.00
```

Chapter 2

Benchmarking

Here we keep a list of scenarios where we compare epiworld with other ABM simulation engines. Although the comparison is made at the speed level, we also list features of capabilities and main differences between the engines.

Chapter 3

Contributor Code of Conduct

As contributors and maintainers of this project, we pledge to respect all people who contribute through reporting issues, posting feature requests, updating documentation, submitting pull requests or patches, and other activities.

We are committed to making participation in this project a harassment-free experience for everyone, regardless of level of experience, gender, gender identity and expression, sexual orientation, disability, personal appearance, body size, race, ethnicity, age, or religion.

Examples of unacceptable behavior by participants include the use of sexual language or imagery, derogatory comments or personal attacks, trolling, public or private harassment, insults, or other unprofessional conduct.

Project maintainers have the right and responsibility to remove, edit, or reject comments, commits, code, wiki edits, issues, and other contributions that are not aligned to this Code of Conduct. Project maintainers who do not follow the Code of Conduct may be removed from the project team.

Instances of abusive, harassing, or otherwise unacceptable behavior may be reported by opening an issue or contacting one or more of the project maintainers.

This Code of Conduct is adapted from the Contributor Covenant (`http://contributor-covenant.org`), version 1.0.0, available at `http://contributor-covenant.org/version/1/0/0/`

Chapter 4

ModelMeaslesMixing

A comprehensive epidemiological model that combines measles-specific disease progression with population mixing and quarantine measures.

4.1 Overview

`ModelMeaslesMixing` implements a measles transmission model that extends the SEIR framework with:

- **Measles-specific disease progression**: Susceptible → Exposed → Prodromal → Rash → Recovered
- **Population mixing**: Uses contact matrices to model heterogeneous mixing between population groups
- **Infectious period**: Agents are infectious during the Prodromal state
- **Detection and isolation**: Detection occurs during the Rash state when symptoms become visible
- **Contact tracing**: Comprehensive contact tracing with configurable success rates
- **Quarantine measures**: Multiple quarantine states for exposed contacts
- **Vaccination**: Vaccine distribution with configurable efficacy and recovery enhancement

4.2 Disease States

The model includes 13 distinct states:

1. **Susceptible** - Can become infected
2. **Exposed** - Infected but not yet infectious (incubation period)
3. **Prodromal** - Infectious individuals (replaces "Infected" in standard SEIR)
4. **Rash** - Non-infectious with visible symptoms (detection occurs here)
5. **Isolated** - Detected individuals in self-isolation
6. **Isolated Recovered** - Recovered individuals still in isolation

7. **Detected Hospitalized** - Hospitalized individuals who were contact-traced
8. **Quarantined Exposed** - Exposed individuals in quarantine
9. **Quarantined Susceptible** - Susceptible individuals in quarantine
10. **Quarantined Prodromal** - Prodromal individuals in quarantine
11. **Quarantined Recovered** - Recovered individuals in quarantine
12. **Hospitalized** - Individuals requiring hospital care
13. **Recovered** - Immune individuals

4.3 Key Features

4.3.1 Disease Progression

- **Incubation Period**: Time from exposure to becoming infectious
- **Prodromal Period**: Duration of infectiousness before rash appears
- **Rash Period**: Duration of visible symptoms (detection window)
- **Detection**: Probabilistic detection during rash period
- **Hospitalization**: Some individuals require hospitalization

4.3.2 Population Mixing

- **Contact Matrices**: Define mixing patterns between population groups
- **Heterogeneous Mixing**: Different contact rates between groups
- **Scalable**: Supports multiple population entities

4.3.3 Public Health Measures

- **Contact Tracing**: Trace contacts of detected individuals
- **Quarantine**: Quarantine exposed contacts with configurable compliance
- **Isolation**: Isolate detected cases with configurable willingness
- **Vaccination**: Reduce susceptibility and enhance recovery

4.4 Parameters

4.4.1 Disease Parameters

- `contact_rate`: Average number of contacts per day
- `transmission_rate`: Probability of transmission per contact
- `incubation_period`: Average incubation period (days)
- `prodromal_period`: Average prodromal period (days)
- `rash_period`: Average rash period (days)
- `hospitalization_rate`: Probability of hospitalization
- `hospitalization_period`: Average hospitalization duration (days)

4.4.2 Detection and Isolation

- `days_undetected`: Average time until detection during rash period
- `isolation_period`: Duration of isolation for detected cases
- `isolation_willingness`: Proportion willing to self-isolate

4.4.3 Contact Tracing and Quarantine

- `contact_tracing_success_rate`: Probability of successfully tracing a contact
- `contact_tracing_days_prior`: Number of days to trace back
- `quarantine_period`: Duration of quarantine for contacts
- `quarantine_willingness`: Proportion willing to quarantine

4.4.4 Vaccination

- `prop_vaccinated`: Proportion of population vaccinated
- `vax_efficacy`: Vaccine efficacy (reduction in susceptibility)
- `vax_reduction_recovery_rate`: Recovery enhancement from vaccination

4.5 Usage Example

```
#include "epiworld.hpp"
// Contact matrix for single homogeneous population
std::vector<double> contact_matrix = {1.0};
// Create the model
epimodels::ModelMeaslesMixing<> model(
    "Measles",          // Virus name
    1000,               // Population size
    0.005,              // Initial prevalence
    4.0,                // Contact rate
    0.9,                // Transmission rate
    0.95,               // Vaccine efficacy
    0.5,                // Vaccine recovery enhancement
    10.0,               // Incubation period
    4.0,                // Prodromal period
    5.0,                // Rash period
    contact_matrix,     // Contact matrix
    0.1,                // Hospitalization rate
    7.0,                // Hospitalization period
    2.0,                // Days undetected
    14,                 // Quarantine period
    0.8,                // Quarantine willingness
    0.9,                // Isolation willingness
    10,                 // Isolation period
    0.7,                // Vaccination rate
    0.8,                // Contact tracing success rate
    3u                  // Contact tracing days prior
);
// Add population entity
model.add_entity(Entity<>("Population", dist_factory<>(0, 1000)));
// Run simulation
model.run(60, 123);
model.print();
```

4.6 Differences from Other Models

4.6.1 vs. ModelMeaslesSchool

- **Population Mixing**: Adds contact matrices for heterogeneous mixing
- **Contact Tracing**: Enhanced contact tracing with configurable success rates
- **Scalability**: Supports multiple population entities

4.6.2 vs. ModelSEIRMixingQuarantine

- **Disease-Specific States**: Uses Prodromal/Rash instead of generic Infected
- **Detection Timing**: Detection occurs during Rash state, not Infected state
- **Infectious Period**: Only Prodromal individuals are infectious
- **Vaccination**: Includes vaccine distribution and efficacy

4.7 Testing

The model includes comprehensive tests that verify:

- Correct transition probabilities between states
- Proper detection and quarantine mechanics
- Population mixing functionality
- Reproductive number calculations
- All quarantine states function correctly

See `tests/19-measles-mixing.cpp` for test examples.

Chapter 5

ModelMeaslesMixingRiskQuarantine

A comprehensive epidemiological model that extends measles transmission modeling with risk-stratified quarantine strategies.

5.1 Overview

`ModelMeaslesMixingRiskQuarantine` implements a measles transmission model based on the `ModelMeaslesMixing` framework, with enhanced quarantine policies that vary based on exposure risk levels. This allows for targeted public health interventions that can optimize resource allocation and epidemic control.

5.1.1 Key Features

- **Measles-specific disease progression**: Susceptible → Exposed → Prodromal → Rash → Recovered
- **Population mixing**: Uses contact matrices to model heterogeneous mixing between population groups
- **Risk-stratified quarantine**: Three-tier system (high/medium/low risk) with customizable durations
- **Enhanced detection**: Detection rate parameter that activates during quarantine periods
- **Contact tracing**: Comprehensive contact tracing with configurable success rates
- **Entity-based risk assessment**: Risk levels determined by shared entity membership
- **Vaccination effects**: Vaccine distribution with configurable efficacy

5.2 Disease States

The model includes 13 distinct states:

1. **Susceptible** - Can become infected
2. **Exposed** - Infected but not yet infectious (incubation period)

3. **Prodromal** - Infectious individuals (replaces "Infected" in standard SEIR)
4. **Rash** - Non-infectious with visible symptoms (detection occurs here)
5. **Isolated** - Detected individuals in self-isolation
6. **Isolated Recovered** - Recovered individuals still in isolation
7. **Detected Hospitalized** - Hospitalized individuals who were contact-traced
8. **Quarantined Exposed** - Exposed individuals in quarantine
9. **Quarantined Susceptible** - Susceptible individuals in quarantine
10. **Quarantined Prodromal** - Prodromal individuals in quarantine
11. **Quarantined Recovered** - Recovered individuals in quarantine
12. **Hospitalized** - Individuals requiring hospital care
13. **Recovered** - Individuals who have recovered and gained immunity

5.3 Risk Classification System

When the quarantine process is triggered by a detected case, contacts are classified into three risk levels:

5.3.1 High Risk

- **Definition**: Unvaccinated agents who share entity membership with the case that triggered quarantine
- **Rationale**: Highest transmission risk due to close, prolonged contact within same household/workplace/school
- **Default quarantine duration**: 21 days (configurable)

5.3.2 Medium Risk

- **Definition**: Unvaccinated agents who had contact with infected individuals but don't share entity membership
- **Rationale**: Moderate transmission risk from community contact
- **Default quarantine duration**: 14 days (configurable)

5.3.3 Low Risk

- **Definition**: All other unvaccinated agents
- **Rationale**: Lowest transmission risk, potential for community spread
- **Default quarantine duration**: 7 days (configurable)

Note: Vaccinated agents (those with tools) are not subject to quarantine regardless of contact patterns.

5.4 Enhanced Detection

The model includes an enhanced detection mechanism that operates during active quarantine periods:

- **Detection rate quarantine**: Additional parameter specifying detection probability for prodromal individuals during active quarantine
- **Mechanism**: When any quarantine process is active, prodromal individuals have an additional chance of being detected and moved to quarantined prodromal state
- **Purpose**: Models increased surveillance and testing during outbreak response

5.5 Parameters

5.5.1 Disease Parameters

- **Contact rate**: Average number of contacts per step
- **Transmission rate**: Probability of transmission per contact
- **Incubation period**: Average time from exposure to becoming infectious
- **Prodromal period**: Average duration of infectious period
- **Rash period**: Average duration of rash symptoms
- **Hospitalization rate**: Probability of requiring hospitalization
- **Hospitalization period**: Average duration of hospital stay

5.5.2 Detection and Isolation

- **Days undetected**: Average time before rash cases are detected
- **Isolation period**: Duration of isolation for detected cases
- **Isolation willingness**: Proportion willing to self-isolate when detected
- **Detection rate quarantine**: Detection rate during active quarantine periods

5.5.3 Risk-based Quarantine

- **Quarantine period high**: Duration for high-risk contacts (days)
- **Quarantine period medium**: Duration for medium-risk contacts (days)
- **Quarantine period low**: Duration for low-risk contacts (days)
- **Quarantine willingness**: Proportion willing to comply with quarantine

5.5.4 Contact Tracing

- **Contact tracing success rate**: Probability of successfully identifying contacts
- **Contact tracing days prior**: Number of days prior to detection for tracing

5.5.5 Vaccination

- **Vaccination rate**: Proportion of agents initially vaccinated
- **Vax efficacy**: Vaccine effectiveness in preventing infection
- **Vax improved recovery**: Enhanced recovery rate for vaccinated individuals

5.6 Usage Example

```
#include <epiworld/epiworld.hpp>
// Contact matrix for 3 population groups
std::vector<double> contact_matrix = {
    0.8, 0.1, 0.1,  // Group 1 mixing
    0.1, 0.8, 0.1,  // Group 2 mixing
    0.1, 0.1, 0.8   // Group 3 mixing
};
// Create model with risk-based quarantine
epimodels::ModelMeaslesMixingRiskQuarantine<> model(
    1000,        // Population size
    0.01,        // Initial prevalence
    2.0,         // Contact rate
    0.2,         // Transmission rate
    0.9,         // Vaccination efficacy
    0.3,         // Vaccine recovery enhancement
    7.0,         // Incubation period
    4.0,         // Prodromal period
    5.0,         // Rash period
    contact_matrix, // Contact matrix
    0.2,         // Hospitalization rate
    7.0,         // Hospitalization duration
    3.0,         // Days undetected
    21,          // Quarantine period high risk
    14,          // Quarantine period medium risk
    7,           // Quarantine period low risk
    0.8,         // Quarantine willingness
    0.8,         // Isolation willingness
    4,           // Isolation period
    0.1,         // Proportion vaccinated
    0.15,        // Detection rate during quarantine
    1.0,         // Contact tracing success rate
    4u           // Contact tracing days prior
);
// Add population entities
model.add_entity(Entity<>("Households", dist_factory<>(0, 400)));
model.add_entity(Entity<>("Schools", dist_factory<>(400, 700)));
model.add_entity(Entity<>("Workplaces", dist_factory<>(700, 1000)));
// Set initial conditions
model.initial_states({1.0, 0.0}); // All infected start as exposed
// Run simulation
model.run(60, 123);
model.print();
```

5.7 Differences from Other Models

5.7.1 vs. ModelMeaslesMixing

- **Risk-stratified quarantine**: Three different quarantine durations based on exposure risk
- **Enhanced detection**: Additional detection during active quarantine periods
- **Entity-based risk assessment**: Risk levels determined by shared entity membership
- **Flexible quarantine policies**: Each risk level can have different quarantine duration or be disabled

5.7.2 vs. ModelMeaslesSchool

- **Population mixing**: Supports contact matrices for heterogeneous mixing
- **Risk stratification**: Multiple quarantine strategies rather than uniform approach
- **Enhanced contact tracing**: Risk-based contact management
- **Scalability**: Supports multiple population entities with different mixing patterns

5.8 Testing

The model includes comprehensive tests that verify:

- Correct transition probabilities between all 13 states
- Proper risk level assignment (high/medium/low)
- Enhanced detection mechanism during quarantine periods
- Different quarantine durations for different risk levels
- Comparison of uniform vs. risk-stratified quarantine strategies
- Population mixing functionality with multiple entities

See `tests/20a-measles-mixing-risk-quarantine.cpp` for test examples.

5.9 Applications

This model is particularly useful for:

1. **Outbreak response planning**: Comparing different quarantine strategies
2. **Resource optimization**: Allocating quarantine resources based on transmission risk
3. **Policy evaluation**: Assessing effectiveness of risk-stratified interventions
4. **Contact tracing optimization**: Understanding impact of enhanced detection during outbreaks
5. **Vaccination strategy**: Evaluating how vaccination coverage affects quarantine effectiveness

5.10 Implementation Notes

- Risk levels are assigned dynamically when quarantine is triggered
- Vaccinated agents are excluded from quarantine regardless of contact patterns
- Enhanced detection only operates when at least one quarantine process is active
- Quarantine durations can be set to -1 to disable quarantine for specific risk levels
- The model maintains backward compatibility with uniform quarantine by setting all periods equal

Chapter 6

epiworld c++ template library

6.1 Main features

This C++ template-header-only library provides a general framework for epidemiologic simulation. The main features of the library are:

1. Four key classes: `Model`, `Person`, `Tool`, and `Virus`.
2. The model features a social networks of `Persons`.
3. `Persons` can have multiple `Tools` as a defense system.
4. `Tools` can reduce contagion rate, transmissibility, death rates, and improve recovery rates.
5. `Viruses` can mutate (generating new variants).
6. `Models` can feature multiple states, e.g., `HEALTHY`, `SUSCEPTIBLE`, etc.
7. `Models` can have an arbitrary number of parameters.
8. **REALLY FAST** About 6.5 Million person/day simulations per second.

6.2 Algorithm

Setup

- Create viruses.
- Create tools (arbitrary).
- Set model parameters (arbitrary).
- Create global events (e.g., surveillance).
- Set up the population: small world network (default).
- Set up rewiring (optional).
- Set states (arbitrary number of them).

Run

1. Distribute the tool(s) and virus(es)
2. For each t in 1 -> Duration:
    - Update state for susceptible/infected/removed(?)
    - Mutate virus(es) (each individual)
    - Run Global events (e.g., surveillance)
    - Run rewiring algorithm

Along update:

- Contagion events are applied recorded.
- New variants are recorded.
- Optional user data is recorded.

6.3 Hello world (C++)

```
#include "include/epiworld/epiworld.hpp"
int main()
{
  // Creating a virus
  epiworld::Virus<> covid19("covid 19", .01, true);
  covid19.set_infectiousness(.8);

  // Creating a tool
  epiworld::Tool<> vax("vaccine", .5, true);
  vax.set_contagion_reduction(.95);
  // Creating a model
  epiworld::Model<> model;
  // Adding the tool and virus
  model.add_virus(covid19);
  model.add_tool(vax);
  // Generating a random pop
  model.population_from_adjlist(
    epiworld::rgraph_smallworld(1000, 5, .2)
  );
  // Initializing setting days and seed
  model.init(60, 123123);
  // Running the model
  model.run();
  model.print();
  return;
}
```

6.4 Surveillance simulation

- Incubation time of the disease ∼ `Gamma(3, 1)`
- Duration of the disease ∼`Gamma(12, 1)`
- Probability of becoming symptomatic: 0.9
- Prob. of transmission: 1.0.
- Vaccinated population: 25%
- Vaccine efficacy: .9.
- Vaccine reduction on transmission: 0.5.
- Surveillance program of x% of the population at random.
- Individuals who test positive become isolated.

6.4.1 Preliminary results

```
# With low surveillance
pop_size <- 20e3
pop_seed <- pop_size * .01
s_levels <- c(0.0001, 0.002)
system(sprintf("./07-surveillance.o %i %i 100 %.04f 2>&1", pop_seed, pop_size, s_levels[1]), intern = TRUE)
       |>
  cat(sep = "\n")
```

```
## Running the model...
## ________________________________________________________________________
## |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| done.
##
## ________________________________________________________________________________
## SIMULATION STUDY
##
## Population size    : 20000
## Days (duration)    : 200 (of 200)
## Number of variants : 1
## Last run elapsed t : 505.00ms
## Rewiring           : off
##
## Virus(es):
##  - Covid19 (baseline prevalence: 100 seeds)
## Tool(s):
##  - Vaccine (baseline prevalence: 25.00%)
##
## Model parameters:
##  - Infect period         : 12.0000
##  - Latent period         : 3.0000
##  - Prob of symptoms      : 0.7000
##  - Prob of transmission  : 1.0000
##  - Prob. death           : 0.0010
##  - Prob. reinfect        : 0.1000
##  - Surveilance prob.     : 1.0e-04
##  - Vax efficacy          : 0.9000
##  - Vax redux transmision : 0.5000
##
## Distribution of the population at time 200:
##  - Total susceptible (S)           :   19900 -> 2106
##  - Total recovered (S)             :       0 -> 17369
##  - Total latent (I)                :     100 -> 109
##  - Total symptomatic (I)           :       0 -> 155
##  - Total symptomatic isolated (I)  :       0 -> 2
##  - Total asymptomatic (I)          :       0 -> 72
##  - Total asymptomatic isolated (I) :       0 -> 0
##  - Total removed (R)               :       0 -> 187
##
## (S): Susceptible, (I): Infected, (R): Recovered
## ________________________________________________________________________________
```

```
hist1 <- read.csv("07-surveillance_hist.txt", sep = " ")
surv1 <- read.csv("07-surveillance_user_data.txt", sep = " ")
# With high surveillance
system(sprintf("./07-surveillance.o %i %i 100 %.04f 2>&1", pop_seed, pop_size, s_levels[2]), intern = TRUE)
       |>
  cat(sep = "\n")
```

```
## Running the model...
## ________________________________________________________________________
## |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| done.
##
## ________________________________________________________________________________
## SIMULATION STUDY
##
## Population size    : 20000
## Days (duration)    : 200 (of 200)
## Number of variants : 1
## Last run elapsed t : 530.00ms
## Rewiring           : off
##
## Virus(es):
```

```
##  - Covid19 (baseline prevalence: 100 seeds)
## Tool(s):
##  - Vaccine (baseline prevalence: 25.00%)
##
## Model parameters:
##  - Infect period         : 12.0000
##  - Latent period         : 3.0000
##  - Prob of symptoms      : 0.7000
##  - Prob of transmission  : 1.0000
##  - Prob. death           : 0.0010
##  - Prob. reinfect        : 0.1000
##  - Surveilance prob.     : 0.0020
##  - Vax efficacy          : 0.9000
##  - Vax redux transmision : 0.5000
##
## Distribution of the population at time 200:
##  - Total susceptible (S)           :   19900 -> 2125
##  - Total recovered (S)             :       0 -> 17325
##  - Total latent (I)                :     100 -> 109
##  - Total symptomatic (I)           :       0 -> 155
##  - Total symptomatic isolated (I)  :       0 -> 8
##  - Total asymptomatic (I)          :       0 -> 76
##  - Total asymptomatic isolated (I) :       0 -> 1
##  - Total removed (R)               :       0 -> 201
##
## (S): Susceptible, (I): Infected, (R): Recovered
## ________________________________________________________________________________
```

```
hist2 <- read.csv("07-surveillance_hist.txt", sep = " ")
surv2 <- read.csv("07-surveillance_user_data.txt", sep = " ")
hist_comb <- rbind(
  cbind(sim = as.character(s_levels[1]), hist1),
  cbind(sim = as.character(s_levels[2]), hist2)
  )
ggplot(hist_comb, aes(x = date, y = counts + 1, colour = state, linetype=sim)) +
  geom_line() +
  # scale_y_log10() +
  labs(y = "Counts (log)")
```

6.4.2 Cases detected

```
survdat <- rbind(
  with(surv1, rbind(
    data.frame(Id = as.character(s_levels[1]), Date = date, Type = "N Sampled",  n = nsampled),
    data.frame(Id = as.character(s_levels[1]), Date = date, Type = "N detected",  n = ndetected),
    data.frame(Id = as.character(s_levels[1]), Date = date, Type = "N detected Asymp",  n =
       ndetected_asympt),
    data.frame(Id = as.character(s_levels[1]), Date = date, Type = "N Asymp",  n = nasymptomatic)
  )),
  with(surv2, rbind(
    data.frame(Id = as.character(s_levels[2]), Date = date, Type = "N Sampled",  n = nsampled),
    data.frame(Id = as.character(s_levels[2]), Date = date, Type = "N detected",  n = ndetected),
    data.frame(Id = as.character(s_levels[2]), Date = date, Type = "N detected Asymp",  n =
       ndetected_asympt),
    data.frame(Id = as.character(s_levels[2]), Date = date, Type = "N Asymp",  n = nasymptomatic)
  ))
)
ggplot(survdat, aes(x = Date, y = n + 1, colour = Type)) +
  geom_line() +
  facet_wrap(~Id) +
  scale_y_log10() +
  labs(y = "Counts (log)")
```

Chapter 7

General parameters

The following are parameters used for both ABM and Compartmental models.

```
EPI_BETA  <- 0.75
EPI_GAMMA <- 0.33
EPI_LATENCY <- 1/0.33
EPI_N     <- 10000
EPI_0     <- 0.01
EPI_NDAYS <- 50
Sys.setenv( # nolint
    EPI_BETA  = EPI_BETA,
    EPI_GAMMA = EPI_GAMMA,
    EPI_LATENCY = EPI_LATENCY,
    EPI_N     = EPI_N,
    EPI_0     = EPI_0,
    EPI_NDAYS = EPI_NDAYS
)
```

7.1 Compartmental Models

7.1.1 SIR Model

```
library(deSolve)
library(ggplot2)
library(data.table)
# Code from
# Chapter 2: SIR
# Book "Epidemics: Models and Data using R."
# By: Ottar N. Bjørnstad
sirmod <- function(t, y, parms) {
    # Pull state variables from the vector y
    S = y[1]
    I = y[2]
    R = y[3]

    # Pull parameter values from parms vector
    beta  = parms["beta"]
    mu    = parms["mu"]
    gamma = parms["gamma"]
    N     = parms["N"]

    # Define equations
    dS  = mu * (N - S) - beta * S * I/N
    dI  = beta * S * I/N - (mu + gamma) * I
    dR  = gamma * I - mu * R
    res = c(dS, dI, dR)

    # Return list of gradients
    list(res)
}
# Initial parameters
times <- seq(0, EPI_NDAYS, by = 1)
parms <- c(mu = 0, N = EPI_N, beta = EPI_BETA, gamma = EPI_GAMMA)
start <- c(S = EPI_N * (1 - EPI_0), I = EPI_N * EPI_0, R = 0)
out <- ode(y = start, times = times, func = sirmod, parms= parms)
out <- as.data.frame(out)
out <- rbind(
```

```
    with(out, data.table(date = time, state = "Susceptible", counts = S)),
    with(out, data.table(date = time, state = "Infected", counts = I)),
    with(out, data.table(date = time, state = "Recovered", counts = R))
)
```

Now we visualize the model

```
ggplot(out, aes(x = date, y = counts)) +
    geom_line(aes(colour = state)) +
    labs(title = "Compartmental SIR")
```

7.1.2 SEIR Model

```
# Code adapted from
# Chapter 2: SIR
# Book "Epidemics: Models and Data using R"
# By: Ottar N. Bjørnstad
seirmod <- function(t, y, parms) {
    # Pull state variables from y vector
    S = y[1]
    E = y[2]
    I = y[3]
    R = y[4]

    # Pull parameter values from parms vector
    beta  = parms["beta"]
    mu    = parms["mu"]
    alpha = parms["alpha"]
    gamma = parms["gamma"]
    N     = parms["N"]

    # Define equations
    dS  = mu * (N - S) - beta * S * I/N - mu * S
    dE  = beta * S * I/N - (mu + alpha) * E
    dI  = alpha * E - (mu + gamma) * I
    dR  = gamma * I - mu * R
    res = c(dS, dE, dI, dR)

    # Return list of gradients
    list(res)
}
# Initial parameters
parms <- c(
    mu = 0, N = EPI_N, beta = EPI_BETA,
    alpha = 1/EPI_LATENCY, gamma = EPI_GAMMA
    )
start <- c(S = EPI_N * (1 - EPI_0), E = EPI_N * EPI_0, I = 0, R = 0)
out_seir <- ode(y = start, times = times, func = seirmod, parms = parms)
out_seir <- as.data.frame(out_seir)
out_seir <- rbind(
    with(out_seir, data.table(date = time, state = "Susceptible", counts = S)),
    with(out_seir, data.table(date = time, state = "Exposed", counts = E)),
    with(out_seir, data.table(date = time, state = "Infected", counts = I)),
    with(out_seir, data.table(date = time, state = "Recovered", counts = R))
)
```

Now we visualize the model

```
ggplot(out_seir, aes(x = date, y = counts)) +
    geom_line(aes(colour = state)) +
    labs(title = "Compartmental SEIR")
```

7.2 Agent-Based Model Approach

Calculation of the expected number of days in state a when prob of changing state equals α is $1/\alpha$

```
set.seed(712)
a <- .3
R <- matrix(runif(2e5 * 50), ncol = 50)
dat <- apply(R, 1, \(x) {
    which.max(x < a)
})
mean(dat) - 1 / a
```

```
[1] -0.01049333
```

7.2.1 Mathematical preliminaries

That agent i becomes infected can be computed as follows:

At the same time, the probability of not becoming infected equals to the probability of no infected agent transmitting the infection. The probability that agent j infects i equals

In this case, β is parametrized such that its values are within $(0,1)$. Since transmission from the I infected agents happens independently, we finally have the following:

With the above equation, we can now calculate the change in the number of susceptible agents. In this case, it equals the expected number of new infections:

With the same parametrization in the canonical SIR model (Kermack and McKendrick), the instantaneous change in the number of susceptible agents equals $\frac{\delta}{\delta t}S = -S \beta I$. Given S and I, we can show that, as $\beta\downarrow 0$, i.e., the population grows, both rates converge to the same number. Formally:

The same can be shown for the change in the number recovered.

7.2.2 Simulation study

Now, what happens with `epiworld`.

```
system("./09-sir-connected.o -n $EPI_N -b $EPI_BETA -d $EPI_NDAYS -p $EPI_0 -r $EPI_GAMMA -i 1.0 -s555599")
library(ggplot2)
epiworld <- data.table::fread("total_hist.txt")
ggplot(epiworld, aes(x = date, y = counts)) +
    geom_line(aes(colour = state)) +
    labs(title = "ABM SIR")
system("./09-seir-connected.o -n $EPI_N -b $EPI_BETA -d $EPI_NDAYS -p $EPI_0 -r $EPI_GAMMA -i 1.0 -s555599
       -l $EPI_LATENCY")
library(ggplot2)
epiworld <- data.table::fread("total_hist.txt")
ggplot(epiworld, aes(x = date, y = counts)) +
    geom_line(aes(colour = state)) +
    labs(title = "ABM SEIR")
```

7.3 Comparing ABM with Compartmental Models

To this end, we will compare the results of the first run of the Compartmental model with 100 runs of the ABM, compute the confidence interval, and see how likely is the compartmental model to fall within the trajectory of the ABM simulation.

7.3.1 SIR

```
system("./09-sir-connected.o -n $EPI_N -b $EPI_BETA -d $EPI_NDAYS -p $EPI_0 -r $EPI_GAMMA -i 1.0 -s555599 -e
       100")
library(ggplot2)
library(data.table)
epiworld <- data.table::fread("09-sir-connected-experiments.csv")
epiworld <- epiworld[, .(
    min  = quantile(counts, probs = .025),
    mean = mean(counts),
    max  = quantile(counts, probs = .975)), by = .(date, state)]
# Merging Compartmental
epiworld <- merge(
    epiworld,
    out[, .(date = date, state = state, compartmental = counts)],
    by = c("date", "state")
)
setorder(epiworld, state, date)
ggplot(epiworld, aes(x = date, y = mean)) +
    geom_ribbon(aes(ymin = min, ymax = max, colour = state), alpha = 0.1) +
    geom_line(aes(x = date, y = compartmental, colour = sprintf("%s (compt)", state)))
```

It seems that, although both yield the same equilibria, compartmental models reach the highest point of the simulation earlier. This makes sense as within a single day of the ABM simulation, compartmental models have more events taking place. Nonetheless, as predicted, as $\beta\downarrow 0$, the differences become lesser. Furthermore, we could use the fact that the transition rates are known to compute an adjustment.

7.3.2 SEIR

```
system("./09-seir-connected.o -n $EPI_N -b $EPI_BETA -d $EPI_NDAYS -p $EPI_0 -r $EPI_GAMMA -i 1.0 -s555599
       -e 100 -l $EPI_LATENCY")
library(ggplot2)
library(data.table)
epiworld_seir <- data.table::fread("09-seir-connected-experiments.csv")
epiworld_seir <- epiworld_seir[, .(
    min  = quantile(counts, probs = .025),
    mean = mean(counts),
    max  = quantile(counts, probs = .975)), by = .(date, state)]
# Merging Compartmental
epiworld_seir <- merge(
    epiworld_seir,
    out_seir[, .(date = date, state = state, compartmental = counts)],
    by = c("date", "state")
)
setorder(epiworld_seir, state, date)
ggplot(epiworld_seir, aes(x = date, y = mean)) +
    geom_ribbon(aes(ymin = min, ymax = max, colour = state), alpha = 0.1) +
    geom_line(aes(x = date, y = compartmental, colour = sprintf("%s (compt)", state)))
```

7.3.3 Rates

```
S <- 1000
rate_comp <- function(I,B) S * B * I
rate_abm <- function(I,B) S * (1 - (1 - B)^I)
op <- par(mfrow = c(3, 2))
for (i in c(1, 10, 100)) {
    curve(rate_comp(i, x), from = .01, to = 0.05)
    curve(rate_abm(i, x), from = .01, to = 0.05, add = FALSE, lty = 2)
}
par(op)
```

Chapter 8

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Chapter 9

model1

The dynamics of the simulation process are:

1. Discrete Markov process.
2. The simulation has the following parameters:

   a. New variant emergence at rate `X.` b. For each variant `k`:

   - Unvaccinated individuals become sick rate `C(k),`
   - Mortality rate `D(k),`
   - Recovery rate `H(k),`
   - Vaccines have an efficaccy rate `E(v,k)` and pseudo vaccines (recovered) have efficacy rate `E(r,k) < E(v,k).` In general, the probability of `i` acquiring the disease `k` from `j` will be equal to

   ``` P(i gets the disease from j | their states) = C(k) * (1 - E(i,k)) * (1 - E(j, k)) ```

   where `(i,j) in (u,v,r).` Efficacy rate for unvaccinated is zero.

   - Vaccinated individuals have a reduced mortality rate `D(k,v) > D(k),` and recovered individuals `D(k,r) in (D(k,v), D(k)]`
   - Vaccinated individuals have an increased recovery rate `H(k,v) > H(k)`, whereas recovered's rate `H(k,r) in [H(k), H(k,v)).`

   The sum of mortality and recovery rates is less than one since the difference represents no change.

   c. Each country vaccinates citizens at rate `V` function of `A` (availability) and `B` (citizens' acceptance rate.) d. In each country `i,` the entire population `N(i)` distributes between the following states:

   - Healthy unvaccinated (`N(i,t,u)`),
   - Healthy vaccinated (`N(i,t,v)`),
   - Deceased (`N(i,t,d)`),
   - Recovered (`N(i,t,r)`),
   - Unvaccinated and sick with variant (`N(i,t,s,k|u)`) `k.`, and
   - Vaccinated and sick with variant (`N(i,t,s,k|v)`) `k.`

   Total sick are `N(i,t,k,s) = sum(g in {u,v}) N(i,t,k,s|g)`

   Globally, we keep track of the prevalence of new variants. Variants can disappear if no more individuals port the variant, i.e., the prevalence rate `P(k,t)=sum(i) N(i,s,k)` equals zero.

   d. Vaccines are manufactured at each country at rates `M(i)` and uniformly shared with other countries at rate `S(i).` c. Population flows between each country pair `(i,j)` at a rate `F(i,j).` Flows between countries do not change Population and are symmetric.
   ```

3. The simulation process is as follows:
   (a) Countries are initialized with a total population `N(i)`.
   (b) Variant zero initializes at a random location `i`, with an initial prevalence `P(k,t) = N(i,t,k)`.
   (c) For time `t` in `(0,T)` do:

      a. Unvaccinated individuals can become sick of variant `k` with probability:

      ``` Pr(h->s|i,t,k,u) ∼ sum(g in {u,v}) (N(i,t - 1,s,k|g) + sum(j != i) F(i,j) ∗ N(j,t-1,s,k|g)) ∗ C(k) / (N(i) + sum(j != i) N(j)) ```

      b. Vaccinated individuals can become sick of variant `k` with probability: `Pr(v->s|i,t,k,v) ∼ Pr(h->s|i,t,k) * (1 - E(v,k))`.

      b. Recovered individuals can become sick of variant `k` with probability: `Pr(v->s|i,t,k,r) ∼ Pr(h->s|i,t,k) * (1 - E(r,k))`.

      c. Sick individuals with variant `k` die with probability `D(k)` or recover with probability `H(k)`, otherwise they stay infected; with the rates depending on their vaccination status `v` or `n`.

      d. Unvaccinated individuals vaccinate in country `i` with probability `P(u->v) ∼ V(A(i,t), B(i))`.

      e. The country vaccine supply changes.
      ```

Chapter 10

Mixing probabilities in connected model

George G. Vega Yon, Ph.D. 2024-04-25

10.1 Case 1: No grouping

We will look into the probability of drawing infected individuals to simplify the algorithm. There are \$I\$ infected individuals at any time in the simulation; thus, instead of drawing from \$Bern(c/N, N)\$, we will be drawing from \$↩
Bern(c/N, I)\$. The next step is to check which infected individuals should be drawn. Let's compare the distributions using the hypergeometric as an example:

```
set.seed(132)
nsims <- 1e4
N <- 400
rate <- 5
p <- rate/N
I <- 10
sim_complex <- parallel::mclapply(1:nsims, \(i) {
  nsamples <- rbinom(N, N, p)
  sum(rbinom(N, size = nsamples, prob = I/N) > 0)
}, mc.cores = 4L) |> unlist()
sim_simple <- parallel::mclapply(1:nsims, \(i) {
  sum(rbinom(N, I, p) > 0)
}, mc.cores = 4L) |> unlist()
op <- par(mfrow = c(1,2))
MASS::truehist(sim_complex)
MASS::truehist(sim_simple)
par(op)
quantile(sim_complex)
```

```
  0%  25%  50%  75% 100%
  27   43   47   51   71
```

```
quantile(sim_simple)
```

```
  0%  25%  50%  75% 100%
  23   43   47   51   71
```

```
plotter(sim_complex, sim_simple)
```

These two approaches are equivalent, but the second one is more efficient from the computational perspective.

10.2 Case 2: Grouping

This explores the case when we have mixing across groups. The question is if we can replicate the effect at the group level.

```
set.seed(123133)
ngroups <- 3
mixing <- matrix(
  c(0.1, 0.2, 0.3, 0.2, 0.1, 0.2, 0.3, 0.2, 0.1),
  nrow = ngroups,
  ncol = ngroups
  )
mixing <- mixing/rowSums(mixing)
mixing
```

```
          [,1]      [,2]      [,3]
[1,] 0.1666667 0.3333333 0.5000000
[2,] 0.4000000 0.2000000 0.4000000
[3,] 0.5000000 0.3333333 0.1666667
```

```
N <- 500
sizes <- c(100, 150, 250)
rate <- 5
p <- rate/N
I <- c(10, 30, 20)
ids <- rep.int(1:ngroups, times = sizes)
nsims <- 1e4
sim_complex <- parallel::mclapply(1:nsims, \(i) {
  # Sampling group first
  sapply(1:ngroups, \(g) {
    # How many each individual will sample from the groups
    ans <- rbinom(
      n = N, size = sizes[g], prob = mixing[ids,][,g] * p
      ) |> sum()
    # Sampling with replacement
    rbinom(ans, size = 1, prob = I[g]/sizes[g]) |> sum()
  }) |> sum()
}, mc.cores = 4L) |> unlist()
```

Using the alternative method in which we directly weight the probabilities:

```
sim_simple <- parallel::mclapply(1:nsims, \(i) {
  # Sampling group first
  sapply(1:ngroups, \(g) {
    rbinom(
      n = N, size = I[g], prob = mixing[cbind(ids,g)] * p
      ) |> sum()
  }) |> sum()
}, mc.cores = 4L) |> unlist()
op <- par(mfrow = c(1,2))
MASS::truehist(sim_complex)
MASS::truehist(sim_simple)
par(op)
quantile(sim_complex)
```

```
  0%  25%  50%  75% 100%
  57   88   94  101  131
```

```
quantile(sim_simple)
```

```
  0%  25%  50%  75% 100%
  58   87   94  101  135
```

```
plotter(sim_complex, sim_simple)
```

Chapter 11

EPI Simulator

11.1 Disease dynamics

Diseases continuously evolve in time. Changes in their genetic sequence make them more or less resistant to the particular version of the vaccine. Mutations also affect the transmissibility level and mortality rate of the disease. Using this approach allows making vaccination efficacy a function of compatibility between the variant and the vaccine.

When an individual becomes infected, the disease accumulates mutations in the new host. Ultimately, there is no single version of the disease present in the model, but rather an infinite number of them, each slightly different from the other.

11.2 Network dynamics

We can assume that the Population is organized in fully connected blocks for the first version of the model. Block sizes and the number of connections between blocks are Poisson random variables. Individuals interact with all the members of their blocks, and bridging individuals allow the disease to move across blocks.

11.3 Contagion dynamics

The transmission of the disease will be governed by the number of vaccinated, infected, and recovered within each block. Transmission between blocks will be treated in the same way, although individuals bridging the block will only interact with others within the block and their direct connections across the blocks.

11.4 Time dynamics

Time dynamics has two components, how biology evolves and how agents react.

The model develops as a continuous-time Markov process. Each block of individuals takes action at rates `L(i|N(i))` function of the local number of infections. This way, if

11.5 Updating agent's status

Like most other components, updating agents' states can be personalized. A naive approach allows agents to get infected with a single virus or stay as-is. The probability of this event is conditional on acquiring at most one virus. Since these are independent events, the conditional probability is computed as follows:

```
P(Variant k|at most 1) = P(at most 1| Variant k) * P(Variant k)/P(at most 1)
                       = P(only variant k)/P(variant k) * P(Variant k)/P(at most 1)
                       = P(only variant k)/P(at most 1)
```

Where

```
P(only variant k) = P(k) * Prod(m!=v) (1 - P(m))
P(at most 1) = P(None) + Sum(v in variants) P(v) * Prod(m != v) (1 - P(m))
P(None) = Prod(v in variants) (1 - P(v))
```

Furthermore, the (Variant, Person) pairs are treated independently.

11.5.1 Other parameters

- Who did you get the infection from.
- Omicron is 1.5 more infectious than delta.
- Surveillance:
  - Pull people to be tested at random.
  - Or at symptoms.
  - A mix of the two.
- Define a class for passing extra functions and datasets, for example, testing surveillance.
- Exposed people become infectious after k days.
- Network changesthe can be a function of an ERGM. Apply K steps throughout time.
- Add progress bar.

Chapter 12

Namespace Index

12.1 Namespace List

Here is a list of all documented namespaces with brief descriptions:

Chapter 13

Hierarchical Index

13.1 Class Hierarchy

This inheritance list is sorted roughly, but not completely, alphabetically:

Chapter 14

Class Index

14.1 Class List

Here are the classes, structs, unions and interfaces with brief descriptions:

Chapter 15

File Index

15.1 File List

Here is a list of all documented files with brief descriptions:

Chapter 16

Namespace Documentation

16.1 epiworld::sampler Namespace Reference

Functions for sampling viruses.

Functions

- template< typename TSeq = EPI_DEFAULT_TSEQ>
  std::function< void(Agent< TSeq > *, Model< TSeq > *)> make_update_susceptible (std::vector< epiworld_fast_uint > exclude={})

    Make a function to sample from neighbors.
- template< typename TSeq = EPI_DEFAULT_TSEQ>
  std::function< Virus< TSeq > *(Agent< TSeq > *, Model< TSeq > *)> make_sample_virus_neighbors (std::vector< epiworld_fast_uint > exclude={})

    Make a function to sample from neighbors.
- template< typename TSeq = EPI_DEFAULT_TSEQ>
  Virus< TSeq > * sample_virus_single (Agent< TSeq > *p, Model< TSeq > *m)

    Sample from neighbors pool of viruses (at most one)

16.1.1 Detailed Description

Functions for sampling viruses.

16.1.2 Function Documentation

16.1.2.1 make_sample_virus_neighbors()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::function<Virus<TSeq>*(Agent<TSeq>*,Model<TSeq>*)> epiworld::sampler::make_sample_↩
virus_neighbors (
            std::vector< epiworld_fast_uint > exclude = {} )  [inline]
```

Make a function to sample from neighbors.

This is akin to the function default_update_susceptible, with the difference that it will create a function that supports excluding states from the sampling frame. For example, individuals who have acquired a virus can be excluded if in incubation state.

Template Parameters

TSeq	

Parameters

exclude	unsigned vector of states that need to be excluded from the sampling

Returns

Virus<TSeq>* of the selected virus. If none selected (or none available,) returns a nullptr;

16.1.2.2 make_update_susceptible()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::function<void(Agent<TSeq>*,Model<TSeq>*)> epiworld::sampler::make_update_susceptible (
            std::vector< epiworld_fast_uint > exclude = {} ) [inline]
```

Make a function to sample from neighbors.

This is akin to the function default_update_susceptible, with the difference that it will create a function that supports excluding states from the sampling frame. For example, individuals who have acquired a virus can be excluded if in incubation state.

Template Parameters

TSeq	

Parameters

exclude	unsigned vector of states that need to be excluded from the sampling

Returns

Virus<TSeq>* of the selected virus. If none selected (or none available,) returns a nullptr;

16.1.2.3 sample_virus_single()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
Virus<TSeq>* epiworld::sampler::sample_virus_single (
            Agent< TSeq > * p,
            Model< TSeq > * m ) [inline]
```

Sample from neighbors pool of viruses (at most one)

This function samples at most one virus from the pool of viruses from its neighbors. If no virus is selected, the function returns a `nullptr`, otherwise it returns a pointer to the selected virus.

This can be used to build a new update function (EPI_NEW_UPDATEFUN.)

Template Parameters

TSeq	

Parameters

p	Pointer to person
m	Pointer to the model

Returns

Virus<TSeq>* of the selected virus. If none selected (or none available,) returns a nullptr;

16.2 sampler Namespace Reference

Functions for sampling viruses.

Functions

- template<typename TSeq = EPI_DEFAULT_TSEQ>
  std::function< void(Agent< TSeq > *, Model< TSeq > *)> make_update_susceptible (std::vector< epiworld_fast_uint > exclude={})

  Make a function to sample from neighbors.
- template<typename TSeq = EPI_DEFAULT_TSEQ>
  std::function< Virus< TSeq > *(Agent< TSeq > *, Model< TSeq > *)> make_sample_virus_neighbors (std::vector< epiworld_fast_uint > exclude={})

  Make a function to sample from neighbors.
- template<typename TSeq = EPI_DEFAULT_TSEQ>
  Virus< TSeq > * sample_virus_single (Agent< TSeq > *p, Model< TSeq > *m)

  Sample from neighbors pool of viruses (at most one)

16.2.1 Detailed Description

Functions for sampling viruses.

16.2.2 Function Documentation

16.2.2.1 make_sample_virus_neighbors()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::function<Virus<TSeq>*(Agent<TSeq>*,Model<TSeq>*)> sampler::make_sample_virus_neighbors
(
            std::vector< epiworld_fast_uint > exclude = {} )  [inline]
```

Make a function to sample from neighbors.

This is akin to the function default_update_susceptible, with the difference that it will create a function that supports excluding states from the sampling frame. For example, individuals who have acquired a virus can be excluded if in incubation state.

Template Parameters

TSeq	

Parameters

exclude	unsigned vector of states that need to be excluded from the sampling

Returns

Virus<TSeq>* of the selected virus. If none selected (or none available,) returns a nullptr;

16.2.2.2 make_update_susceptible()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::function<void(Agent<TSeq>*,Model<TSeq>*)> sampler::make_update_susceptible (
            std::vector< epiworld_fast_uint > exclude = {} ) [inline]
```

Make a function to sample from neighbors.

This is akin to the function default_update_susceptible, with the difference that it will create a function that supports excluding states from the sampling frame. For example, individuals who have acquired a virus can be excluded if in incubation state.

Template Parameters

TSeq	

Parameters

exclude	unsigned vector of states that need to be excluded from the sampling

Returns

Virus<TSeq>* of the selected virus. If none selected (or none available,) returns a nullptr;

16.2.2.3 sample_virus_single()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
Virus<TSeq>* sampler::sample_virus_single (
            Agent< TSeq > * p,
            Model< TSeq > * m ) [inline]
```

Sample from neighbors pool of viruses (at most one)

This function samples at most one virus from the pool of viruses from its neighbors. If no virus is selected, the function returns a `nullptr`, otherwise it returns a pointer to the selected virus.

This can be used to build a new update function (EPI_NEW_UPDATEFUN.)

Template Parameters

TSeq	

Parameters

p	Pointer to person
m	Pointer to the model

Returns

Virus<TSeq>* of the selected virus. If none selected (or none available,) returns a nullptr;

Chapter 17

Class Documentation

17.1 AdjList Class Reference

Public Member Functions

- AdjList (const std::vector< int > &source, const std::vector< int > &target, int size, bool directed)

    Construct a new Adj List object.
- **AdjList** (AdjList &&a)
- **AdjList** (const AdjList &a)
- AdjList & **operator=** (const AdjList &a)
- void read_edgelist (std::string fn, int size, int skip=0, bool directed=true)

    Read an edgelist.
- std::map< int, int > **operator()** (epiworld_fast_uint i) const
- void **print** (epiworld_fast_uint limit=20u) const
- size_t vcount () const

    Number of vertices/nodes in the network.
- size_t ecount () const

    Number of edges/arcs/ties in the network.
- std::vector< std::map< int, int > > & **get_dat** ()
- bool is_directed () const

    `true` *if the network is directed.*

17.1.1 Constructor & Destructor Documentation

17.1.1.1 AdjList()

```
AdjList::AdjList (
            const std::vector< int > & source,
            const std::vector< int > & target,
            int size,
            bool directed ) [inline]
```

Construct a new Adj List object.

Ids in the network are assume to range from `0` to `size - 1`.

Parameters

source	Unsigned int vector with the source
target	Unsigned int vector with the target
size	Number of vertices in the network.
directed	Bool true if the network is directed

17.1.2 Member Function Documentation

17.1.2.1 read_edgelist()

```
void AdjList::read_edgelist (
            std::string fn,
            int size,
            int skip = 0,
            bool directed = true )  [inline]
```

Read an edgelist.

Ids in the network are assume to range from `0` to `size - 1`.

Parameters

fn	Path to the file
skip	Number of lines to skip (e.g., 1 if there's a header)
directed	`true` if the network is directed
size	Number of vertices in the network.

The documentation for this class was generated from the following files:

- include/epiworld/adjlist-bones.hpp
- include/epiworld/adjlist-meat.hpp

17.2 epiworld::AdjList Class Reference

Public Member Functions

- AdjList (const std::vector< int > &source, const std::vector< int > &target, int size, bool directed)

  Construct a new Adj List object.
- **AdjList** (AdjList &&a)
- **AdjList** (const AdjList &a)
- AdjList & **operator=** (const AdjList &a)
- void read_edgelist (std::string fn, int size, int skip=0, bool directed=true)

  Read an edgelist.

- std::map< int, int > **operator()** (epiworld_fast_uint i) const
- void **print** (epiworld_fast_uint limit=20u) const
- size_t vcount () const

    Number of vertices/nodes in the network.
- size_t ecount () const

    Number of edges/arcs/ties in the network.
- std::vector< std::map< int, int > > & **get_dat** ()
- bool is_directed () const

    `true` *if the network is directed.*

17.2.1 Constructor & Destructor Documentation

17.2.1.1 AdjList()

```
AdjList::AdjList (
            const std::vector< int > & source,
            const std::vector< int > & target,
            int size,
            bool directed ) [inline]
```

Construct a new Adj List object.

Ids in the network are assume to range from `0` to `size - 1`.

Parameters

source	Unsigned int vector with the source
target	Unsigned int vector with the target
size	Number of vertices in the network.
directed	Bool true if the network is directed

17.2.2 Member Function Documentation

17.2.2.1 read_edgelist()

```
void AdjList::read_edgelist (
            std::string fn,
            int size,
            int skip = 0,
            bool directed = true ) [inline]
```

Read an edgelist.

Ids in the network are assume to range from `0` to `size - 1`.

Parameters

fn	Path to the file
skip	Number of lines to skip (e.g., 1 if there's a header)
directed	`true` if the network is directed
size	Number of vertices in the network.

The documentation for this class was generated from the following file:

- epiworld.hpp

17.3 Agent< TSeq > Class Template Reference

Agent (agents)

`#include <agent-bones.hpp>`

Public Member Functions

- **Agent** (Agent< TSeq > &&p)
- **Agent** (const Agent< TSeq > &p)
- Agent< TSeq > & **operator=** (const Agent< TSeq > &other_agent)
- int get_id () const

  Id of the individual.
- VirusPtr< TSeq > & **get_virus** ()
- const VirusPtr< TSeq > & **get_virus** () const
- ToolPtr< TSeq > & **get_tool** (int i)
- Tools< TSeq > **get_tools** ()
- const Tools_const< TSeq > **get_tools** () const
- size_t **get_n_tools** () const noexcept
- void **mutate_virus** ()
- void **add_neighbor** (Agent< TSeq > &p, bool check_source=true, bool check_target=true)
- void swap_neighbors (Agent< TSeq > &other, size_t n_this, size_t n_other)

  Swaps neighbors between the current agent and agent `other`
- std::vector< Agent< TSeq > * > **get_neighbors** ()
- size_t **get_n_neighbors** () const
- void **change_state** (Model< TSeq > *model, epiworld_fast_uint new_state, epiworld_fast_int queue=0)
- const unsigned int & **get_state** () const
- void **reset** ()
- bool **has_tool** (epiworld_fast_uint t) const
- bool **has_tool** (std::string name) const
- bool **has_tool** (const Tool< TSeq > &t) const
- bool **has_virus** (epiworld_fast_uint t) const
- bool **has_virus** (std::string name) const
- bool **has_virus** (const Virus< TSeq > &v) const
- bool **has_entity** (epiworld_fast_uint t) const
- bool **has_entity** (std::string name) const
- void **print** (bool compressed=false) const
- Entities< TSeq > **get_entities** ()
- const Entities_const< TSeq > **get_entities** () const

- const Entity< TSeq > & **get_entity** (size_t i) const
- Entity< TSeq > & **get_entity** (size_t i)
- size_t **get_n_entities** () const
- bool **operator==** (const Agent< TSeq > &other) const
- bool **operator!=** (const Agent< TSeq > &other) const

Add/Remove Virus/Tool

Any of these is ultimately reflected at the end of the iteration.

Parameters

tool	*Tool to add*
virus	*Virus to add*
state_new	*state after the change*
queue	

- void **add_tool** (ToolPtr< TSeq > &tool, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **add_tool** (const Tool< TSeq > &tool, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **set_virus** (VirusPtr< TSeq > &virus, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **set_virus** (const Virus< TSeq > &virus, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **add_entity** (Entity< TSeq > &entity, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_tool** (epiworld_fast_uint tool_idx, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_tool** (ToolPtr< TSeq > &tool, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_virus** (Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_entity** (epiworld_fast_uint entity_idx, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_entity** (Entity< TSeq > &entity, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void rm_agent_by_virus (Model< TSeq > *model)

  Agent removed by virus.

Get the rates (multipliers) for the agent

Parameters

v	*A pointer to a virus.*

Returns

epiworld_double

- epiworld_double **get_susceptibility_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_transmission_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_recovery_enhancer** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_death_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)

- double & operator() (size_t j)

  Access the j-th column of the agent.
- double & **operator[ ]** (size_t j)
- double **operator()** (size_t j) const
- double **operator[ ]** (size_t j) const

Friends

- class **Model**< **TSeq** >
- class **Virus**< **TSeq** >
- class **Tool**< **TSeq** >
- class **Tools**< **TSeq** >
- class **Tools_const**< **TSeq** >
- class **Queue**< **TSeq** >
- class **Entities**< **TSeq** >
- class **AgentsSample**< **TSeq** >
- void **default_add_virus** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_add_tool** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_add_entity** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_virus** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_tool** (Event< TSeq > &a, Model< TSeq > *m)
- void default_rm_entity (Event< TSeq > &a, Model< TSeq > *m)
- void **default_change_state** (Event< TSeq > &a, Model< TSeq > *m)

17.3.1 Detailed Description

template<typename TSeq>
class Agent< TSeq >

Agent (agents)

Template Parameters

TSeq	Sequence type (should match `TSeq` across the model)

17.3.2 Member Function Documentation

17.3.2.1 operator()()

```
template<typename TSeq >
double & Agent< TSeq >::operator() (
            size_t j ) [inline]
```

Access the j-th column of the agent.

If an external array has been specified, then these two functions can be used to access additional agent's features not included in the model.

The `operator[]` method is with no boundary check, whereas the `operator()` method checks boundaries. The former can result in a segfault.

Parameters

j	

Returns

double&

17.3.2.2 swap_neighbors()

```
template<typename TSeq >
void Agent< TSeq >::swap_neighbors (
            Agent< TSeq > & other,
            size_t n_this,
            size_t n_other ) [inline]
```

Swaps neighbors between the current agent and agent `other`

Parameters

other	
n_this	
n_other	

17.3.3 Friends And Related Function Documentation

17.3.3.1 default_rm_entity

```
template<typename TSeq >
void default_rm_entity (
            Event< TSeq > & a,
            Model< TSeq > * m ) [friend]
```

< Last entity of the agent

< Last agent of the entity

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/agent-meat.hpp

17.4 epiworld::Agent< TSeq > Class Template Reference

Agent (agents)

```
#include <epiworld.hpp>
```

Public Member Functions

- **Agent** (Agent< TSeq > &&p)
- **Agent** (const Agent< TSeq > &p)
- Agent< TSeq > & **operator=** (const Agent< TSeq > &other_agent)
- int get_id () const

  Id of the individual.
- VirusPtr< TSeq > & **get_virus** ()
- const VirusPtr< TSeq > & **get_virus** () const
- ToolPtr< TSeq > & **get_tool** (int i)
- Tools< TSeq > **get_tools** ()
- const Tools_const< TSeq > **get_tools** () const
- size_t **get_n_tools** () const noexcept
- void **mutate_virus** ()
- void **add_neighbor** (Agent< TSeq > &p, bool check_source=true, bool check_target=true)
- void swap_neighbors (Agent< TSeq > &other, size_t n_this, size_t n_other)

  Swaps neighbors between the current agent and agent `other`
- std::vector< Agent< TSeq > * > **get_neighbors** ()
- size_t **get_n_neighbors** () const
- void **change_state** (Model< TSeq > *model, epiworld_fast_uint new_state, epiworld_fast_int queue=0)
- const unsigned int & **get_state** () const
- void **reset** ()
- bool **has_tool** (epiworld_fast_uint t) const
- bool **has_tool** (std::string name) const
- bool **has_tool** (const Tool< TSeq > &t) const
- bool **has_virus** (epiworld_fast_uint t) const
- bool **has_virus** (std::string name) const
- bool **has_virus** (const Virus< TSeq > &v) const
- bool **has_entity** (epiworld_fast_uint t) const
- bool **has_entity** (std::string name) const
- void **print** (bool compressed=false) const
- Entities< TSeq > **get_entities** ()
- const Entities_const< TSeq > **get_entities** () const
- const Entity< TSeq > & **get_entity** (size_t i) const
- Entity< TSeq > & **get_entity** (size_t i)
- size_t **get_n_entities** () const
- bool **operator==** (const Agent< TSeq > &other) const
- bool **operator!=** (const Agent< TSeq > &other) const

Add/Remove Virus/Tool

Any of these is ultimately reflected at the end of the iteration.

Parameters

tool	*Tool to add*
virus	*Virus to add*
state_new	*state after the change*
queue	

- void **add_tool** (ToolPtr< TSeq > &tool, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **add_tool** (const Tool< TSeq > &tool, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **set_virus** (VirusPtr< TSeq > &virus, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **set_virus** (const Virus< TSeq > &virus, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **add_entity** (Entity< TSeq > &entity, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_tool** (epiworld_fast_uint tool_idx, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_tool** (ToolPtr< TSeq > &tool, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_virus** (Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_entity** (epiworld_fast_uint entity_idx, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void **rm_entity** (Entity< TSeq > &entity, Model< TSeq > *model, epiworld_fast_int state_new=-99, epiworld_fast_int queue=-99)
- void rm_agent_by_virus (Model< TSeq > *model)

  Agent removed by virus.

Get the rates (multipliers) for the agent

Parameters

v	*A pointer to a virus.*

Returns

epiworld_double

- epiworld_double **get_susceptibility_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_transmission_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_recovery_enhancer** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_death_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)

- double & operator() (size_t j)

  Access the j-th column of the agent.
- double & **operator[ ]** (size_t j)
- double **operator()** (size_t j) const
- double **operator[ ]** (size_t j) const

Friends

- class **Model**< **TSeq** >
- class **Virus**< **TSeq** >
- class **Tool**< **TSeq** >
- class **Tools**< **TSeq** >
- class **Tools_const**< **TSeq** >
- class **Queue**< **TSeq** >
- class **Entities**< **TSeq** >
- class **AgentsSample**< **TSeq** >

- void **default_add_virus** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_add_tool** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_add_entity** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_virus** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_tool** (Event< TSeq > &a, Model< TSeq > *m)
- void default_rm_entity (Event< TSeq > &a, Model< TSeq > *m)
- void **default_change_state** (Event< TSeq > &a, Model< TSeq > *m)

17.4.1 Detailed Description

template<typename TSeq>
class epiworld::Agent< TSeq >

Agent (agents)

Template Parameters

TSeq	Sequence type (should match `TSeq` across the model)

17.4.2 Member Function Documentation

17.4.2.1 operator()()

```
template<typename TSeq >
double & Agent< TSeq >::operator() (
            size_t j ) [inline]
```

Access the j-th column of the agent.

If an external array has been specified, then these two functions can be used to access additional agent's features not included in the model.

The `operator[]` method is with no boundary check, whereas the `operator()` method checks boundaries. The former can result in a segfault.

Parameters

j	

Returns

double&

17.4.2.2 swap_neighbors()

```
template<typename TSeq >
void Agent< TSeq >::swap_neighbors (
            Agent< TSeq > & other,
            size_t n_this,
            size_t n_other ) [inline]
```

Swaps neighbors between the current agent and agent `other`

Parameters

other	
n_this	
n_other	

17.4.3 Friends And Related Function Documentation

17.4.3.1 default_rm_entity

```
template<typename TSeq >
void default_rm_entity (
            Event< TSeq > & a,
            Model< TSeq > * m ) [friend]
```

< Last entity of the agent

< Last agent of the entity

The documentation for this class was generated from the following file:

- epiworld.hpp

17.5 AgentsSample< TSeq > Class Template Reference

Sample of agents.

`#include <agentssample-bones.hpp>`

Public Member Functions

- AgentsSample ()=delete

    Default constructor.
- AgentsSample (const AgentsSample< TSeq > &a)=delete

    Copy constructor.
- AgentsSample (AgentsSample< TSeq > &&a)=delete

    Move constructor.
- **AgentsSample** (Model< TSeq > &model_, size_t n, std::vector< size_t > states_={}, bool truncate=false)
- **AgentsSample** (Model< TSeq > *model, Entity< TSeq > &entity_, size_t n, std::vector< size_t > states↩
_={}, bool truncate=false)
- AgentsSample (Model< TSeq > *model, Agent< TSeq > &agent_, size_t n, std::vector< size_t > states↩
_={}, bool truncate=false)

    Sample from the agent's entities.
- std::vector< Agent< TSeq > * >::iterator **begin** ()
- std::vector< Agent< TSeq > * >::iterator **end** ()
- Agent< TSeq > * **operator[ ]** (size_t n)
- Agent< TSeq > * **operator()** (size_t n)
- size_t **size** () const noexcept

17.5.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class AgentsSample< TSeq >

Sample of agents.

This class allows sampling agents from Entity<TSeq> and Model<TSeq>.

Template Parameters

TSeq	

17.5.2 Constructor & Destructor Documentation

17.5.2.1 AgentsSample()

```
template<typename TSeq >
AgentsSample< TSeq >::AgentsSample (
            Model< TSeq > * model,
            Agent< TSeq > & agent_,
            size_t n,
            std::vector< size_t > states_ = {},
            bool truncate = false )  [inline]
```

Sample from the agent's entities.

For example, how many individuals the agent contacts in a given point in time.

Template Parameters

TSeq	

Parameters

agent↩ _	
n	Sample size
truncate	If the agent has fewer than `n` connections, then truncate = true will automatically reduce the number of possible samples. Otherwise, if false, then it returns an error.

The documentation for this class was generated from the following file:

- include/epiworld/agentssample-bones.hpp

17.6 epiworld::AgentsSample< TSeq > Class Template Reference

Sample of agents.

`#include <epiworld.hpp>`

Public Member Functions

- AgentsSample ()=delete

  Default constructor.
- AgentsSample (const AgentsSample< TSeq > &a)=delete

  Copy constructor.
- AgentsSample (AgentsSample< TSeq > &&a)=delete

  Move constructor.
- **AgentsSample** (Model< TSeq > &model_, size_t n, std::vector< size_t > states_={}, bool truncate=false)
- **AgentsSample** (Model< TSeq > *model, Entity< TSeq > &entity_, size_t n, std::vector< size_t > states↩ _={}, bool truncate=false)
- AgentsSample (Model< TSeq > *model, Agent< TSeq > &agent_, size_t n, std::vector< size_t > states↩ _={}, bool truncate=false)

  Sample from the agent's entities.
- std::vector< Agent< TSeq > * >::iterator **begin** ()
- std::vector< Agent< TSeq > * >::iterator **end** ()
- Agent< TSeq > * **operator[ ]** (size_t n)
- Agent< TSeq > * **operator()** (size_t n)
- size_t **size** () const noexcept

17.6.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::AgentsSample< TSeq >

Sample of agents.

This class allows sampling agents from Entity<TSeq> and Model<TSeq>.

Template Parameters

TSeq	

17.6.2 Constructor & Destructor Documentation

17.6.2.1 AgentsSample()

```
template<typename TSeq >
AgentsSample< TSeq >::AgentsSample (
            Model< TSeq > * model,
            Agent< TSeq > & agent_,
            size_t n,
            std::vector< size_t > states_ = {},
            bool truncate = false )  [inline]
```

Sample from the agent's entities.

For example, how many individuals the agent contacts in a given point in time.

Template Parameters

TSeq	

Parameters

*agent_*	
n	Sample size
truncate	If the agent has fewer than `n` connections, then truncate = true will automatically reduce the number of possible samples. Otherwise, if false, then it returns an error.

The documentation for this class was generated from the following file:

- epiworld.hpp

17.7 ContactTracing Class Reference

Public Member Functions

- **ContactTracing** (size_t n_agents, size_t max_contacts)
- void **add_contact** (size_t agent_a, size_t agent_b, size_t day)
- size_t **get_n_contacts** (size_t agent)
- std::pair< size_t, size_t > **get_contact** (size_t agent, size_t idx)

- void **reset** (size_t n_agents, size_t max_contacts)
- void **print** (size_t agent)

The documentation for this class was generated from the following file:

- include/epiworld/contacttracing-bones.hpp

17.8 epiworld::ContactTracing Class Reference

Public Member Functions

- **ContactTracing** (size_t n_agents, size_t max_contacts)
- void **add_contact** (size_t agent_a, size_t agent_b, size_t day)
- size_t **get_n_contacts** (size_t agent)
- std::pair< size_t, size_t > **get_contact** (size_t agent, size_t idx)
- void **reset** (size_t n_agents, size_t max_contacts)
- void **print** (size_t agent)

The documentation for this class was generated from the following file:

- epiworld.hpp

17.9 DataBase< TSeq > Class Template Reference

Statistical data about the process.

```
#include <database-bones.hpp>
```

Public Member Functions

- **DataBase** (Model< TSeq > &m)
- **DataBase** (const DataBase< TSeq > &db)
- void record_virus (Virus< TSeq > &v)

  Registering a new variant.
- void **record_tool** (Tool< TSeq > &t)
- void **set_seq_hasher** (std::function< std::vector< int >(TSeq)> fun)
- void **reset** ()
- Model< TSeq > * **get_model** ()
- void **record** ()
- const std::vector< TSeq > & **get_sequence** () const
- const std::vector< int > & **get_nexposed** () const
- size_t **size** () const
- void **write_data** (std::string fn_virus_info, std::string fn_virus_hist, std::string fn_tool_info, std::string fn_tool_hist, std::string fn_total_hist, std::string fn_transmission, std::string fn_transition, std::string fn_reproductive_number, std::string fn_generation_time) const
- void **record_transmission** (int i, int j, int virus, int i_expo_date)
- size_t get_n_viruses () const

Get the number of viruses.

- size_t get_n_tools () const

  Get the number of tools.

- void **set_user_data** (std::vector< std::string > names)
- void **add_user_data** (std::vector< epiworld_double > x)
- void **add_user_data** (epiworld_fast_uint j, epiworld_double x)
- UserData< TSeq > & **get_user_data** ()
- std::vector< epiworld_double > get_transition_probability (bool print=true, bool normalize=true) const

  Calculates the transition probabilities.

- bool operator== (const DataBase< TSeq > &other) const
- bool **operator!=** (const DataBase< TSeq > &other) const
- bool operator== (const DataBase< std::vector< int >> &other) const
- bool operator== (const DataBase< std::vector< int >> &other) const

Get recorded information from the model

Parameters

what	*std::string, The state, e.g., 0, 1, 2, ...*

Returns

In `get_today_total`, the current counts of `what`.

In `get_today_virus`, the current counts of `what` for each virus.

In `get_hist_total`, the time series of `what`

In `get_hist_virus`, the time series of what for each virus.

In `get_hist_total_date` and `get_hist_virus_date` the corresponding date

- int **get_today_total** (const std::string &what) const
- int **get_today_total** (const epiworld_fast_uint &what) const
- void **get_today_total** (std::vector< std::string > ∗state=nullptr, std::vector< int > ∗counts=nullptr) const
- void **get_today_virus** (std::vector< std::string > &state, std::vector< int > &id, std::vector< int > &counts) const
- void **get_today_transition_matrix** (std::vector< int > &counts) const
- void **get_hist_total** (std::vector< int > ∗date, std::vector< std::string > ∗state, std::vector< int > ∗counts) const
- void **get_hist_virus** (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &state, std::vector< int > &counts) const
- void **get_hist_tool** (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &state, std::vector< int > &counts) const
- void **get_hist_transition_matrix** (std::vector< std::string > &state_from, std::vector< std::string > &state_to, std::vector< int > &date, std::vector< int > &counts, bool skip_zeros) const

- void get_transmissions (std::vector< int > &date, std::vector< int > &source, std::vector< int > &target, std::vector< int > &virus, std::vector< int > &source_exposure_date) const

  Get the transmissions object.

- void **get_transmissions** (int ∗date, int ∗source, int ∗target, int ∗virus, int ∗source_exposure_date) const

- MapVec_type< int, int > get_reproductive_number () const

Computes the reproductive number of each case.
- void **get_reproductive_number** (std::string fn) const

- void get_generation_time (std::vector< int > &agent_id, std::vector< int > &virus_id, std::vector< int > &time, std::vector< int > &gentime) const

  Get the generation time.
- void get_generation_time (std::string fn) const

  Write the generation time to a file.

Friends

- class **Model**< **TSeq** >
- void **default_add_virus** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_add_tool** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_virus** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_tool** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_change_state** (Event< TSeq > &a, Model< TSeq > *m)

17.9.1 Detailed Description

template<typename TSeq>
class DataBase< TSeq >

Statistical data about the process.

Template Parameters

TSeq	

17.9.2 Member Function Documentation

17.9.2.1 get_generation_time()

```
template<typename TSeq >
void DataBase< TSeq >::get_generation_time (
            std::vector< int > & agent_id,
            std::vector< int > & virus_id,
            std::vector< int > & time,
            std::vector< int > & gentime ) const  [inline]
```

Get the generation time.

Calculates the generating time

Parameters

agent_id,virus_id,time,gentime	vectors where to save the values

The generation time is the time between the infection of the source and the infection of the target.

17.9.2.2 get_reproductive_number()

```
template<typename TSeq >
MapVec_type< int, int > DataBase< TSeq >::get_reproductive_number  [inline]
```

Computes the reproductive number of each case.

By definition, whereas it computes R0 (basic reproductive number) or Rt/R (the effective reproductive number) will depend on whether the virus is allowed to circulate naïvely or not, respectively.

Parameters

fn	File where to write out the reproductive number.

In the case of `MapVec_type<int,int>`, the key is a vector of 3 integers:

- Virus id
- Source id
- Date when the source was infected

17.9.2.3 get_transition_probability()

```
template<typename TSeq >
std::vector< epiworld_double > DataBase< TSeq >::get_transition_probability (
            bool print = true,
            bool normalize = true ) const  [inline]
```

Calculates the transition probabilities.

Parameters

print	Print the transition matrix.
normalize	Normalize the transition matrix. Otherwise, it returns raw counts.

The transition matrix is the matrix of the counts of transitions from one state to another. So the ij-th element of the matrix is the number of transitions from state i to state j (when not normalized), or the probability of transitioning from state i to state j (when normalized).

Returns

std::vector< epiworld_double >

17.9.2.4 get_transmissions()

```
template<typename TSeq >
void DataBase< TSeq >::get_transmissions (
            std::vector< int > & date,
            std::vector< int > & source,
            std::vector< int > & target,
            std::vector< int > & virus,
            std::vector< int > & source_exposure_date ) const [inline]
```

Get the transmissions object.

Parameters

date	
source	
target	
virus	
source_exposure_date	

17.9.2.5 operator==() [1/3]

```
bool DataBase< std::vector< int > >::operator== (
            const DataBase< std::vector< int >> & other ) const [inline]
```

< Date of the transmission eve,

< Id of the sour,

< Id of the targ,

< Id of the varia,

< Date when the source acquired the varia,

17.9.2.6 operator==() [2/3]

```
bool DataBase< std::vector< int > >::operator== (
            const DataBase< std::vector< int >> & other ) const [inline]
```

< Date of the transmission eve,

< Id of the sour,

< Id of the targ,

< Id of the varia,

< Date when the source acquired the varia,

17.9.2.7 operator==() [3/3]

```
template<typename TSeq >
bool DataBase< TSeq >::operator== (
            const DataBase< TSeq > & other ) const  [inline]
```

< Date of the transmission eve

< Id of the sour

< Id of the targ

< Id of the varia

< Date when the source acquired the varia

17.9.2.8 record_virus()

```
template<typename TSeq >
void DataBase< TSeq >::record_virus (
            Virus< TSeq > & v )  [inline]
```

Registering a new variant.

Parameters

v	Pointer to the new virus. Since viruses are originated in the agent, the numbers simply move around. From the parent virus to the new virus. And the total number of infected does not change.

The documentation for this class was generated from the following files:

- include/epiworld/database-bones.hpp
- include/epiworld/database-meat.hpp

17.10 epiworld::DataBase< TSeq > Class Template Reference

Statistical data about the process.

`#include <epiworld.hpp>`

Public Member Functions

- **DataBase** (Model< TSeq > &m)
- **DataBase** (const DataBase< TSeq > &db)
- void record_virus (Virus< TSeq > &v)

    Registering a new variant.
- void **record_tool** (Tool< TSeq > &t)
- void **set_seq_hasher** (std::function< std::vector< int >(TSeq)> fun)
- void **reset** ()

- Model< TSeq > * **get_model** ()
- void **record** ()
- const std::vector< TSeq > & **get_sequence** () const
- const std::vector< int > & **get_nexposed** () const
- size_t **size** () const
- void **write_data** (std::string fn_virus_info, std::string fn_virus_hist, std::string fn_tool_info, std::string fn_tool_hist, std::string fn_total_hist, std::string fn_transmission, std::string fn_transition, std::string fn_reproductive_number, std::string fn_generation_time) const
- void **record_transmission** (int i, int j, int virus, int i_expo_date)
- size_t get_n_viruses () const

  Get the number of viruses.
- size_t get_n_tools () const

  Get the number of tools.
- void **set_user_data** (std::vector< std::string > names)
- void **add_user_data** (std::vector< epiworld_double > x)
- void **add_user_data** (epiworld_fast_uint j, epiworld_double x)
- UserData< TSeq > & **get_user_data** ()
- std::vector< epiworld_double > get_transition_probability (bool print=true, bool normalize=true) const

  Calculates the transition probabilities.
- bool operator== (const DataBase< TSeq > &other) const
- bool **operator!=** (const DataBase< TSeq > &other) const

Get recorded information from the model

Parameters

what	*std::string, The state, e.g., 0, 1, 2, ...*

Returns

In `get_today_total`, the current counts of `what`.

In `get_today_virus`, the current counts of `what` for each virus.

In `get_hist_total`, the time series of `what`

In `get_hist_virus`, the time series of what for each virus.

In `get_hist_total_date` and `get_hist_virus_date` the corresponding date

- int **get_today_total** (const std::string &what) const
- int **get_today_total** (const epiworld_fast_uint &what) const
- void **get_today_total** (std::vector< std::string > *state=nullptr, std::vector< int > *counts=nullptr) const
- void **get_today_virus** (std::vector< std::string > &state, std::vector< int > &id, std::vector< int > &counts) const
- void **get_today_transition_matrix** (std::vector< int > &counts) const
- void **get_hist_total** (std::vector< int > *date, std::vector< std::string > *state, std::vector< int > *counts) const
- void **get_hist_virus** (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &state, std::vector< int > &counts) const
- void **get_hist_tool** (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &state, std::vector< int > &counts) const
- void **get_hist_transition_matrix** (std::vector< std::string > &state_from, std::vector< std::string > &state_to, std::vector< int > &date, std::vector< int > &counts, bool skip_zeros) const

- void get_transmissions (std::vector< int > &date, std::vector< int > &source, std::vector< int > &target, std::vector< int > &virus, std::vector< int > &source_exposure_date) const

Get the transmissions object.

- void **get_transmissions** (int ∗date, int ∗source, int ∗target, int ∗virus, int ∗source_exposure_date) const
- MapVec_type< int, int > get_reproductive_number () const

  Computes the reproductive number of each case.
- void **get_reproductive_number** (std::string fn) const
- void get_generation_time (std::vector< int > &agent_id, std::vector< int > &virus_id, std::vector< int > &time, std::vector< int > &gentime) const

  Get the generation time.
- void get_generation_time (std::string fn) const

  Write the generation time to a file.

Friends

- class **Model**< **TSeq** >
- void **default_add_virus** (Event< TSeq > &a, Model< TSeq > ∗m)
- void **default_add_tool** (Event< TSeq > &a, Model< TSeq > ∗m)
- void **default_rm_virus** (Event< TSeq > &a, Model< TSeq > ∗m)
- void **default_rm_tool** (Event< TSeq > &a, Model< TSeq > ∗m)
- void **default_change_state** (Event< TSeq > &a, Model< TSeq > ∗m)

17.10.1 Detailed Description

template<typename TSeq>
class epiworld::DataBase< TSeq >

Statistical data about the process.

Template Parameters

TSeq	

17.10.2 Member Function Documentation

17.10.2.1 get_generation_time()

```
template<typename TSeq >
void DataBase< TSeq >::get_generation_time (
```

```
std::vector< int > & agent_id,
std::vector< int > & virus_id,
std::vector< int > & time,
std::vector< int > & gentime ) const [inline]
```

Get the generation time.

Calculates the generating time

Parameters

agent_id,virus_id,time,gentime	vectors where to save the values

The generation time is the time between the infection of the source and the infection of the target.

17.10.2.2 get_reproductive_number()

```
template<typename TSeq >
MapVec_type< int, int > DataBase< TSeq >::get_reproductive_number [inline]
```

Computes the reproductive number of each case.

By definition, whereas it computes R0 (basic reproductive number) or Rt/R (the effective reproductive number) will depend on whether the virus is allowed to circulate naïvely or not, respectively.

Parameters

fn	File where to write out the reproductive number.

In the case of `MapVec_type<int,int>`, the key is a vector of 3 integers:

- Virus id
- Source id
- Date when the source was infected

17.10.2.3 get_transition_probability()

```
template<typename TSeq >
std::vector< epiworld_double > DataBase< TSeq >::get_transition_probability (
            bool print = true,
            bool normalize = true ) const [inline]
```

Calculates the transition probabilities.

Parameters

print	Print the transition matrix.
normalize	Normalize the transition matrix. Otherwise, it returns raw counts.

The transition matrix is the matrix of the counts of transitions from one state to another. So the ij-th element of the matrix is the number of transitions from state i to state j (when not normalized), or the probability of transitioning from state i to state j (when normalized).

Returns

std::vector< epiworld_double >

17.10.2.4 get_transmissions()

```
template<typename TSeq >
void DataBase< TSeq >::get_transmissions (
            std::vector< int > & date,
            std::vector< int > & source,
            std::vector< int > & target,
            std::vector< int > & virus,
            std::vector< int > & source_exposure_date ) const  [inline]
```

Get the transmissions object.

Parameters

date	
source	
target	
virus	
source_exposure_date	

17.10.2.5 operator==()

```
template<typename TSeq >
bool DataBase< TSeq >::operator== (
            const DataBase< TSeq > & other ) const  [inline]
```

< Date of the transmission eve

< Id of the sour

< Id of the targ

< Id of the varia

< Date when the source acquired the varia

17.10.2.6 record_virus()

```
template<typename TSeq >
void DataBase< TSeq >::record_virus (
            Virus< TSeq > & v )  [inline]
```

Registering a new variant.

Parameters

v	Pointer to the new virus. Since viruses are originated in the agent, the numbers simply move around. From the parent virus to the new virus. And the total number of infected does not change.

The documentation for this class was generated from the following file:

- epiworld.hpp

17.11 Entities< TSeq > Class Template Reference

Set of Entities (useful for building iterators)

```
#include <entities-bones.hpp>
```

Public Member Functions

- **Entities** (Agent< TSeq > &p)
- std::vector< Entity< TSeq > * >::iterator **begin** ()
- std::vector< Entity< TSeq > * >::iterator **end** ()
- Entity< TSeq > & **operator()** (size_t i)
- Entity< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- bool **operator==** (const Entities< TSeq > &other) const

Friends

- class **Entity**< **TSeq** >
- class **Agent**< **TSeq** >

17.11.1 Detailed Description

template<typename TSeq>
class Entities< TSeq >

Set of Entities (useful for building iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/entities-bones.hpp

17.12 epiworld::Entities< TSeq > Class Template Reference

Set of Entities (useful for building iterators)

```
#include <epiworld.hpp>
```

Public Member Functions

- **Entities** (Agent< TSeq > &p)
- std::vector< Entity< TSeq > * >::iterator **begin** ()
- std::vector< Entity< TSeq > * >::iterator **end** ()
- Entity< TSeq > & **operator()** (size_t i)
- Entity< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- bool **operator==** (const Entities< TSeq > &other) const

Friends

- class **Entity**< **TSeq** >
- class **Agent**< **TSeq** >

17.12.1 Detailed Description

template<typename TSeq>
class epiworld::Entities< TSeq >

Set of Entities (useful for building iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following file:

- epiworld.hpp

17.13 Entities_const< TSeq > Class Template Reference

Set of Entities (const) (useful for iterators)

```
#include <entities-bones.hpp>
```

Public Member Functions

- **Entities_const** (const Agent< TSeq > &p)
- std::vector< Entity< TSeq > * >::const_iterator **begin** ()
- std::vector< Entity< TSeq > * >::const_iterator **end** ()
- const Entity< TSeq > & **operator()** (size_t i)
- const Entity< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- bool **operator==** (const Entities_const< TSeq > &other) const

Friends

- class **Virus**< **TSeq** >
- class **Agent**< **TSeq** >

17.13.1 Detailed Description

template<typename TSeq>
class Entities_const< TSeq >

Set of Entities (const) (useful for iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following file:

- include/epiworld/entities-bones.hpp

17.14 epiworld::Entities_const< TSeq > Class Template Reference

Set of Entities (const) (useful for iterators)

```
#include <epiworld.hpp>
```

Public Member Functions

- **Entities_const** (const Agent< TSeq > &p)
- std::vector< Entity< TSeq > * >::const_iterator **begin** ()
- std::vector< Entity< TSeq > * >::const_iterator **end** ()
- const Entity< TSeq > & **operator()** (size_t i)
- const Entity< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- bool **operator==** (const Entities_const< TSeq > &other) const

Friends

- class **Virus**< **TSeq** >
- class **Agent**< **TSeq** >

17.14.1 Detailed Description

template<typename TSeq>
class epiworld::Entities_const< TSeq >

Set of Entities (const) (useful for iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following file:

- epiworld.hpp

17.15 Entity< TSeq > Class Template Reference

Public Member Functions

- Entity (std::string name, EntityToAgentFun< TSeq > fun=nullptr)
  Constructs an Entity object.
- void **add_agent** (Agent< TSeq > &p, Model< TSeq > ∗model)
- void **add_agent** (Agent< TSeq > ∗p, Model< TSeq > ∗model)
- void **rm_agent** (size_t idx, Model< TSeq > ∗model)
- size_t **size** () const noexcept
- void **set_location** (std::vector< epiworld_double > loc)
- std::vector< epiworld_double > & **get_location** ()
- std::vector< size_t >::iterator **begin** ()
- std::vector< size_t >::iterator **end** ()
- std::vector< size_t >::const_iterator **begin** () const
- std::vector< size_t >::const_iterator **end** () const
- size_t **operator[ ]** (size_t i)
- int **get_id** () const noexcept
- const std::string & **get_name** () const noexcept
- void **set_state** (epiworld_fast_int init, epiworld_fast_int post)
- void **set_queue** (epiworld_fast_int init, epiworld_fast_int post)
- void **get_state** (epiworld_fast_int ∗init, epiworld_fast_int ∗post)
- void **get_queue** (epiworld_fast_int ∗init, epiworld_fast_int ∗post)
- void **reset** ()
- bool **operator==** (const Entity< TSeq > &other) const
- bool **operator!=** (const Entity< TSeq > &other) const

Entity distribution

These functions are used for distributing agents among entities. The idea is to have a flexible way of distributing agents among entities.

- void **distribute** (Model< TSeq > ∗model)
- std::vector< size_t > & **get_agents** ()
- void **print** () const
- void **set_distribution** (EntityToAgentFun< TSeq > fun)

Friends

- class **Agent**< **TSeq** >
- class **AgentsSample**< **TSeq** >
- class **Model**< **TSeq** >
- void **default_add_entity** (Event< TSeq > &a, Model< TSeq > *m)
- void default_rm_entity (Event< TSeq > &a, Model< TSeq > *m)

17.15.1 Constructor & Destructor Documentation

17.15.1.1 Entity()

```
template<typename TSeq >
Entity< TSeq >::Entity (
            std::string name,
            EntityToAgentFun< TSeq > fun = nullptr )  [inline]
```

Constructs an Entity object.

This constructor initializes an Entity object with the specified parameters.

Parameters

name	The name of the entity.
fun	A function pointer to a function that maps the entity to an agent.

17.15.2 Friends And Related Function Documentation

17.15.2.1 default_rm_entity

```
template<typename TSeq >
void default_rm_entity (
            Event< TSeq > & a,
            Model< TSeq > * m )  [friend]
```

< Last entity of the agent

< Last agent of the entity

< Last entity of the agent

< Last agent of the entity

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/entity-bones.hpp
- include/epiworld/entity-meat.hpp

17.16 epiworld::Entity< TSeq > Class Template Reference

Public Member Functions

- Entity (std::string name, EntityToAgentFun< TSeq > fun=nullptr)

  Constructs an Entity object.
- void **add_agent** (Agent< TSeq > &p, Model< TSeq > *model)
- void **add_agent** (Agent< TSeq > *p, Model< TSeq > *model)
- void **rm_agent** (size_t idx, Model< TSeq > *model)
- size_t **size** () const noexcept
- void **set_location** (std::vector< epiworld_double > loc)
- std::vector< epiworld_double > & **get_location** ()
- std::vector< size_t >::iterator **begin** ()
- std::vector< size_t >::iterator **end** ()
- std::vector< size_t >::const_iterator **begin** () const
- std::vector< size_t >::const_iterator **end** () const
- size_t **operator[ ]** (size_t i)
- int **get_id** () const noexcept
- const std::string & **get_name** () const noexcept
- void **set_state** (epiworld_fast_int init, epiworld_fast_int post)
- void **set_queue** (epiworld_fast_int init, epiworld_fast_int post)
- void **get_state** (epiworld_fast_int *init, epiworld_fast_int *post)
- void **get_queue** (epiworld_fast_int *init, epiworld_fast_int *post)
- void **reset** ()
- bool **operator==** (const Entity< TSeq > &other) const
- bool **operator!=** (const Entity< TSeq > &other) const

Entity distribution

These functions are used for distributing agents among entities. The idea is to have a flexible way of distributing agents among entities.

- void **distribute** (Model< TSeq > *model)
- std::vector< size_t > & **get_agents** ()
- void **print** () const
- void **set_distribution** (EntityToAgentFun< TSeq > fun)

Friends

- class **Agent< TSeq >**
- class **AgentsSample< TSeq >**
- class **Model< TSeq >**
- void **default_add_entity** (Event< TSeq > &a, Model< TSeq > *m)
- void default_rm_entity (Event< TSeq > &a, Model< TSeq > *m)

17.16.1 Constructor & Destructor Documentation

17.16.1.1 Entity()

```
template<typename TSeq >
epiworld::Entity< TSeq >::Entity (
            std::string name,
            EntityToAgentFun< TSeq > fun = nullptr )  [inline]
```

Constructs an Entity object.

This constructor initializes an Entity object with the specified parameters.

Parameters

name	The name of the entity.
fun	A function pointer to a function that maps the entity to an agent.

17.16.2 Friends And Related Function Documentation

17.16.2.1 default_rm_entity

```
template<typename TSeq >
void default_rm_entity (
            Event< TSeq > & a,
            Model< TSeq > * m )  [friend]
```

< Last entity of the agent

< Last agent of the entity

The documentation for this class was generated from the following file:

- epiworld.hpp

17.17 epiworld::Event< TSeq > Struct Template Reference

Event data for update an agent.

`#include <epiworld.hpp>`

Public Member Functions

- Event (Agent< TSeq > *agent_, VirusPtr< TSeq > &virus_, ToolPtr< TSeq > &tool_, Entity< TSeq > *entity_, epiworld_fast_int new_state_, epiworld_fast_int queue_, EventFun< TSeq > &call_, int idx_agent↩ _, int idx_object_)

    Construct a new Event object.

Public Attributes

- Agent< TSeq > * **agent**
- VirusPtr< TSeq > **virus**
- ToolPtr< TSeq > **tool**
- Entity< TSeq > * **entity**
- epiworld_fast_int **new_state**
- epiworld_fast_int **queue**
- EventFun< TSeq > **call**
- int **idx_agent**
- int **idx_object**

17.17.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
struct epiworld::Event< TSeq >

Event data for update an agent.

Template Parameters

TSeq	

17.17.2 Constructor & Destructor Documentation

17.17.2.1 Event()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
epiworld::Event< TSeq >::Event (
            Agent< TSeq > * agent_,
            VirusPtr< TSeq > & virus_,
            ToolPtr< TSeq > & tool_,
            Entity< TSeq > * entity_,
            epiworld_fast_int new_state_,
            epiworld_fast_int queue_,
            EventFun< TSeq > & call_,
            int idx_agent_,
            int idx_object_ )  [inline]
```

Construct a new Event object.

All the parameters are rather optional.

Parameters

*agent_*	Agent over who the action will happen
*virus_*	Virus to add
*tool_*	Tool to add
virus_idx	Index of virus to be removed (if needed)
tool_idx	Index of tool to be removed (if needed)
*new_↩ state_*	Next state
*queue_*	Efect on the queue
*call_*	The action call (if needed)
*idx_↩ agent_*	Location of agent in object.
*idx_↩ object_*	Location of object in agent.

The documentation for this struct was generated from the following file:

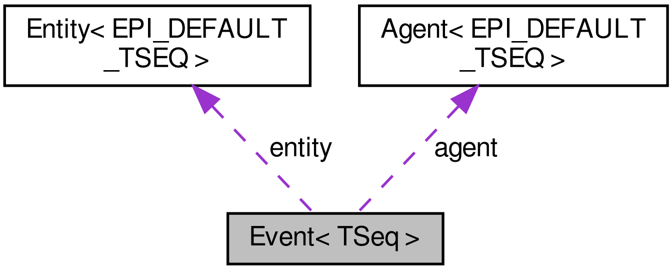
- epiworld.hpp

17.18 Event< TSeq > Struct Template Reference

Event data for update an agent.

```
#include <config.hpp>
```

Collaboration diagram for Event< TSeq >:



Public Member Functions

- Event (Agent< TSeq > *agent_, VirusPtr< TSeq > &virus_, ToolPtr< TSeq > &tool_, Entity< TSeq > *entity_, epiworld_fast_int new_state_, epiworld_fast_int queue_, EventFun< TSeq > &call_, int idx_agent↩ _, int idx_object_)

    Construct a new Event object.

Public Attributes

- Agent< TSeq > * **agent**
- VirusPtr< TSeq > **virus**
- ToolPtr< TSeq > **tool**
- Entity< TSeq > * **entity**
- epiworld_fast_int **new_state**
- epiworld_fast_int **queue**
- EventFun< TSeq > **call**
- int **idx_agent**
- int **idx_object**

17.18.1 Detailed Description

template< typename TSeq = EPI_DEFAULT_TSEQ >
struct Event< TSeq >

Event data for update an agent.

Template Parameters

TSeq	

17.18.2 Constructor & Destructor Documentation

17.18.2.1 Event()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
Event< TSeq >::Event (
            Agent< TSeq > * agent_,
            VirusPtr< TSeq > & virus_,
            ToolPtr< TSeq > & tool_,
            Entity< TSeq > * entity_,
            epiworld_fast_int new_state_,
            epiworld_fast_int queue_,
            EventFun< TSeq > & call_,
            int idx_agent_,
            int idx_object_ )  [inline]
```

Construct a new Event object.

All the parameters are rather optional.

Parameters

*agent_*	Agent over who the action will happen
*virus_*	Virus to add
*tool_*	Tool to add
virus_idx	Index of virus to be removed (if needed)
tool_idx	Index of tool to be removed (if needed)
*new_↩ state_*	Next state
*queue_*	Efect on the queue
*call_*	The action call (if needed)
*idx_↩ agent_*	Location of agent in object.
*idx_↩ object_*	Location of object in agent.

The documentation for this struct was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/config.hpp

17.19 epiworld::GlobalEvent< TSeq > Class Template Reference

Template for a Global Event.

```
#include <epiworld.hpp>
```

Public Member Functions

- GlobalEvent (GlobalFun< TSeq > fun, std::string name, int day=-99)
  Construct a new Global Event object.
- void **operator()** (Model< TSeq > ∗m, int day)
- void **set_name** (std::string name)
- std::string **get_name** () const
- void **set_day** (int day)
- int **get_day** () const
- void **print** () const
- bool **operator==** (const GlobalEvent< TSeq > &other) const
- bool **operator!=** (const GlobalEvent< TSeq > &other) const

17.19.1 Detailed Description

template<typename TSeq>
class epiworld::GlobalEvent< TSeq >

Template for a Global Event.

Global events are functions that Model<TSeq> executes at the end of a day.

17.19.2 Constructor & Destructor Documentation

17.19.2.1 GlobalEvent()

```
template<typename TSeq >
GlobalEvent< TSeq >::GlobalEvent (
            GlobalFun< TSeq > fun,
            std::string name,
            int day = -99 )  [inline]
```

Construct a new Global Event object.

Parameters

fun	A function that takes a Model<TSeq> ∗ as argument and returns void.
name	A descriptive name for the action.
day	The day when the action will be executed. If negative, it will be executed every day.

The documentation for this class was generated from the following file:

- epiworld.hpp

17.20 GlobalEvent< TSeq > Class Template Reference

Template for a Global Event.

```
#include <globalevent-bones.hpp>
```

Public Member Functions

- GlobalEvent (GlobalFun< TSeq > fun, std::string name, int day=-99)
  Construct a new Global Event object.
- void **operator()** (Model< TSeq > *m, int day)
- void **set_name** (std::string name)
- std::string **get_name** () const
- void **set_day** (int day)
- int **get_day** () const
- void **print** () const
- bool **operator==** (const GlobalEvent< TSeq > &other) const
- bool **operator!=** (const GlobalEvent< TSeq > &other) const

17.20.1 Detailed Description

template<typename TSeq>
class GlobalEvent< TSeq >

Template for a Global Event.

Global events are functions that Model<TSeq> executes at the end of a day.

17.20.2 Constructor & Destructor Documentation

17.20.2.1 GlobalEvent()

```
template<typename TSeq >
GlobalEvent< TSeq >::GlobalEvent (
            GlobalFun< TSeq > fun,
            std::string name,
            int day = -99 )  [inline]
```

Construct a new Global Event object.

Parameters

fun	A function that takes a Model<TSeq> * as argument and returns void.
name	A descriptive name for the action.
day	The day when the action will be executed. If negative, it will be executed every day.

The documentation for this class was generated from the following files:

- include/epiworld/globalevent-bones.hpp
- include/epiworld/globalevent-meat.hpp

17.21 epiworld::LFMCMC< TData > Class Template Reference

Likelihood-Free Markov Chain Monte Carlo.

```
#include <epiworld.hpp>
```

Public Member Functions

- void **run** (std::vector< epiworld_double > params_init_, size_t n_samples_, epiworld_double epsilon_, int seed=-1)
- **LFMCMC** (const TData &observed_data_)
- void **set_observed_data** (const TData &observed_data_)
- void **set_proposal_fun** (LFMCMCProposalFun< TData > fun)
- void **set_simulation_fun** (LFMCMCSimFun< TData > fun)
- void **set_summary_fun** (LFMCMCSummaryFun< TData > fun)
- void **set_kernel_fun** (LFMCMCKernelFun< TData > fun)
- void **set_params_names** (std::vector< std::string > names)
- void **set_stats_names** (std::vector< std::string > names)
- size_t **get_n_samples** () const
- size_t **get_n_stats** () const
- size_t **get_n_params** () const
- epiworld_double **get_epsilon** () const
- const std::vector< epiworld_double > & **get_initial_params** () const
- const std::vector< epiworld_double > & **get_current_proposed_params** () const
- const std::vector< epiworld_double > & **get_current_accepted_params** () const
- const std::vector< epiworld_double > & **get_current_proposed_stats** () const
- const std::vector< epiworld_double > & **get_current_accepted_stats** () const
- const std::vector< epiworld_double > & **get_observed_stats** () const
- const std::vector< epiworld_double > & **get_all_sample_params** () const
- const std::vector< epiworld_double > & **get_all_sample_stats** () const
- const std::vector< bool > & **get_all_sample_acceptance** () const
- const std::vector< epiworld_double > & **get_all_sample_drawn_prob** () const
- const std::vector< epiworld_double > & **get_all_sample_kernel_scores** () const
- const std::vector< epiworld_double > & **get_all_accepted_params** () const
- const std::vector< epiworld_double > & **get_all_accepted_stats** () const
- const std::vector< epiworld_double > & **get_all_accepted_kernel_scores** () const
- std::vector< TData > * **get_simulated_data** () const
- std::vector< epiworld_double > **get_mean_params** ()
- std::vector< epiworld_double > **get_mean_stats** ()
- LFMCMC< TData > & **verbose_off** ()
- LFMCMC< TData > & **verbose_on** ()
- void **print** (size_t burnin=0u) const

Random number generation

Parameters

eng	

- void **set_rand_engine** (std::shared_ptr< std::mt19937 > &eng)
- std::shared_ptr< std::mt19937 > & **get_rand_endgine** ()
- void **seed** (epiworld_fast_uint s)
- void **set_rand_gamma** (epiworld_double alpha, epiworld_double beta)
- epiworld_double **runif** ()
- epiworld_double **rnorm** ()
- epiworld_double **rgamma** ()
- epiworld_double **runif** (epiworld_double lb, epiworld_double ub)
- epiworld_double **rnorm** (epiworld_double mean, epiworld_double sd)
- epiworld_double **rgamma** (epiworld_double alpha, epiworld_double beta)

17.21.1 Detailed Description

template<typename TData>
class epiworld::LFMCMC< TData >

Likelihood-Free Markov Chain Monte Carlo.

Template Parameters

TData	Type of data that is generated

The documentation for this class was generated from the following file:

- epiworld.hpp

17.22 LFMCMC< TData > Class Template Reference

Likelihood-Free Markov Chain Monte Carlo.

```
#include <lfmcmc-bones.hpp>
```

Public Member Functions

- void **run** (std::vector< epiworld_double > params_init_, size_t n_samples_, epiworld_double epsilon_, int seed=-1)
- **LFMCMC** (const TData &observed_data_)
- void **set_observed_data** (const TData &observed_data_)
- void **set_proposal_fun** (LFMCMCProposalFun< TData > fun)
- void **set_simulation_fun** (LFMCMCSimFun< TData > fun)
- void **set_summary_fun** (LFMCMCSummaryFun< TData > fun)
- void **set_kernel_fun** (LFMCMCKernelFun< TData > fun)
- void **set_params_names** (std::vector< std::string > names)
- void **set_stats_names** (std::vector< std::string > names)
- size_t **get_n_samples** () const

- size_t **get_n_stats** () const
- size_t **get_n_params** () const
- epiworld_double **get_epsilon** () const
- const std::vector< epiworld_double > & **get_initial_params** () const
- const std::vector< epiworld_double > & **get_current_proposed_params** () const
- const std::vector< epiworld_double > & **get_current_accepted_params** () const
- const std::vector< epiworld_double > & **get_current_proposed_stats** () const
- const std::vector< epiworld_double > & **get_current_accepted_stats** () const
- const std::vector< epiworld_double > & **get_observed_stats** () const
- const std::vector< epiworld_double > & **get_all_sample_params** () const
- const std::vector< epiworld_double > & **get_all_sample_stats** () const
- const std::vector< bool > & **get_all_sample_acceptance** () const
- const std::vector< epiworld_double > & **get_all_sample_drawn_prob** () const
- const std::vector< epiworld_double > & **get_all_sample_kernel_scores** () const
- const std::vector< epiworld_double > & **get_all_accepted_params** () const
- const std::vector< epiworld_double > & **get_all_accepted_stats** () const
- const std::vector< epiworld_double > & **get_all_accepted_kernel_scores** () const
- std::vector< TData > * **get_simulated_data** () const
- std::vector< epiworld_double > **get_mean_params** ()
- std::vector< epiworld_double > **get_mean_stats** ()
- LFMCMC< TData > & **verbose_off** ()
- LFMCMC< TData > & **verbose_on** ()
- void **print** (size_t burnin=0u) const

Random number generation

Parameters

eng	

- void **set_rand_engine** (std::shared_ptr< std::mt19937 > &eng)
- std::shared_ptr< std::mt19937 > & **get_rand_endgine** ()
- void **seed** (epiworld_fast_uint s)
- void **set_rand_gamma** (epiworld_double alpha, epiworld_double beta)
- epiworld_double **runif** ()
- epiworld_double **rnorm** ()
- epiworld_double **rgamma** ()
- epiworld_double **runif** (epiworld_double lb, epiworld_double ub)
- epiworld_double **rnorm** (epiworld_double mean, epiworld_double sd)
- epiworld_double **rgamma** (epiworld_double alpha, epiworld_double beta)

17.22.1 Detailed Description

template<typename TData>
class LFMCMC< TData >

Likelihood-Free Markov Chain Monte Carlo.

Template Parameters

TData	Type of data that is generated

The documentation for this class was generated from the following files:

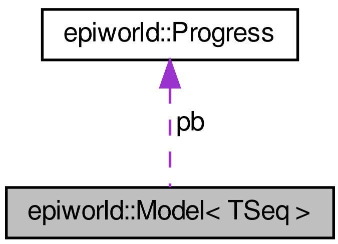
- include/epiworld/math/lfmcmc/lfmcmc-bones.hpp
- include/epiworld/math/lfmcmc/lfmcmc-meat-print.hpp
- include/epiworld/math/lfmcmc/lfmcmc-meat.hpp

17.23 epiworld::Model< TSeq > Class Template Reference

Core class of epiworld.

```
#include <epiworld.hpp>
```

Collaboration diagram for epiworld::Model< TSeq >:



Public Member Functions

- DataBase< TSeq > & **get_db** ()
- const DataBase< TSeq > & **get_db** () const
- epiworld_double & **operator()** (std::string pname)
- size_t **size** () const
- void load_agents_entities_ties (std::string fn, int skip)

  Associate agents-entities from a file.
- void load_agents_entities_ties (const std::vector< int > &agents_ids, const std::vector< int > &entities_ids)

  Associate agents-entities from data.
- void **load_agents_entities_ties** (const int *agents_id, const int *entities_id, size_t n)
- size_t get_n_viruses () const

  Number of viruses in the model.
- size_t get_n_tools () const

  Number of tools in the model.
- epiworld_fast_uint **get_ndays** () const
- epiworld_fast_uint **get_n_replicates** () const
- size_t **get_n_entities** () const
- void **set_ndays** (epiworld_fast_uint ndays)
- bool **get_verbose** () const
- Model< TSeq > & **verbose_off** ()
- Model< TSeq > & **verbose_on** ()

- int today () const

  The current time of the model.
- void write_data (std::string fn_virus_info, std::string fn_virus_hist, std::string fn_tool_info, std::string fn↩ _tool_hist, std::string fn_total_hist, std::string fn_transmission, std::string fn_transition, std::string fn_↩ reproductive_number, std::string fn_generation_time) const

  Wrapper of `DataBase::write_data`
- std::map< std::string, epiworld_double > & **params** ()
- virtual void reset ()

  Reset the model.
- const Model< TSeq > & **print** (bool lite=false) const
- void **get_elapsed** (std::string unit="auto", epiworld_double *last_elapsed=nullptr, epiworld_double *total_↩ elapsed=nullptr, std::string *unit_abbr=nullptr, bool print=true) const
- void add_globalevent (std::function< void(Model< TSeq > *)> fun, std::string name="A global action", int date=-99)

  Set a global action.
- void **add_globalevent** (GlobalEvent< TSeq > action)
- GlobalEvent< TSeq > & get_globalevent (std::string name)

  Retrieve a global action by name.
- GlobalEvent< TSeq > & get_globalevent (size_t i)

  Retrieve a global action by index.
- void rm_globalevent (std::string name)

  Remove a global action by name.
- void rm_globalevent (size_t i)

  Remove a global action by index.
- void **run_globalevents** ()
- void **clear_state_set** ()
- const std::vector< VirusPtr< TSeq > > & **get_viruses** () const
- const std::vector< ToolPtr< TSeq > > & **get_tools** () const
- Virus< TSeq > & **get_virus** (size_t id)
- Tool< TSeq > & **get_tool** (size_t id)
- void set_agents_data (double *data_, size_t ncols_)

  Set the agents data object.
- double * **get_agents_data** ()
- size_t **get_agents_data_ncols** () const
- void set_name (std::string name)

  Set the name object.
- std::string **get_name** () const
- bool **operator==** (const Model< TSeq > &other) const
- bool **operator!=** (const Model< TSeq > &other) const
- void events_run ()

  Executes the stored action.
- void draw (DiagramType diagram_type=DiagramType::Mermaid, const std::string &fn_output="", bool self=false)

  Draws a mermaid diagram of the model.

Set the backup object

`backup` can be used to restore the entire object after a run. This can be useful if the user wishes to have individuals start with the same network from the beginning.

- void **set_backup** ()

Random number generation

Parameters

eng	*Random number generator*
s	*Seed*

- void **set_rand_engine** (std::shared_ptr< std::mt19937 > &eng)
- std::shared_ptr< std::mt19937 > & **get_rand_endgine** ()
- void **seed** (size_t s)
- void **set_rand_norm** (epiworld_double mean, epiworld_double sd)
- void **set_rand_unif** (epiworld_double a, epiworld_double b)
- void **set_rand_exp** (epiworld_double lambda)
- void **set_rand_gamma** (epiworld_double alpha, epiworld_double beta)
- void **set_rand_lognormal** (epiworld_double mean, epiworld_double shape)
- void **set_rand_binom** (int n, epiworld_double p)
- void **set_rand_nbinom** (int n, epiworld_double p)
- void **set_rand_geom** (epiworld_double p)
- void **set_rand_poiss** (epiworld_double lambda)
- epiworld_double **runif** ()
- epiworld_double **runif** (epiworld_double a, epiworld_double b)
- epiworld_double **rnorm** ()
- epiworld_double **rnorm** (epiworld_double mean, epiworld_double sd)
- epiworld_double **rgamma** ()
- epiworld_double **rgamma** (epiworld_double alpha, epiworld_double beta)
- epiworld_double **rexp** ()
- epiworld_double **rexp** (epiworld_double lambda)
- epiworld_double **rlognormal** ()
- epiworld_double **rlognormal** (epiworld_double mean, epiworld_double shape)
- int **rbinom** ()
- int **rbinom** (int n, epiworld_double p)
- int **rnbinom** ()
- int **rnbinom** (int n, epiworld_double p)
- int **rgeom** ()
- int **rgeom** (epiworld_double p)
- int **rpoiss** ()
- int **rpoiss** (epiworld_double lambda)

Add Virus/Tool to the model

This is done before the model has been initialized.

Parameters

v	*Virus to be added*
t	*Tool to be added*
preval	*Initial prevalence (initial state.) It can be specified as a proportion (between zero and one,) or an integer indicating number of individuals.*

- void **add_virus** (Virus< TSeq > &v)
- void **add_tool** (Tool< TSeq > &t)
- void **add_entity** (Entity< TSeq > e)
- void **rm_virus** (size_t virus_pos)
- void **rm_tool** (size_t tool_pos)
- void **rm_entity** (size_t entity_id)

Accessing population of the model

Parameters

fn	*std::string Filename of the edgelist file.*
skip	*int Number of lines to skip in `fn`.*
directed	*bool Whether the graph is directed or not.*
size	*Size of the network.*
al	*AdjList to read into the model.*

- void **agents_from_adjlist** (std::string fn, int size, int skip=0, bool directed=false)
- void **agents_from_edgelist** (const std::vector< int > &source, const std::vector< int > &target, int size, bool directed)
- void **agents_from_adjlist** (AdjList al)
- bool **is_directed** () const
- std::vector< Agent< TSeq > > & get_agents ()

  Returns a reference to the vector of agents.
- Agent< TSeq > & **get_agent** (size_t i)
- std::vector< epiworld_fast_uint > get_agents_states () const

  Returns a vector with the states of the agents.
- std::vector< Viruses_const< TSeq > > get_agents_viruses () const

  Returns a const vector with the viruses of the agents.
- std::vector< Viruses< TSeq > > get_agents_viruses ()

  Returns a vector with the viruses of the agents.
- std::vector< Entity< TSeq > > & **get_entities** ()
- Entity< TSeq > & **get_entity** (size_t entity_id, int ∗entity_pos=nullptr)
- Model< TSeq > & **agents_smallworld** (epiworld_fast_uint n=1000, epiworld_fast_uint k=5, bool d=false, epiworld_double p=.01)
- void **agents_empty_graph** (epiworld_fast_uint n=1000)

Functions to run the model

Parameters

seed	*Seed to be used for Pseudo-RNG.*
ndays	*Number of days (steps) of the simulation.*
fun	*In the case of `run_multiple`, a function that is called after each experiment.*

- void **update_state** ()
- void **mutate_virus** ()
- void **next** ()
- virtual Model< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

  Runs the simulation (after initialization)
- void run_multiple (epiworld_fast_uint ndays, epiworld_fast_uint nexperiments, int seed_=-1, std::function< void(size_t, Model< TSeq > ∗)> fun=make_save_run< TSeq >(), bool reset=true, bool verbose=true, int nthreads=1)

Rewire the network preserving the degree sequence.

This implementation assumes an undirected network, thus if {(i,j), (k,l)} -> {(i,l), (k,j)}, the reciprocal is also true, i.e., {(j,i), (l,k)} -> {(j,k), (l,i)}.

Parameters

proportion	*Proportion of ties to be rewired.*

Returns

A rewired version of the network.

- void **set_rewire_fun** (std::function< void(std::vector< Agent< TSeq >> *, Model< TSeq > *, epiworld_double)> fun)
- void **set_rewire_prop** (epiworld_double prop)
- epiworld_double **get_rewire_prop** () const
- void **rewire** ()

Export the network data in edgelist form

Parameters

fn	*std::string. File name.*
source	*Integer vector*
target	*Integer vector*

When passing the source and target, the function will write the edgelist on those.

- void **write_edgelist** (std::string fn) const
- void **write_edgelist** (std::vector< int > &source, std::vector< int > &target) const

Manage state (states) in the model

The functions `get_state` return the current values for the states included in the model.

Parameters

lab	*`std::string` Name of the state.*

Returns

`add_state*` returns nothing.

`get_state_*` returns a vector of pairs with the states and their labels.

- void **add_state** (std::string lab, UpdateFun< TSeq > fun=nullptr)
- const std::vector< std::string > & **get_states** () const
- size_t **get_n_states** () const
- const std::vector< UpdateFun< TSeq > > & **get_state_fun** () const
- void **print_state_codes** () const

Initial states

These functions are called before the simulation starts.

Parameters

proportions_	*Vector of proportions for each state.*
queue_	*Vector of queue for each state.*

- virtual Model< TSeq > & **initial_states** (std::vector< double >, std::vector< int >)

Setting and accessing parameters from the model

Tools can incorporate parameters included in the model. Internally, parameters in the tool are stored as pointers to an std::map<> of parameters in the model. Using the `epiworld_fast_uint` method directly fetches the parameters in the order these were added to the tool. Accessing parameters via the `std::string` method involves searching the parameter directly in the std::map<> member of the model (so it is not recommended.)

The `par()` function members are aliases for `get_param()`.

In the case of the function `read_params`, users can pass a file listing parameters to be included in the model. Each line in the file should have the following structure:

```
[name of parameter 1]: [value in double]
[name of parameter 2]: [value in double]
...
```

The only condition for parameter names is that these do not include a colon.

Parameters

initial_val	
pname	*Name of the parameter to add or to fetch*
fn	*Path to the file containing parameters*

Returns

The current value of the parameter in the model.

- epiworld_double **add_param** (epiworld_double initial_val, std::string pname, bool overwrite=false)
- Model< TSeq > & **read_params** (std::string fn, bool overwrite=false)
- epiworld_double **get_param** (epiworld_fast_uint k)
- epiworld_double **get_param** (std::string pname)
- void **set_param** (std::string pname, epiworld_double val)
- epiworld_double **par** (std::string pname) const

Set the user data object

Parameters

names	*string vector with the names of the variables.*

- void set_user_data (std::vector< std::string > names)

  [@
- void **add_user_data** (epiworld_fast_uint j, epiworld_double x)
- void **add_user_data** (std::vector< epiworld_double > x)
- UserData< TSeq > & **get_user_data** ()

Queuing system

When queueing is on, the model will keep track of which agents are either in risk of exposure or exposed. This then is used at each step to act only on the aforementioned agents.

- void queuing_on ()

  Activates the queuing system (default.)
- Model< TSeq > & queuing_off ()

  Deactivates the queuing system.
- bool is_queuing_on () const

  Query if the queuing system is on.
- Queue< TSeq > & get_queue ()

  Retrieve the `Queue` object.

Get the susceptibility reduction object

Parameters

v	

Returns

epiworld_double

- void **set_susceptibility_reduction_mixer** (MixerFun< TSeq > fun)
- void **set_transmission_reduction_mixer** (MixerFun< TSeq > fun)
- void **set_recovery_enhancer_mixer** (MixerFun< TSeq > fun)
- void **set_death_reduction_mixer** (MixerFun< TSeq > fun)

Protected Member Functions

- void **dist_tools** ()
- void **dist_virus** ()
- void **dist_entities** ()
- void **chrono_start** ()
- void **chrono_end** ()
- void events_add (Agent< TSeq > ∗agent_, VirusPtr< TSeq > virus_, ToolPtr< TSeq > tool_, Entity< TSeq > ∗entity_, epiworld_fast_int new_state_, epiworld_fast_int queue_, EventFun< TSeq > call_, int idx_agent_, int idx_object_)

    Construct a new Event object.

Protected Attributes

- std::string name = ""

    Name of the model.
- DataBase< TSeq > **db** = DataBase<TSeq>(∗this)
- std::vector< Agent< TSeq > > **population** = {}
- bool **using_backup** = true
- std::vector< Agent< TSeq > > **population_backup** = {}
- bool **directed** = false
- std::vector< VirusPtr< TSeq > > **viruses** = {}
- std::vector< ToolPtr< TSeq > > **tools** = {}
- std::vector< Entity< TSeq > > **entities** = {}
- std::vector< Entity< TSeq > > **entities_backup** = {}
- std::shared_ptr< std::mt19937 > **engine** = std::make_shared< std::mt19937 >()
- std::uniform_real_distribution **runifd**
- std::normal_distribution **rnormd**
- std::gamma_distribution **rgammad**
- std::lognormal_distribution **rlognormald**
- std::exponential_distribution **rexpd**
- std::binomial_distribution **rbinomd**
- std::negative_binomial_distribution **rnbinomd**
- std::geometric_distribution **rgeomd**
- std::poisson_distribution **rpoissd**
- std::function< void(std::vector< Agent< TSeq >> ∗, Model< TSeq > ∗, epiworld_double)> **rewire_fun**
- epiworld_double **rewire_prop** = 0.0
- std::map< std::string, epiworld_double > **parameters**
- epiworld_fast_uint **ndays** = 0
- Progress **pb**

- std::vector< UpdateFun< TSeq > > state_fun = {}

  Functions to update states.
- std::vector< std::string > states_labels = {}

  Labels of the states.
- std::function< void(Model< TSeq > *)> initial_states_fun
- epiworld_fast_uint **nstates** = 0u
- bool **verbose** = true
- int **current_date** = 0
- std::chrono::time_point< std::chrono::steady_clock > **time_start**
- std::chrono::time_point< std::chrono::steady_clock > **time_end**
- std::chrono::duration< epiworld_double, std::micro > **time_elapsed**
- epiworld_fast_uint **n_replicates** = 0u
- std::vector< GlobalEvent< TSeq > > **globalevents**
- Queue< TSeq > **queue**
- bool **use_queuing** = true
- std::vector< Event< TSeq > > events = {}

  Variables used to keep track of the events to be made regarding viruses.
- epiworld_fast_uint **nactions** = 0u

Auxiliary variables for AgentsSample<TSeq> iterators

These variables+objects are used by the AgentsSample<TSeq> class for building efficient iterators over agents. The idea is to reduce the memory allocation, so only during the first call of AgentsSample<TSeq>::AgentsSample(Model<TSeq>) these vectors are allocated.

- std::vector< Agent< TSeq > * > **sampled_population**
- size_t **sampled_population_n** = 0u
- std::vector< size_t > **population_left**
- size_t **population_left_n** = 0u

Agents features

Optionally, a model can include an external data source pointing to agents information. The data can then be access through the `Agent::operator()` method.

- double * **agents_data** = nullptr
- size_t **agents_data_ncols** = 0u

Friends

- class **Agent< TSeq >**
- class **AgentsSample< TSeq >**
- class **DataBase< TSeq >**
- class **Queue< TSeq >**

Tool Mixers

These functions combine the effects tools have to deliver a single effect. For example, wearing a mask, been vaccinated, and the immune system combine together to jointly reduce the susceptibility for a given virus.

- MixerFun< TSeq > **susceptibility_reduction_mixer** = susceptibility_reduction_mixer_default<TSeq>
- MixerFun< TSeq > **transmission_reduction_mixer** = transmission_reduction_mixer_default<TSeq>
- MixerFun< TSeq > **recovery_enhancer_mixer** = recovery_enhancer_mixer_default<TSeq>

- MixerFun< TSeq > **death_reduction_mixer** = death_reduction_mixer_default<TSeq>
- std::vector< epiworld_double > **array_double_tmp**
- std::vector< Virus< TSeq > * > **array_virus_tmp**
- virtual Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- **Model** ()
- **Model** (const Model< TSeq > &m)
- **Model** (Model< TSeq > &m)
- **Model** (Model< TSeq > &&m)
- Model< TSeq > & **operator=** (const Model< TSeq > &m)
- virtual ∼**Model** ()

17.23.1 Detailed Description

template<typename TSeq>
class epiworld::Model< TSeq >

Core class of epiworld.

The model class provides the wrapper that puts together `Agent`, `Virus`, and `Tools`.

Template Parameters

TSeq	Type of sequence. In principle, users can build models in which virus and human sequence is represented as numeric vectors (if needed.)

17.23.2 Member Function Documentation

17.23.2.1 add_globalevent()

```
template<typename TSeq >
void Model< TSeq >::add_globalevent (
            std::function< void(Model< TSeq > *)> fun,
            std::string name = "A global action",
            int date = -99 )  [inline]
```

Set a global action.

Parameters

fun	A function to be called on the prescribed date
name	Name of the action.
date	Integer indicating when the function is called (see details)

When date is less than zero, then the function is called at the end of every day. Otherwise, the function will be called only at the end of the indicated date.

17.23.2.2 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * Model< TSeq >::clone_ptr [inline], [protected], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented in ModelSIRMixing< TSeq >, ModelSIRLogit< TSeq >, ModelSIRDCONN< TSeq >, ModelSIRCONN< TSeq >, ModelSEIRMixingQuarantine< TSeq >, ModelSEIRMixing< TSeq >, ModelSEIRDCONN< TSeq >, ModelSEIRCONN< TSeq >, ModelMeaslesMixing< TSeq >, epiworld::epimodels::ModelMeaslesMixing< TSeq >, epiworld::epimodels::ModelSEIRMixingQuara epiworld::epimodels::ModelMeaslesSchool< TSeq >, epiworld::epimodels::ModelSIRMixing< TSeq >, epiworld::epimodels::ModelS epiworld::epimodels::ModelSIRLogit< TSeq >, epiworld::epimodels::ModelSEIRDCONN< TSeq >, epiworld::epimodels::ModelSIRD epiworld::epimodels::ModelSEIRCONN< TSeq >, and epiworld::epimodels::ModelSIRCONN< TSeq >.

17.23.2.3 draw()

```
template<typename TSeq >
void Model< TSeq >::draw (
            DiagramType diagram_type = DiagramType::Mermaid,
            const std::string & fn_output = "",
            bool self = false ) [inline]
```

Draws a mermaid diagram of the model.

Parameters

model	The model to draw.
fn_output	The name of the file to write the diagram. If empty, the diagram will be printed to the standard output.
self	Whether to allow self-transitions.

17.23.2.4 events_add()

```
template<typename TSeq >
void Model< TSeq >::events_add (
            Agent< TSeq > * agent_,
            VirusPtr< TSeq > virus_,
            ToolPtr< TSeq > tool_,
            Entity< TSeq > * entity_,
            epiworld_fast_int new_state_,
            epiworld_fast_int queue_,
            EventFun< TSeq > call_,
            int idx_agent_,
            int idx_object_ ) [inline], [protected]
```

Construct a new Event object.

Parameters

*agent_*	Agent over which the action will be called
*virus_*	Virus pointer included in the action
*tool_*	Tool pointer included in the action
*entity_*	Entity pointer included in the action
*new_↩ state_*	New state of the agent
*call_*	Function the action will call
*queue_*	Change in the queue
*idx_↩ agent_*	Location of agent in object.
*idx_↩ object_*	Location of object in agent.

17.23.2.5 events_run()

```
template<typename TSeq >
void Model< TSeq >::events_run  [inline]
```

Executes the stored action.

Parameters

model↩ _	Model over which it will be executed.

17.23.2.6 load_agents_entities_ties()

```
template<typename TSeq >
void Model< TSeq >::load_agents_entities_ties (
            std::string fn,
            int skip )  [inline]
```

Associate agents-entities from a file.

The structure of the file should be two columns separated by space. The first column indexing between 0 and nagents-1, and the second column between 0 and nentities - 1.

Parameters

fn	Path to the file.
skip	How many rows to skip.

17.23.2.7 reset()

```
template<typename TSeq >
void Model< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented in ModelSURV< TSeq >, ModelSIRMixing< TSeq >, ModelSIRLogit< TSeq >, ModelSIRDCONN< TSeq >, ModelSIRCONN< TSeq >, ModelSEIRMixingQuarantine< TSeq >, ModelSEIRMixing< TSeq >, ModelSEIRDCONN< TSeq >, ModelSEIRCONN< TSeq >, ModelMeaslesMixing< TSeq >, epiworld::epimodels::ModelMeaslesMixing< TSeq >, epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >, epiworld::epimodels::ModelMeaslesSchool< TSeq >, epiworld::epimodels::ModelSIRMixing< TSeq >, epiworld::epimodels::ModelSEIRMixing< TSeq >, epiworld::epimodels::ModelSIRL epiworld::epimodels::ModelSEIRDCONN< TSeq >, epiworld::epimodels::ModelSIRDCONN< TSeq >, epiworld::epimodels::ModelS epiworld::epimodels::ModelSIRCONN< TSeq >, and epiworld::epimodels::ModelSURV< TSeq >.

17.23.2.8 run_multiple()

```
template<typename TSeq >
void Model< TSeq >::run_multiple (
            epiworld_fast_uint ndays,
            epiworld_fast_uint nexperiments,
            int seed_ = -1,
            std::function< void(size_t, Model< TSeq > *)> fun = make_save_run<TSeq>(),
            bool reset = true,
            bool verbose = true,
            int nthreads = 1 )  [inline]
```

Parameters

ndays	Multiple runs of the simulation

17.23.2.9 set_agents_data()

```
template<typename TSeq >
void Model< TSeq >::set_agents_data (
            double * data_,
            size_t ncols_ )  [inline]
```

Set the agents data object.

The data should be an array with the data stored in a column major order, i.e., by column.

Parameters

*data_*	Pointer to the first element of an array of size `size() * ncols_`.
*ncols_*	Number of features included in the data.

17.23.2.10 set_name()

```
template<typename TSeq >
void Model< TSeq >::set_name (
            std::string name ) [inline]
```

Set the name object.

Parameters

name	

17.23.2.11 write_data()

```
template<typename TSeq >
void Model< TSeq >::write_data (
            std::string fn_virus_info,
            std::string fn_virus_hist,
            std::string fn_tool_info,
            std::string fn_tool_hist,
            std::string fn_total_hist,
            std::string fn_transmission,
            std::string fn_transition,
            std::string fn_reproductive_number,
            std::string fn_generation_time ) const [inline]
```

Wrapper of `DataBase::write_data`

Parameters

fn_virus_info	Filename. Information about the virus.
fn_virus_hist	Filename. History of the virus.
fn_tool_info	Filename. Information about the tool.
fn_tool_hist	Filename. History of the tool.
fn_total_hist	Filename. Aggregated history (state)
fn_transmission	Filename. Transmission history.
fn_transition	Filename. Markov transition history.
fn_reproductive_number	Filename. Case by case reproductive number

17.23.3 Member Data Documentation

17.23.3.1 initial_states_fun

```
template<typename TSeq >
std::function<void(Model<TSeq>*)> epiworld::Model< TSeq >::initial_states_fun [protected]
```

Initial value:

```
= [](Model<TSeq> * )
    -> void {}
```

Function to distribute states. Goes along with the function

17.23.3.2 rbinomd

```
template<typename TSeq >
std::binomial_distribution epiworld::Model< TSeq >::rbinomd [protected]
```

Initial value:

```
=
        std::binomial_distribution<>()
```

17.23.3.3 rexpd

```
template<typename TSeq >
std::exponential_distribution epiworld::Model< TSeq >::rexpd [protected]
```

Initial value:

```
=
        std::exponential_distribution<>()
```

17.23.3.4 rgammad

```
template<typename TSeq >
std::gamma_distribution epiworld::Model< TSeq >::rgammad [protected]
```

Initial value:

```
=
        std::gamma_distribution<>()
```

17.23.3.5 rgeomd

```
template<typename TSeq >
std::geometric_distribution epiworld::Model< TSeq >::rgeomd [protected]
```

Initial value:

```
=
        std::geometric_distribution<>()
```

17.23.3.6 rlognormald

```
template<typename TSeq >
std::lognormal_distribution epiworld::Model< TSeq >::rlognormald [protected]
```

Initial value:

```
=
        std::lognormal_distribution<>()
```

17.23.3.7 rnbinomd

```
template<typename TSeq >
std::negative_binomial_distribution epiworld::Model< TSeq >::rnbinomd [protected]
```

Initial value:

```
=
        std::negative_binomial_distribution<>()
```

17.23.3.8 rnormd

```
template<typename TSeq >
std::normal_distribution epiworld::Model< TSeq >::rnormd [protected]
```

Initial value:

```
=
        std::normal_distribution<>(0.0)
```

17.23.3.9 rpoissd

```
template<typename TSeq >
std::poisson_distribution epiworld::Model< TSeq >::rpoissd [protected]
```

Initial value:

```
=
        std::poisson_distribution<>()
```

17.23.3.10 runifd

```
template<typename TSeq >
std::uniform_real_distribution epiworld::Model< TSeq >::runifd [protected]
```

Initial value:

```
=
        std::uniform_real_distribution<> (0.0, 1.0)
```

17.23.3.11 time_elapsed

```
template<typename TSeq >
std::chrono::duration<epiworld_double,std::micro> epiworld::Model< TSeq >::time_elapsed [protected]
```

Initial value:

```
=
        std::chrono::duration<epiworld_double,std::micro>::zero()
```

The documentation for this class was generated from the following file:

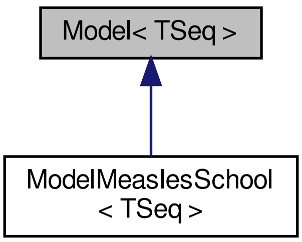
- epiworld.hpp

17.24 Model< TSeq > Class Template Reference

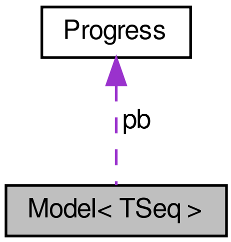
Core class of epiworld.

```
#include <model-bones.hpp>
```

Inheritance diagram for Model< TSeq >:



Collaboration diagram for Model< TSeq >:



Public Member Functions

- DataBase< TSeq > & **get_db** ()
- const DataBase< TSeq > & **get_db** () const
- epiworld_double & **operator()** (std::string pname)
- size_t **size** () const
- void load_agents_entities_ties (std::string fn, int skip)

  Associate agents-entities from a file.
- void load_agents_entities_ties (const std::vector< int > &agents_ids, const std::vector< int > &entities_ids)

  Associate agents-entities from data.
- void **load_agents_entities_ties** (const int *agents_id, const int *entities_id, size_t n)
- size_t get_n_viruses () const

  Number of viruses in the model.
- size_t get_n_tools () const

  Number of tools in the model.
- epiworld_fast_uint **get_ndays** () const
- epiworld_fast_uint **get_n_replicates** () const
- size_t **get_n_entities** () const
- void **set_ndays** (epiworld_fast_uint ndays)
- bool **get_verbose** () const
- Model< TSeq > & **verbose_off** ()
- Model< TSeq > & **verbose_on** ()
- int today () const

  The current time of the model.
- void write_data (std::string fn_virus_info, std::string fn_virus_hist, std::string fn_tool_info, std::string fn←_tool_hist, std::string fn_total_hist, std::string fn_transmission, std::string fn_transition, std::string fn_←reproductive_number, std::string fn_generation_time) const

  Wrapper of `DataBase::write_data`
- std::map< std::string, epiworld_double > & **params** ()
- virtual void reset ()

  Reset the model.
- const Model< TSeq > & **print** (bool lite=false) const
- void **get_elapsed** (std::string unit="auto", epiworld_double *last_elapsed=nullptr, epiworld_double *total_←elapsed=nullptr, std::string *unit_abbr=nullptr, bool print=true) const
- void add_globalevent (std::function< void(Model< TSeq > *)> fun, std::string name="A global action", int date=-99)

Set a global action.

- void **add_globalevent** (GlobalEvent< TSeq > action)
- GlobalEvent< TSeq > & get_globalevent (std::string name)

  Retrieve a global action by name.
- GlobalEvent< TSeq > & get_globalevent (size_t i)

  Retrieve a global action by index.
- void rm_globalevent (std::string name)

  Remove a global action by name.
- void rm_globalevent (size_t i)

  Remove a global action by index.
- void **run_globalevents** ()
- void **clear_state_set** ()
- const std::vector< VirusPtr< TSeq > > & **get_viruses** () const
- const std::vector< ToolPtr< TSeq > > & **get_tools** () const
- Virus< TSeq > & **get_virus** (size_t id)
- Tool< TSeq > & **get_tool** (size_t id)
- void set_agents_data (double ∗data_, size_t ncols_)

  Set the agents data object.
- double ∗ **get_agents_data** ()
- size_t **get_agents_data_ncols** () const
- void set_name (std::string name)

  Set the name object.
- std::string **get_name** () const
- bool **operator==** (const Model< TSeq > &other) const
- bool **operator!=** (const Model< TSeq > &other) const
- void events_run ()

  Executes the stored action.
- void draw (DiagramType diagram_type=DiagramType::Mermaid, const std::string &fn_output="", bool self=false)

  Draws a mermaid diagram of the model.

Set the backup object

`backup` can be used to restore the entire object after a run. This can be useful if the user wishes to have individuals start with the same network from the beginning.

- void **set_backup** ()

Random number generation

Parameters

eng	*Random number generator*
s	*Seed*

- void **set_rand_engine** (std::shared_ptr< std::mt19937 > &eng)
- std::shared_ptr< std::mt19937 > & **get_rand_endgine** ()
- void **seed** (size_t s)
- void **set_rand_norm** (epiworld_double mean, epiworld_double sd)
- void **set_rand_unif** (epiworld_double a, epiworld_double b)
- void **set_rand_exp** (epiworld_double lambda)
- void **set_rand_gamma** (epiworld_double alpha, epiworld_double beta)
- void **set_rand_lognormal** (epiworld_double mean, epiworld_double shape)
- void **set_rand_binom** (int n, epiworld_double p)

- void **set_rand_nbinom** (int n, epiworld_double p)
- void **set_rand_geom** (epiworld_double p)
- void **set_rand_poiss** (epiworld_double lambda)
- epiworld_double **runif** ()
- epiworld_double **runif** (epiworld_double a, epiworld_double b)
- epiworld_double **rnorm** ()
- epiworld_double **rnorm** (epiworld_double mean, epiworld_double sd)
- epiworld_double **rgamma** ()
- epiworld_double **rgamma** (epiworld_double alpha, epiworld_double beta)
- epiworld_double **rexp** ()
- epiworld_double **rexp** (epiworld_double lambda)
- epiworld_double **rlognormal** ()
- epiworld_double **rlognormal** (epiworld_double mean, epiworld_double shape)
- int **rbinom** ()
- int **rbinom** (int n, epiworld_double p)
- int **rnbinom** ()
- int **rnbinom** (int n, epiworld_double p)
- int **rgeom** ()
- int **rgeom** (epiworld_double p)
- int **rpoiss** ()
- int **rpoiss** (epiworld_double lambda)

Add Virus/Tool to the model

This is done before the model has been initialized.

Parameters

v	*Virus to be added*
t	*Tool to be added*
preval	*Initial prevalence (initial state.) It can be specified as a proportion (between zero and one,) or an integer indicating number of individuals.*

- void **add_virus** (Virus< TSeq > &v)
- void **add_tool** (Tool< TSeq > &t)
- void **add_entity** (Entity< TSeq > e)
- void **rm_virus** (size_t virus_pos)
- void **rm_tool** (size_t tool_pos)
- void **rm_entity** (size_t entity_id)

Accessing population of the model

Parameters

fn	*std::string Filename of the edgelist file.*
skip	*int Number of lines to skip in `fn`.*
directed	*bool Whether the graph is directed or not.*
size	*Size of the network.*
al	*AdjList to read into the model.*

- void **agents_from_adjlist** (std::string fn, int size, int skip=0, bool directed=false)
- void **agents_from_edgelist** (const std::vector< int > &source, const std::vector< int > &target, int size, bool directed)
- void **agents_from_adjlist** (AdjList al)
- bool **is_directed** () const
- std::vector< Agent< TSeq > > & get_agents ()
  Returns a reference to the vector of agents.

- Agent< TSeq > & **get_agent** (size_t i)
- std::vector< epiworld_fast_uint > get_agents_states () const

    Returns a vector with the states of the agents.
- std::vector< Viruses_const< TSeq > > get_agents_viruses () const

    Returns a const vector with the viruses of the agents.
- std::vector< Viruses< TSeq > > get_agents_viruses ()

    Returns a vector with the viruses of the agents.
- std::vector< Entity< TSeq > > & **get_entities** ()
- Entity< TSeq > & **get_entity** (size_t entity_id, int ∗entity_pos=nullptr)
- Model< TSeq > & **agents_smallworld** (epiworld_fast_uint n=1000, epiworld_fast_uint k=5, bool d=false, epiworld_double p=.01)
- void **agents_empty_graph** (epiworld_fast_uint n=1000)

Functions to run the model

Parameters

seed	*Seed to be used for Pseudo-RNG.*
ndays	*Number of days (steps) of the simulation.*
fun	*In the case of `run_multiple`, a function that is called after each experiment.*

- void **update_state** ()
- void **mutate_virus** ()
- void **next** ()
- virtual Model< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void run_multiple (epiworld_fast_uint ndays, epiworld_fast_uint nexperiments, int seed_=-1, std::function< void(size_t, Model< TSeq > ∗)> fun=make_save_run< TSeq >(), bool reset=true, bool verbose=true, int nthreads=1)

Rewire the network preserving the degree sequence.

This implementation assumes an undirected network, thus if {(i,j), (k,l)} -> {(i,l), (k,j)}, the reciprocal is also true, i.e., {(j,i), (l,k)} -> {(j,k), (l,i)}.

Parameters

proportion	*Proportion of ties to be rewired.*

Returns

A rewired version of the network.

- void **set_rewire_fun** (std::function< void(std::vector< Agent< TSeq >> ∗, Model< TSeq > ∗, epiworld_double)> fun)
- void **set_rewire_prop** (epiworld_double prop)
- epiworld_double **get_rewire_prop** () const
- void **rewire** ()

Export the network data in edgelist form

Parameters

fn	*std::string. File name.*
source	*Integer vector*
target	*Integer vector*

When passing the source and target, the function will write the edgelist on those.

- void **write_edgelist** (std::string fn) const
- void **write_edgelist** (std::vector< int > &source, std::vector< int > &target) const

Manage state (states) in the model

The functions `get_state` return the current values for the states included in the model.

Parameters

lab	*`std::string` Name of the state.*

Returns

`add_state*` returns nothing.

`get_state_*` returns a vector of pairs with the states and their labels.

- void **add_state** (std::string lab, UpdateFun< TSeq > fun=nullptr)
- const std::vector< std::string > & **get_states** () const
- size_t **get_n_states** () const
- const std::vector< UpdateFun< TSeq > > & **get_state_fun** () const
- void **print_state_codes** () const

Initial states

These functions are called before the simulation starts.

Parameters

proportions↩ _	*Vector of proportions for each state.*
queue_	*Vector of queue for each state.*

- virtual Model< TSeq > & **initial_states** (std::vector< double >, std::vector< int >)

Setting and accessing parameters from the model

Tools can incorporate parameters included in the model. Internally, parameters in the tool are stored as pointers to an std::map<> of parameters in the model. Using the `epiworld_fast_uint` method directly fetches the parameters in the order these were added to the tool. Accessing parameters via the `std::string` method involves searching the parameter directly in the std::map<> member of the model (so it is not recommended.)

The `par()` function members are aliases for `get_param()`.

In the case of the function `read_params`, users can pass a file listing parameters to be included in the model. Each line in the file should have the following structure:

```
[name of parameter 1]: [value in double]
[name of parameter 2]: [value in double]
...
```

The only condition for parameter names is that these do not include a colon.

Parameters

initial_val	
pname	*Name of the parameter to add or to fetch*
fn	*Path to the file containing parameters*

Returns

The current value of the parameter in the model.

- epiworld_double **add_param** (epiworld_double initial_val, std::string pname, bool overwrite=false)
- Model< TSeq > & **read_params** (std::string fn, bool overwrite=false)
- epiworld_double **get_param** (epiworld_fast_uint k)
- epiworld_double **get_param** (std::string pname)
- void **set_param** (std::string pname, epiworld_double val)
- epiworld_double **par** (std::string pname) const

Set the user data object

Parameters

names	*string vector with the names of the variables.*

- void set_user_data (std::vector< std::string > names)
  [@
- void **add_user_data** (epiworld_fast_uint j, epiworld_double x)
- void **add_user_data** (std::vector< epiworld_double > x)
- UserData< TSeq > & **get_user_data** ()

Queuing system

When queueing is on, the model will keep track of which agents are either in risk of exposure or exposed. This then is used at each step to act only on the aforementioned agents.

- void queuing_on ()
  Activates the queuing system (default.)
- Model< TSeq > & queuing_off ()
  Deactivates the queuing system.
- bool is_queuing_on () const
  Query if the queuing system is on.
- Queue< TSeq > & get_queue ()
  Retrieve the `Queue` object.

Get the susceptibility reduction object

Parameters

v	

Returns

epiworld_double

- void **set_susceptibility_reduction_mixer** (MixerFun< TSeq > fun)
- void **set_transmission_reduction_mixer** (MixerFun< TSeq > fun)
- void **set_recovery_enhancer_mixer** (MixerFun< TSeq > fun)
- void **set_death_reduction_mixer** (MixerFun< TSeq > fun)

Protected Member Functions

- void **dist_tools** ()
- void **dist_virus** ()

- void **dist_entities** ()
- void **chrono_start** ()
- void **chrono_end** ()
- void events_add (Agent< TSeq > *agent_, VirusPtr< TSeq > virus_, ToolPtr< TSeq > tool_, Entity< TSeq > *entity_, epiworld_fast_int new_state_, epiworld_fast_int queue_, EventFun< TSeq > call_, int idx_←agent_, int idx_object_)

    Construct a new Event object.

Protected Attributes

- std::string name = ""

    Name of the model.
- DataBase< TSeq > **db** = DataBase<TSeq>(*this)
- std::vector< Agent< TSeq > > **population** = {}
- bool **using_backup** = true
- std::vector< Agent< TSeq > > **population_backup** = {}
- bool **directed** = false
- std::vector< VirusPtr< TSeq > > **viruses** = {}
- std::vector< ToolPtr< TSeq > > **tools** = {}
- std::vector< Entity< TSeq > > **entities** = {}
- std::vector< Entity< TSeq > > **entities_backup** = {}
- std::shared_ptr< std::mt19937 > **engine** = std::make_shared< std::mt19937 >()
- std::uniform_real_distribution **runifd**
- std::normal_distribution **rnormd**
- std::gamma_distribution **rgammad**
- std::lognormal_distribution **rlognormald**
- std::exponential_distribution **rexpd**
- std::binomial_distribution **rbinomd**
- std::negative_binomial_distribution **rnbinomd**
- std::geometric_distribution **rgeomd**
- std::poisson_distribution **rpoissd**
- std::function< void(std::vector< Agent< TSeq >> *, Model< TSeq > *, epiworld_double)> **rewire_fun**
- epiworld_double **rewire_prop** = 0.0
- std::map< std::string, epiworld_double > **parameters**
- epiworld_fast_uint **ndays** = 0
- Progress **pb**
- std::vector< UpdateFun< TSeq > > state_fun = {}

    Functions to update states.
- std::vector< std::string > states_labels = {}

    Labels of the states.
- std::function< void(Model< TSeq > *)> initial_states_fun
- epiworld_fast_uint **nstates** = 0u
- bool **verbose** = true
- int **current_date** = 0
- std::chrono::time_point< std::chrono::steady_clock > **time_start**
- std::chrono::time_point< std::chrono::steady_clock > **time_end**
- std::chrono::duration< epiworld_double, std::micro > **time_elapsed**
- epiworld_fast_uint **n_replicates** = 0u
- std::vector< GlobalEvent< TSeq > > **globalevents**
- Queue< TSeq > **queue**
- bool **use_queuing** = true
- std::vector< Event< TSeq > > events = {}

    Variables used to keep track of the events to be made regarding viruses.

- epiworld_fast_uint **nactions** = 0u

Auxiliary variables for AgentsSample< TSeq > iterators

These variables+objects are used by the AgentsSample< TSeq> class for building efficient iterators over agents. The idea is to reduce the memory allocation, so only during the first call of AgentsSample< TSeq>::Agents←Sample(Model< TSeq>) these vectors are allocated.

- std::vector< Agent< TSeq > * > **sampled_population**
- size_t **sampled_population_n** = 0u
- std::vector< size_t > **population_left**
- size_t **population_left_n** = 0u

Agents features

Optionally, a model can include an external data source pointing to agents information. The data can then be access through the `Agent::operator()` method.

- double * **agents_data** = nullptr
- size_t **agents_data_ncols** = 0u

Friends

- class **Agent**< **TSeq** >
- class **AgentsSample**< **TSeq** >
- class **DataBase**< **TSeq** >
- class **Queue**< **TSeq** >

Tool Mixers

These functions combine the effects tools have to deliver a single effect. For example, wearing a mask, been vaccinated, and the immune system combine together to jointly reduce the susceptibility for a given virus.

- MixerFun< TSeq > **susceptibility_reduction_mixer** = susceptibility_reduction_mixer_default<TSeq>
- MixerFun< TSeq > **transmission_reduction_mixer** = transmission_reduction_mixer_default<TSeq>
- MixerFun< TSeq > **recovery_enhancer_mixer** = recovery_enhancer_mixer_default<TSeq>
- MixerFun< TSeq > **death_reduction_mixer** = death_reduction_mixer_default<TSeq>
- std::vector< epiworld_double > **array_double_tmp**
- std::vector< Virus< TSeq > * > **array_virus_tmp**
- virtual Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- **Model** ()
- **Model** (const Model< TSeq > &m)
- **Model** (Model< TSeq > &m)
- **Model** (Model< TSeq > &&m)
- Model< TSeq > & **operator=** (const Model< TSeq > &m)
- virtual ~**Model** ()

17.24.1 Detailed Description

template<typename TSeq>
class Model< TSeq >

Core class of epiworld.

The model class provides the wrapper that puts together `Agent`, `Virus`, and `Tools`.

Template Parameters

TSeq	Type of sequence. In principle, users can build models in which virus and human sequence is represented as numeric vectors (if needed.)

17.24.2 Member Function Documentation

17.24.2.1 add_globalevent()

```
template<typename TSeq >
void Model< TSeq >::add_globalevent (
            std::function< void(Model< TSeq > *)> fun,
            std::string name = "A global action",
            int date = -99 ) [inline]
```

Set a global action.

Parameters

fun	A function to be called on the prescribed date
name	Name of the action.
date	Integer indicating when the function is called (see details)

When date is less than zero, then the function is called at the end of every day. Otherwise, the function will be called only at the end of the indicated date.

17.24.2.2 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * Model< TSeq >::clone_ptr [inline], [protected], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented in ModelMeaslesSchool< TSeq >.

17.24.2.3 draw()

```
template<typename TSeq >
void Model< TSeq >::draw (
```

```
            DiagramType diagram_type = DiagramType::Mermaid,
            const std::string & fn_output = "",
            bool self = false )  [inline]
```

Draws a mermaid diagram of the model.

Parameters

model	The model to draw.
fn_output	The name of the file to write the diagram. If empty, the diagram will be printed to the standard output.
self	Whether to allow self-transitions.

17.24.2.4 events_add()

```
template<typename TSeq >
void Model< TSeq >::events_add (
            Agent< TSeq > * agent_,
            VirusPtr< TSeq > virus_,
            ToolPtr< TSeq > tool_,
            Entity< TSeq > * entity_,
            epiworld_fast_int new_state_,
            epiworld_fast_int queue_,
            EventFun< TSeq > call_,
            int idx_agent_,
            int idx_object_ )  [inline], [protected]
```

Construct a new Event object.

Parameters

*agent_*	Agent over which the action will be called
*virus_*	Virus pointer included in the action
*tool_*	Tool pointer included in the action
*entity_*	Entity pointer included in the action
*new_↩ state_*	New state of the agent
*call_*	Function the action will call
*queue_*	Change in the queue
*idx_↩ agent_*	Location of agent in object.
*idx_↩ object_*	Location of object in agent.

17.24.2.5 events_run()

```
template<typename TSeq >
void Model< TSeq >::events_run  [inline]
```

Executes the stored action.

Parameters

model←_	Model over which it will be executed.

17.24.2.6 load_agents_entities_ties()

```
template<typename TSeq >
void Model< TSeq >::load_agents_entities_ties (
            std::string fn,
            int skip )  [inline]
```

Associate agents-entities from a file.

The structure of the file should be two columns separated by space. The first column indexing between 0 and nagents-1, and the second column between 0 and nentities - 1.

Parameters

fn	Path to the file.
skip	How many rows to skip.

17.24.2.7 reset()

```
template<typename TSeq >
void Model< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented in ModelMeaslesSchool< TSeq >.

17.24.2.8 run_multiple()

```
template<typename TSeq >
void Model< TSeq >::run_multiple (
            epiworld_fast_uint ndays,
            epiworld_fast_uint nexperiments,
            int seed_ = -1,
            std::function< void(size_t, Model< TSeq > *)> fun = make_save_run<TSeq>(),
            bool reset = true,
            bool verbose = true,
            int nthreads = 1 )  [inline]
```

Parameters

ndays	Multiple runs of the simulation

17.24.2.9 set_agents_data()

```
template<typename TSeq >
void Model< TSeq >::set_agents_data (
            double * data_,
            size_t ncols_ )  [inline]
```

Set the agents data object.

The data should be an array with the data stored in a column major order, i.e., by column.

Parameters

*data_*	Pointer to the first element of an array of size `size() * ncols_`.
*ncols_*	Number of features included in the data.

17.24.2.10 set_name()

```
template<typename TSeq >
void Model< TSeq >::set_name (
            std::string name )  [inline]
```

Set the name object.

Parameters

name	

17.24.2.11 write_data()

```
template<typename TSeq >
void Model< TSeq >::write_data (
            std::string fn_virus_info,
            std::string fn_virus_hist,
            std::string fn_tool_info,
            std::string fn_tool_hist,
            std::string fn_total_hist,
            std::string fn_transmission,
            std::string fn_transition,
            std::string fn_reproductive_number,
            std::string fn_generation_time ) const  [inline]
```

Wrapper of `DataBase::write_data`

Parameters

fn_virus_info	Filename. Information about the virus.
fn_virus_hist	Filename. History of the virus.
fn_tool_info	Filename. Information about the tool.
fn_tool_hist	Filename. History of the tool.
fn_total_hist	Filename. Aggregated history (state)
fn_transmission	Filename. Transmission history.
fn_transition	Filename. Markov transition history.
fn_reproductive_number	Filename. Case by case reproductive number

17.24.3 Member Data Documentation

17.24.3.1 initial_states_fun

```
template<typename TSeq >
std::function<void(Model<TSeq>*)> Model< TSeq >::initial_states_fun  [protected]
```

Initial value:

```
= [](Model<TSeq> * )
    -> void {}
```

Function to distribute states. Goes along with the function

17.24.3.2 rbinomd

```
template<typename TSeq >
std::binomial_distribution Model< TSeq >::rbinomd  [protected]
```

Initial value:

```
=
        std::binomial_distribution<>()
```

17.24.3.3 rexpd

```
template<typename TSeq >
std::exponential_distribution Model< TSeq >::rexpd [protected]
```

Initial value:

```
=
        std::exponential_distribution<>()
```

17.24.3.4 rgammad

```
template<typename TSeq >
std::gamma_distribution Model< TSeq >::rgammad [protected]
```

Initial value:

```
=
        std::gamma_distribution<>()
```

17.24.3.5 rgeomd

```
template<typename TSeq >
std::geometric_distribution Model< TSeq >::rgeomd [protected]
```

Initial value:

```
=
        std::geometric_distribution<>()
```

17.24.3.6 rlognormald

```
template<typename TSeq >
std::lognormal_distribution Model< TSeq >::rlognormald [protected]
```

Initial value:

```
=
        std::lognormal_distribution<>()
```

17.24.3.7 rnbinomd

```
template<typename TSeq >
std::negative_binomial_distribution Model< TSeq >::rnbinomd [protected]
```

Initial value:

```
=
        std::negative_binomial_distribution<>()
```

17.24.3.8 rnormd

```
template<typename TSeq >
std::normal_distribution Model< TSeq >::rnormd [protected]
```

Initial value:

```
=
        std::normal_distribution<>(0.0)
```

17.24.3.9 rpoissd

```
template<typename TSeq >
std::poisson_distribution Model< TSeq >::rpoissd [protected]
```

Initial value:

```
=
        std::poisson_distribution<>()
```

17.24.3.10 runifd

```
template<typename TSeq >
std::uniform_real_distribution Model< TSeq >::runifd [protected]
```

Initial value:

```
=
        std::uniform_real_distribution<> (0.0, 1.0)
```

17.24.3.11 time_elapsed

```
template<typename TSeq >
std::chrono::duration<epiworld_double,std::micro> Model< TSeq >::time_elapsed [protected]
```

Initial value:

```
=
        std::chrono::duration<epiworld_double,std::micro>::zero()
```

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/model-bones.hpp
- include/epiworld/model-meat-print.hpp
- include/epiworld/model-meat.hpp

17.25 epiworld::ModelDiagram Class Reference

Public Member Functions

- void **draw_from_data** (DiagramType diagram_type, const std::vector< std::string > &states, const std::vector< epiworld_double > &tprob, const std::string &fn_output="", bool self=false)
- void **draw_from_file** (DiagramType diagram_type, const std::string &fn_transition, const std::string &fn_output="", bool self=false)
- void **draw_from_files** (DiagramType diagram_type, const std::vector< std::string > &fns_transition, const std::string &fn_output="", bool self=false)

The documentation for this class was generated from the following file:

- epiworld.hpp

17.26 ModelDiagram Class Reference

Public Member Functions

- void **draw_from_data** (DiagramType diagram_type, const std::vector< std::string > &states, const std::vector< epiworld_double > &tprob, const std::string &fn_output="", bool self=false)
- void **draw_from_file** (DiagramType diagram_type, const std::string &fn_transition, const std::string &fn_output="", bool self=false)
- void **draw_from_files** (DiagramType diagram_type, const std::vector< std::string > &fns_transition, const std::string &fn_output="", bool self=false)

The documentation for this class was generated from the following files:

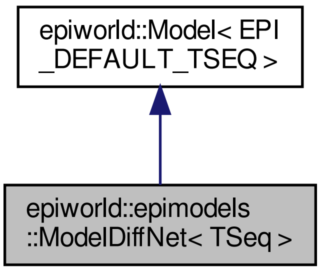
- include/epiworld/modeldiagram-bones.hpp
- include/epiworld/modeldiagram-meat.hpp

17.27 epiworld::epimodels::ModelDiffNet< TSeq > Class Template Reference

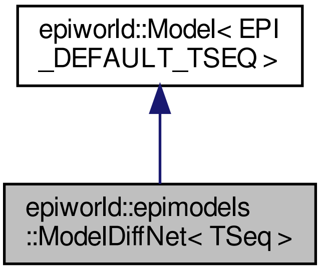
Template for a Network Diffusion Model.

`#include <epiworld.hpp>`

Inheritance diagram for epiworld::epimodels::ModelDiffNet< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelDiffNet< TSeq >:



Public Member Functions

- **ModelDiffNet** (ModelDiffNet< TSeq > &model, const std::string &innovation_name, epiworld_double prevalence, epiworld_double prob_adopt, bool normalize_exposure=true, double ∗agents_data=nullptr, size_t data_ncols=0u, std::vector< size_t > data_cols={}, std::vector< double > params={})
- **ModelDiffNet** (const std::string &innovation_name, epiworld_double prevalence, epiworld_double prob_adopt, bool normalize_exposure=true, double ∗agents_data=nullptr, size_t data_ncols=0u, std::vector< size_t > data_cols={}, std::vector< double > params={})

Public Attributes

- bool **normalize_exposure** = true
- std::vector< size_t > **data_cols**
- std::vector< double > **params**

Static Public Attributes

- static const int **NONADOPTER** = 0
- static const int **ADOPTER** = 1

Additional Inherited Members

17.27.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelDiffNet< TSeq >

Template for a Network Diffusion Model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
initial_prevalence	epiworld_double Initial prevalence
initial_efficacy	epiworld_double Initial susceptibility_reduction of the immune system
initial_recovery	epiworld_double Initial recovery rate of the immune system

The documentation for this class was generated from the following file:

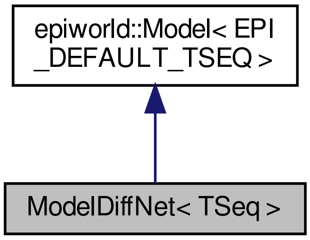
- epiworld.hpp

17.28 ModelDiffNet< TSeq > Class Template Reference

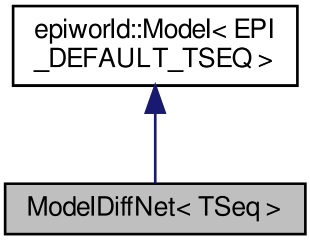
Template for a Network Diffusion Model.

`#include <diffnet.hpp>`

Inheritance diagram for ModelDiffNet< TSeq >:



Collaboration diagram for ModelDiffNet< TSeq >:



Public Member Functions

- **ModelDiffNet** (ModelDiffNet< TSeq > &model, const std::string &innovation_name, epiworld_double prevalence, epiworld_double prob_adopt, bool normalize_exposure=true, double *agents_data=nullptr, size_t data_ncols=0u, std::vector< size_t > data_cols={}, std::vector< double > params={})
- **ModelDiffNet** (const std::string &innovation_name, epiworld_double prevalence, epiworld_double prob_adopt, bool normalize_exposure=true, double *agents_data=nullptr, size_t data_ncols=0u, std::vector< size_t > data_cols={}, std::vector< double > params={})

Public Attributes

- bool **normalize_exposure** = true
- std::vector< size_t > **data_cols**
- std::vector< double > **params**

Static Public Attributes

- static const int **NONADOPTER** = 0
- static const int **ADOPTER** = 1

Additional Inherited Members

17.28.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelDiffNet< TSeq >

Template for a Network Diffusion Model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
initial_prevalence	epiworld_double Initial prevalence
initial_efficacy	epiworld_double Initial susceptibility_reduction of the immune system
initial_recovery	epiworld_double Initial recovery rate of the immune system

The documentation for this class was generated from the following file:

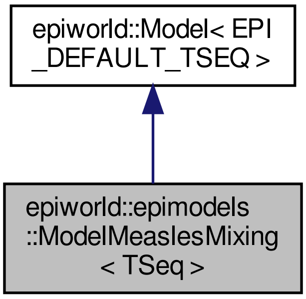
- include/epiworld/models/diffnet.hpp

17.29 epiworld::epimodels::ModelMeaslesMixing< TSeq > Class Template Reference

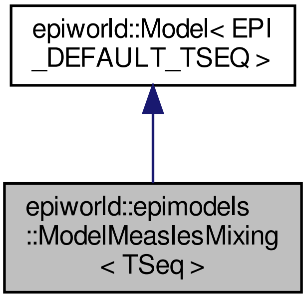
Measles model with population mixing, quarantine, and contact tracing.

```
#include <epiworld.hpp>
```

Inheritance diagram for epiworld::epimodels::ModelMeaslesMixing< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelMeaslesMixing< TSeq >:



Public Member Functions

- ModelMeaslesMixing (ModelMeaslesMixing< TSeq > &model, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double vax_efficacy, epiworld_double vax_reduction_recovery_rate, epiworld_double incubation_period, epiworld_double prodromal_period, epiworld_double rash_period, std::vector< double > contact_matrix, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double days_undetected, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_double isolation_willingness, epiworld_fast_int isolation_period, epiworld_double prop_vaccinated, epiworld_double contact_tracing_success_rate=1.0, epiworld_fast_uint contact_tracing_days_prior=4u)

    Constructs a ModelMeaslesMixing object.
- ModelMeaslesMixing (epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double vax_efficacy, epiworld_double vax_reduction_recovery_rate, epiworld_double incubation_period, epiworld_double prodromal_period, epiworld_double rash_period, std::vector< double > contact_matrix, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double days_undetected, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_double isolation_willingness, epiworld_fast_int isolation_period,

epiworld_double prop_vaccinated, epiworld_double contact_tracing_success_rate=1.0, epiworld_fast_uint contact_tracing_days_prior=4u)

Constructs a ModelMeaslesMixing object.

- ModelMeaslesMixing< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

  Run the model simulation.
- void reset ()

  Reset the model to initial state.
- Model< TSeq > * clone_ptr ()

  Create a clone of this model.
- ModelMeaslesMixing< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

  Set the initial states of the model.
- void set_contact_matrix (std::vector< double > cmat)

  Set the contact matrix for population mixing.
- std::vector< double > get_contact_matrix () const

  Get the current contact matrix.
- std::vector< size_t > get_agent_quarantine_triggered () const

  Get the quarantine trigger status for all agents.
- std::vector< bool > get_quarantine_willingness () const

  Get the quarantine willingness for all agents.
- std::vector< bool > get_isolation_willingness () const

  Get the isolation willingness for all agents.

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **PRODROMAL** = 2
- static const int **RASH** = 3
- static const int **ISOLATED** = 4
- static const int **ISOLATED_RECOVERED** = 5
- static const int **DETECTED_HOSPITALIZED** = 6
- static const int **QUARANTINED_EXPOSED** = 7
- static const int **QUARANTINED_SUSCEPTIBLE** = 8
- static const int **QUARANTINED_PRODROMAL** = 9
- static const int **QUARANTINED_RECOVERED** = 10
- static const int **HOSPITALIZED** = 11
- static const int **RECOVERED** = 12
- static const size_t **QUARANTINE_PROCESS_INACTIVE** = 0u
- static const size_t **QUARANTINE_PROCESS_ACTIVE** = 1u
- static const size_t **QUARANTINE_PROCESS_DONE** = 2u

Additional Inherited Members

17.29.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelMeaslesMixing< TSeq >

Measles model with population mixing, quarantine, and contact tracing.

This class implements a Measles epidemiological model based on the SEIR framework with additional features including:

- Population mixing based on contact matrices
- Measles-specific disease progression: Susceptible → Exposed → Prodromal → Rash
- Prodromal individuals are infectious (replace the "Infected" state in SEIR)
- Rash individuals are no longer infectious but can be detected for isolation
- Quarantine measures for exposed contacts during contact tracing
- Isolation policies for detected individuals during the rash state
- Contact tracing with configurable success rates
- Hospitalization of severe cases
- Individual willingness to comply with public health measures

The model supports 13 distinct states:

- Susceptible: Individuals who can become infected
- Exposed: Infected but not yet infectious (incubation period)
- Prodromal: Infectious individuals in the community (replaces "Infected" in SEIR)
- Rash: Non-infectious individuals with visible symptoms (detection occurs here)
- Isolated: Detected individuals in self-isolation
- Isolated Recovered: Recovered individuals still in isolation
- Detected Hospitalized: Hospitalized individuals who were contact-traced
- Quarantined Exposed: Exposed individuals in quarantine due to contact tracing
- Quarantined Susceptible: Susceptible individuals in quarantine due to contact tracing
- Quarantined Prodromal: Prodromal individuals in quarantine due to contact tracing
- Quarantined Recovered: Recovered individuals in quarantine due to contact tracing
- Hospitalized: Individuals requiring hospital care
- Recovered: Individuals who have recovered and gained immunity

Template Parameters

TSeq	Type for genetic sequences (default: EPI_DEFAULT_TSEQ)

17.29.2 Constructor & Destructor Documentation

17.29.2.1 ModelMeaslesMixing() [1/2]

```
template<typename TSeq >
ModelMeaslesMixing< TSeq >::ModelMeaslesMixing (
```

```
ModelMeaslesMixing< TSeq > & model,
epiworld_fast_uint n,
epiworld_double prevalence,
epiworld_double contact_rate,
epiworld_double transmission_rate,
epiworld_double vax_efficacy,
epiworld_double vax_reduction_recovery_rate,
epiworld_double incubation_period,
epiworld_double prodromal_period,
epiworld_double rash_period,
std::vector< double > contact_matrix,
epiworld_double hospitalization_rate,
epiworld_double hospitalization_period,
epiworld_double days_undetected,
epiworld_fast_int quarantine_period,
epiworld_double quarantine_willingness,
epiworld_double isolation_willingness,
epiworld_fast_int isolation_period,
epiworld_double prop_vaccinated,
epiworld_double contact_tracing_success_rate = 1.0,
epiworld_fast_uint contact_tracing_days_prior = 4u )  [inline]
```

Constructs a ModelMeaslesMixing object.

Template for a Measles model with population mixing, quarantine, and contact tracing.

Parameters

model	A reference to an existing ModelMeaslesMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
vax_efficacy	The efficacy of the vaccine.
vax_reduction_recovery_rate	The reduction in recovery rate due to the vaccine.
incubation_period	The incubation period of the disease in the model.
prodromal_period	The prodromal period of the disease in the model.
rash_period	The rash period of the disease in the model.
contact_matrix	The contact matrix between entities in the model. Specified in column-major order.
hospitalization_rate	The rate at which infected individuals are hospitalized.
hospitalization_period	The average duration of hospitalization in days.
days_undetected	The average number of days an infected individual remains undetected.
quarantine_period	The duration of quarantine in days for exposed contacts.
quarantine_willingness	The proportion of individuals willing to comply with quarantine measures.
isolation_willingness	The proportion of individuals willing to self-isolate when detected.
isolation_period	The duration of isolation in days for detected infected individuals.
prop_vaccinated	The proportion of vaccinated agents.
contact_tracing_success_rate	The probability of successfully identifying and tracing contacts (default: 1.0).
contact_tracing_days_prior	The number of days prior to detection for which contacts are traced (default: 4).
model	A ModelMeaslesMixing<TSeq> object where to set up the model.
n	Number of agents in the population
prevalence	Initial prevalence (proportion of infected individuals)

Parameters

contact_rate	Average number of contacts (interactions) per step
transmission_rate	Probability of transmission per contact
vax_efficacy	The efficacy of the vaccine
vax_reduction_recovery_rate	The reduction in recovery rate due to the vaccine
incubation_period	Average incubation period in days
prodromal_period	Average prodromal period in days
rash_period	Average rash period in days
contact_matrix	Contact matrix specifying mixing patterns between population groups
hospitalization_rate	Rate at which infected individuals are hospitalized
hospitalization_period	Average duration of hospitalization in days
days_undetected	Average number of days an infected individual remains undetected
quarantine_period	Duration of quarantine in days for exposed contacts
quarantine_willingness	Proportion of individuals willing to comply with quarantine
isolation_willingness	Proportion of individuals willing to self-isolate when detected
isolation_period	Duration of isolation in days for detected infected individuals
prop_vaccinated	Proportion of vaccinated agents
contact_tracing_success_rate	Probability of successfully identifying contacts during tracing
contact_tracing_days_prior	Number of days prior to detection for contact tracing

17.29.2.2 ModelMeaslesMixing() [2/2]

```
template<typename TSeq >
ModelMeaslesMixing< TSeq >::ModelMeaslesMixing (
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double vax_efficacy,
            epiworld_double vax_reduction_recovery_rate,
            epiworld_double incubation_period,
            epiworld_double prodromal_period,
            epiworld_double rash_period,
            std::vector< double > contact_matrix,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double days_undetected,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_double isolation_willingness,
            epiworld_fast_int isolation_period,
            epiworld_double prop_vaccinated,
            epiworld_double contact_tracing_success_rate = 1.0,
            epiworld_fast_uint contact_tracing_days_prior = 4u )  [inline]
```

Constructs a ModelMeaslesMixing object.

Parameters

n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
vax_efficacy	The efficacy of the vaccine.
vax_reduction_recovery_rate	The reduction in recovery rate due to the vaccine.
incubation_period	The incubation period of the disease in the model.
prodromal_period	The prodromal period of the disease in the model.
rash_period	The rash period of the disease in the model.
contact_matrix	The contact matrix between entities in the model.
hospitalization_rate	The rate at which infected individuals are hospitalized.
hospitalization_period	The average duration of hospitalization in days.
days_undetected	The average number of days an infected individual remains undetected.
quarantine_period	The duration of quarantine in days for exposed contacts.
quarantine_willingness	The proportion of individuals willing to comply with quarantine measures.
isolation_willingness	The proportion of individuals willing to self-isolate when detected.
isolation_period	The duration of isolation in days for detected infected individuals.
prop_vaccinated	The proportion of vaccinated agents.
contact_tracing_success_rate	The probability of successfully identifying and tracing contacts (default: 1.0).
contact_tracing_days_prior	The number of days prior to detection for which contacts are traced (default: 4).

17.29.3 Member Function Documentation

17.29.3.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelMeaslesMixing< TSeq >::clone_ptr  [inline], [virtual]
```

Create a clone of this model.

Returns

Pointer to a new model instance with the same configuration

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.29.3.2 get_agent_quarantine_triggered()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< size_t > epiworld::epimodels::ModelMeaslesMixing< TSeq >::get_agent_quarantine↩
_triggered ( ) const  [inline]
```

Get the quarantine trigger status for all agents.

Returns

Vector indicating quarantine process status for each agent

17.29.3.3 get_contact_matrix()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< double > epiworld::epimodels::ModelMeaslesMixing< TSeq >::get_contact_matrix ( )
const [inline]
```

Get the current contact matrix.

Returns

Vector representing the contact matrix

17.29.3.4 get_isolation_willingness()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< bool > epiworld::epimodels::ModelMeaslesMixing< TSeq >::get_isolation_willingness
( ) const [inline]
```

Get the isolation willingness for all agents.

Returns

Vector of boolean values indicating each agent's willingness to self-isolate

17.29.3.5 get_quarantine_willingness()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< bool > epiworld::epimodels::ModelMeaslesMixing< TSeq >::get_quarantine_willingness
( ) const [inline]
```

Get the quarantine willingness for all agents.

Returns

Vector of boolean values indicating each agent's willingness to quarantine

17.29.3.6 initial_states()

```
template<typename TSeq >
ModelMeaslesMixing< TSeq > & ModelMeaslesMixing< TSeq >::initial_states (
             std::vector< double > proportions_,
             std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set the initial states of the model.

Parameters

proportions←↩_	Double vector with two elements: • [0]: The proportion of initially infected individuals who start in the exposed state. • [1]: The proportion of initially non-infected individuals who have recovered (immune).
*queue_*	Optional vector for queuing specifications (default: empty).

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.29.3.7 run()

```
template<typename TSeq >
ModelMeaslesMixing< TSeq > & ModelMeaslesMixing< TSeq >::run (
            epiworld_fast_uint ndays,
            int seed = -1 ) [inline], [virtual]
```

Run the model simulation.

Parameters

ndays	Number of days to simulate
seed	Random seed for reproducibility (default: -1 for random seed)

Returns

Reference to this model instance

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.29.3.8 set_contact_matrix()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
void epiworld::epimodels::ModelMeaslesMixing< TSeq >::set_contact_matrix (
            std::vector< double > cmat ) [inline]
```

Set the contact matrix for population mixing.

Parameters

cmat	Contact matrix specifying interaction rates between groups

The documentation for this class was generated from the following file:

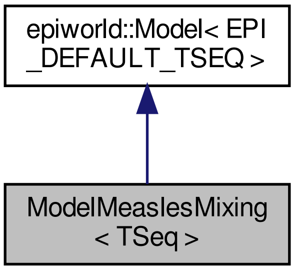
- epiworld.hpp

17.30 ModelMeaslesMixing< TSeq > Class Template Reference

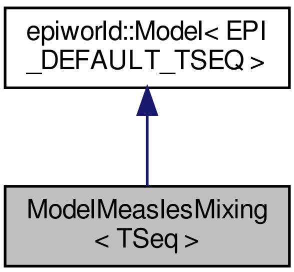
Measles model with population mixing, quarantine, and contact tracing.

```
#include <measlesmixing.hpp>
```

Inheritance diagram for ModelMeaslesMixing< TSeq >:



Collaboration diagram for ModelMeaslesMixing< TSeq >:



Public Member Functions

- ModelMeaslesMixing (ModelMeaslesMixing< TSeq > &model, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double vax_efficacy, epiworld_double vax_reduction_recovery_rate, epiworld_double incubation_period, epiworld_double prodromal_period, epiworld_double rash_period, std::vector< double > contact_matrix, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double days_undetected, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_double isolation_willingness, epiworld_fast_int isolation_period, epiworld_double prop_vaccinated, epiworld_double contact_tracing_success_rate=1.0, epiworld_fast_uint contact_tracing_days_prior=4u)

    Constructs a ModelMeaslesMixing object.

- ModelMeaslesMixing (epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double vax_efficacy, epiworld_double vax_reduction_recovery_rate, epiworld_double incubation_period, epiworld_double prodromal_period, epiworld_double rash_period, std::vector< double > contact_matrix, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double days_undetected, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_double isolation_willingness, epiworld_fast_int isolation_period, epiworld_double prop_vaccinated, epiworld_double contact_tracing_success_rate=1.0, epiworld_fast_uint contact_tracing_days_prior=4u)

    Constructs a ModelMeaslesMixing object.
- ModelMeaslesMixing< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Run the model simulation.
- void reset ()

    Reset the model to initial state.
- Model< TSeq > * clone_ptr ()

    Create a clone of this model.
- ModelMeaslesMixing< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set the initial states of the model.
- void set_contact_matrix (std::vector< double > cmat)

    Set the contact matrix for population mixing.
- std::vector< double > get_contact_matrix () const

    Get the current contact matrix.
- std::vector< size_t > get_agent_quarantine_triggered () const

    Get the quarantine trigger status for all agents.
- std::vector< bool > get_quarantine_willingness () const

    Get the quarantine willingness for all agents.
- std::vector< bool > get_isolation_willingness () const

    Get the isolation willingness for all agents.

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **PRODROMAL** = 2
- static const int **RASH** = 3
- static const int **ISOLATED** = 4
- static const int **ISOLATED_RECOVERED** = 5
- static const int **DETECTED_HOSPITALIZED** = 6
- static const int **QUARANTINED_EXPOSED** = 7
- static const int **QUARANTINED_SUSCEPTIBLE** = 8
- static const int **QUARANTINED_PRODROMAL** = 9
- static const int **QUARANTINED_RECOVERED** = 10
- static const int **HOSPITALIZED** = 11
- static const int **RECOVERED** = 12
- static const size_t **QUARANTINE_PROCESS_INACTIVE** = 0u
- static const size_t **QUARANTINE_PROCESS_ACTIVE** = 1u
- static const size_t **QUARANTINE_PROCESS_DONE** = 2u

Additional Inherited Members

17.30.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelMeaslesMixing< TSeq >

Measles model with population mixing, quarantine, and contact tracing.

This class implements a Measles epidemiological model based on the SEIR framework with additional features including:

- Population mixing based on contact matrices
- Measles-specific disease progression: Susceptible → Exposed → Prodromal → Rash
- Prodromal individuals are infectious (replace the "Infected" state in SEIR)
- Rash individuals are no longer infectious but can be detected for isolation
- Quarantine measures for exposed contacts during contact tracing
- Isolation policies for detected individuals during the rash state
- Contact tracing with configurable success rates
- Hospitalization of severe cases
- Individual willingness to comply with public health measures

The model supports 13 distinct states:

- Susceptible: Individuals who can become infected
- Exposed: Infected but not yet infectious (incubation period)
- Prodromal: Infectious individuals in the community (replaces "Infected" in SEIR)
- Rash: Non-infectious individuals with visible symptoms (detection occurs here)
- Isolated: Detected individuals in self-isolation
- Isolated Recovered: Recovered individuals still in isolation
- Detected Hospitalized: Hospitalized individuals who were contact-traced
- Quarantined Exposed: Exposed individuals in quarantine due to contact tracing
- Quarantined Susceptible: Susceptible individuals in quarantine due to contact tracing
- Quarantined Prodromal: Prodromal individuals in quarantine due to contact tracing
- Quarantined Recovered: Recovered individuals in quarantine due to contact tracing
- Hospitalized: Individuals requiring hospital care
- Recovered: Individuals who have recovered and gained immunity

Template Parameters

TSeq	Type for genetic sequences (default: EPI_DEFAULT_TSEQ)

17.30.2 Constructor & Destructor Documentation

17.30.2.1 ModelMeaslesMixing() [1/2]

```
template<typename TSeq >
ModelMeaslesMixing< TSeq >::ModelMeaslesMixing (
            ModelMeaslesMixing< TSeq > & model,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double vax_efficacy,
            epiworld_double vax_reduction_recovery_rate,
            epiworld_double incubation_period,
            epiworld_double prodromal_period,
            epiworld_double rash_period,
            std::vector< double > contact_matrix,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double days_undetected,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_double isolation_willingness,
            epiworld_fast_int isolation_period,
            epiworld_double prop_vaccinated,
            epiworld_double contact_tracing_success_rate = 1.0,
            epiworld_fast_uint contact_tracing_days_prior = 4u )  [inline]
```

Constructs a ModelMeaslesMixing object.

Template for a Measles model with population mixing, quarantine, and contact tracing.

Parameters

model	A reference to an existing ModelMeaslesMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
vax_efficacy	The efficacy of the vaccine.
vax_reduction_recovery_rate	The reduction in recovery rate due to the vaccine.
incubation_period	The incubation period of the disease in the model.
prodromal_period	The prodromal period of the disease in the model.
rash_period	The rash period of the disease in the model.
contact_matrix	The contact matrix between entities in the model. Specified in column-major order.

Parameters

hospitalization_rate	The rate at which infected individuals are hospitalized.
hospitalization_period	The average duration of hospitalization in days.
days_undetected	The average number of days an infected individual remains undetected.
quarantine_period	The duration of quarantine in days for exposed contacts.
quarantine_willingness	The proportion of individuals willing to comply with quarantine measures.
isolation_willingness	The proportion of individuals willing to self-isolate when detected.
isolation_period	The duration of isolation in days for detected infected individuals.
prop_vaccinated	The proportion of vaccinated agents.
contact_tracing_success_rate	The probability of successfully identifying and tracing contacts (default: 1.0).
contact_tracing_days_prior	The number of days prior to detection for which contacts are traced (default: 4).
model	A ModelMeaslesMixing<TSeq> object where to set up the model.
n	Number of agents in the population
prevalence	Initial prevalence (proportion of infected individuals)
contact_rate	Average number of contacts (interactions) per step
transmission_rate	Probability of transmission per contact
vax_efficacy	The efficacy of the vaccine
vax_reduction_recovery_rate	The reduction in recovery rate due to the vaccine
incubation_period	Average incubation period in days
prodromal_period	Average prodromal period in days
rash_period	Average rash period in days
contact_matrix	Contact matrix specifying mixing patterns between population groups
hospitalization_rate	Rate at which infected individuals are hospitalized
hospitalization_period	Average duration of hospitalization in days
days_undetected	Average number of days an infected individual remains undetected
quarantine_period	Duration of quarantine in days for exposed contacts
quarantine_willingness	Proportion of individuals willing to comply with quarantine
isolation_willingness	Proportion of individuals willing to self-isolate when detected
isolation_period	Duration of isolation in days for detected infected individuals
prop_vaccinated	Proportion of vaccinated agents
contact_tracing_success_rate	Probability of successfully identifying contacts during tracing
contact_tracing_days_prior	Number of days prior to detection for contact tracing

17.30.2.2 ModelMeaslesMixing() [2/2]

```
template<typename TSeq >
ModelMeaslesMixing< TSeq >::ModelMeaslesMixing (
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double vax_efficacy,
            epiworld_double vax_reduction_recovery_rate,
            epiworld_double incubation_period,
            epiworld_double prodromal_period,
```

```
            epiworld_double rash_period,
            std::vector< double > contact_matrix,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double days_undetected,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_double isolation_willingness,
            epiworld_fast_int isolation_period,
            epiworld_double prop_vaccinated,
            epiworld_double contact_tracing_success_rate = 1.0,
            epiworld_fast_uint contact_tracing_days_prior = 4u )  [inline]
```

Constructs a ModelMeaslesMixing object.

Parameters

n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
vax_efficacy	The efficacy of the vaccine.
vax_reduction_recovery_rate	The reduction in recovery rate due to the vaccine.
incubation_period	The incubation period of the disease in the model.
prodromal_period	The prodromal period of the disease in the model.
rash_period	The rash period of the disease in the model.
contact_matrix	The contact matrix between entities in the model.
hospitalization_rate	The rate at which infected individuals are hospitalized.
hospitalization_period	The average duration of hospitalization in days.
days_undetected	The average number of days an infected individual remains undetected.
quarantine_period	The duration of quarantine in days for exposed contacts.
quarantine_willingness	The proportion of individuals willing to comply with quarantine measures.
isolation_willingness	The proportion of individuals willing to self-isolate when detected.
isolation_period	The duration of isolation in days for detected infected individuals.
prop_vaccinated	The proportion of vaccinated agents.
contact_tracing_success_rate	The probability of successfully identifying and tracing contacts (default: 1.0).
contact_tracing_days_prior	The number of days prior to detection for which contacts are traced (default: 4).

17.30.3 Member Function Documentation

17.30.3.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelMeaslesMixing< TSeq >::clone_ptr  [inline], [virtual]
```

Create a clone of this model.

Returns

Pointer to a new model instance with the same configuration

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.30.3.2 get_agent_quarantine_triggered()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< size_t > ModelMeaslesMixing< TSeq >::get_agent_quarantine_triggered ( ) const
[inline]
```

Get the quarantine trigger status for all agents.

Returns

Vector indicating quarantine process status for each agent

17.30.3.3 get_contact_matrix()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< double > ModelMeaslesMixing< TSeq >::get_contact_matrix ( ) const [inline]
```

Get the current contact matrix.

Returns

Vector representing the contact matrix

17.30.3.4 get_isolation_willingness()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< bool > ModelMeaslesMixing< TSeq >::get_isolation_willingness ( ) const [inline]
```

Get the isolation willingness for all agents.

Returns

Vector of boolean values indicating each agent's willingness to self-isolate

17.30.3.5 get_quarantine_willingness()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< bool > ModelMeaslesMixing< TSeq >::get_quarantine_willingness ( ) const [inline]
```

Get the quarantine willingness for all agents.

Returns

Vector of boolean values indicating each agent's willingness to quarantine

17.30.3.6 initial_states()

```
template<typename TSeq >
ModelMeaslesMixing< TSeq > & ModelMeaslesMixing< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with two elements: • [0]: The proportion of initially infected individuals who start in the exposed state. • [1]: The proportion of initially non-infected individuals who have recovered (immune).
*queue_*	Optional vector for queuing specifications (default: empty).

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.30.3.7 run()

```
template<typename TSeq >
ModelMeaslesMixing< TSeq > & ModelMeaslesMixing< TSeq >::run (
            epiworld_fast_uint ndays,
            int seed = -1 ) [inline], [virtual]
```

Run the model simulation.

Parameters

ndays	Number of days to simulate
seed	Random seed for reproducibility (default: -1 for random seed)

Returns

Reference to this model instance

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.30.3.8 set_contact_matrix()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
void ModelMeaslesMixing< TSeq >::set_contact_matrix (
             std::vector< double > cmat )  [inline]
```

Set the contact matrix for population mixing.

Parameters

cmat	Contact matrix specifying interaction rates between groups

The documentation for this class was generated from the following file:

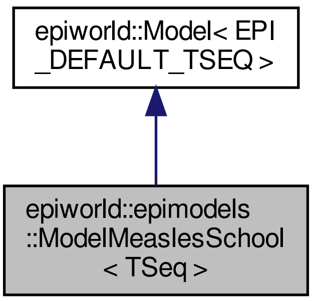
- include/epiworld/models/measlesmixing.hpp

17.31 epiworld::epimodels::ModelMeaslesSchool< TSeq > Class Template Reference

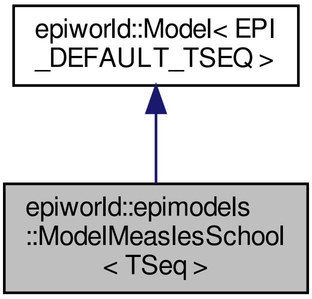
Template for a Measles model with quarantine.

```
#include <epiworld.hpp>
```

Inheritance diagram for epiworld::epimodels::ModelMeaslesSchool< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelMeaslesSchool< TSeq >:



Public Member Functions

- void quarantine_agents ()

  Quarantine agents that are in the system.
- void reset ()

  Reset the model.
- void **update_infectious** ()
- Model< TSeq > * clone_ptr ()

  Advanced usage: Makes a copy of data and returns it as undeleted pointer.

- ModelMeaslesSchool (ModelMeaslesSchool< TSeq > &model, epiworld_fast_uint n, epiworld_fast_uint n_exposed, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double vax_efficacy, epiworld_double vax_reduction_recovery_rate, epiworld_double incubation_period, epiworld_double prodromal_period, epiworld_double rash_period, epiworld_double days_undetected, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double prop_vaccinated, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_fast_int isolation_period)
- **ModelMeaslesSchool** (epiworld_fast_uint n, epiworld_fast_uint n_exposed, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double vax_efficacy, epiworld_double vax_reduction_recovery_rate, epiworld_double incubation_period, epiworld_double prodromal_period, epiworld_double rash_period, epiworld_double days_undetected, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double prop_vaccinated, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_fast_int isolation_period)

Public Attributes

- std::vector< Agent< TSeq > * > infectious

  Agents infectious for contact.
- bool **system_quarantine_triggered** = false
- std::vector< int > day_flagged

  Either detected or started quarantine.
- std::vector< int > day_rash_onset

  Day of rash onset.

Static Public Attributes

- static constexpr epiworld_fast_uint **SUSCEPTIBLE** = 0u
- static constexpr epiworld_fast_uint **EXPOSED** = 1u
- static constexpr epiworld_fast_uint **PRODROMAL** = 2u
- static constexpr epiworld_fast_uint **RASH** = 3u
- static constexpr epiworld_fast_uint **ISOLATED** = 4u
- static constexpr epiworld_fast_uint **ISOLATED_RECOVERED** = 5u
- static constexpr epiworld_fast_uint **DETECTED_HOSPITALIZED** = 6u
- static constexpr epiworld_fast_uint **QUARANTINED_EXPOSED** = 7u
- static constexpr epiworld_fast_uint **QUARANTINED_SUSCEPTIBLE** = 8u
- static constexpr epiworld_fast_uint **QUARANTINED_PRODROMAL** = 9u
- static constexpr epiworld_fast_uint **QUARANTINED_RECOVERED** = 10u
- static constexpr epiworld_fast_uint **HOSPITALIZED** = 11u
- static constexpr epiworld_fast_uint **RECOVERED** = 12u

Additional Inherited Members

17.31.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelMeaslesSchool< TSeq >

Template for a Measles model with quarantine.

Parameters

TSeq	The type of the sequence to be used.

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 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. Isolated agents then may be moved out of the isolation in isolation↩_period days.

17.31.2 Constructor & Destructor Documentation

17.31.2.1 ModelMeaslesSchool()

```
template<typename TSeq >
ModelMeaslesSchool< TSeq >::ModelMeaslesSchool (
            ModelMeaslesSchool< TSeq > & model,
            epiworld_fast_uint n,
            epiworld_fast_uint n_exposed,
            epiworld_double contact_rate,
```

```
            epiworld_double transmission_rate,
            epiworld_double vax_efficacy,
            epiworld_double vax_reduction_recovery_rate,
            epiworld_double incubation_period,
            epiworld_double prodromal_period,
            epiworld_double rash_period,
            epiworld_double days_undetected,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double prop_vaccinated,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_fast_int isolation_period )  [inline]
```

Parameters

n	The number of agents in the system.
n_exposed	The number of exposed agents in the system.
contact_rate	The rate of contact between agents.
transmission_rate	The rate of transmission of the virus.
vax_efficacy	The efficacy of the vaccine.
vax_reduction_recovery_rate	The reduction in recovery rate due to the vaccine.
incubation_period	The incubation period of the virus.
prodromal_period	The prodromal period of the virus.
rash_period	The rash period of the virus.
days_undetected	The number of days the virus goes undetected.
hospitalization_rate	The rate of hospitalization.
hospitalization_period	The duration of hospitalization.
prop_vaccinated	The proportion of vaccinated agents.
quarantine_period	The number of days for quarantine.
quarantine_willingness	The willingness to be quarantined.
isolation_period	The number of days for isolation.

17.31.3 Member Function Documentation

17.31.3.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelMeaslesSchool< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.31.3.2 quarantine_agents()

```
template<typename TSeq >
void ModelMeaslesSchool< TSeq >::quarantine_agents  [inline]
```

Quarantine agents that are in the system.

The flow should be:

- The function only runs if the quarantine status is active.
- Agents who are in quarantine, isolation, removed, or hospitalized are ignored.
- Agents who are in the RASH state are isolated.
- Vaccinated agents are ignored.
- Susceptible, Exposed, and Prodromal agents are moved to the QUARANTINED_* state.
- At the end of the function, the quarantine status is set false.

17.31.3.3 reset()

```
template<typename TSeq >
void ModelMeaslesSchool< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

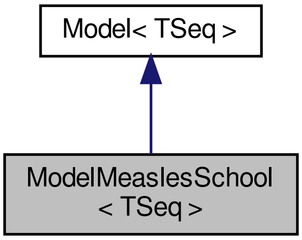
- epiworld.hpp

17.32 ModelMeaslesSchool< TSeq > Class Template Reference

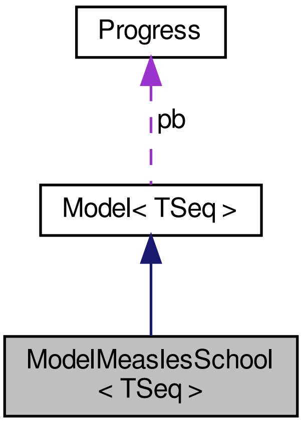
Template for a Measles model with quarantine.

```
#include <measlesquarantine.hpp>
```

Inheritance diagram for ModelMeaslesSchool< TSeq >:



Collaboration diagram for ModelMeaslesSchool< TSeq >:



Public Member Functions

- void quarantine_agents ()

  Quarantine agents that are in the system.
- void reset ()

  Reset the model.
- void **update_infectious** ()

- Model< TSeq > ∗ clone_ptr ()

  Advanced usage: Makes a copy of data and returns it as undeleted pointer.

- ModelMeaslesSchool (ModelMeaslesSchool< TSeq > &model, epiworld_fast_uint n, epiworld_fast_uint n_exposed, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double vax↔_efficacy, epiworld_double vax_reduction_recovery_rate, epiworld_double incubation_period, epiworld_↔double prodromal_period, epiworld_double rash_period, epiworld_double days_undetected, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double prop_vaccinated, epiworld_↔fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_fast_int isolation_period)
- **ModelMeaslesSchool** (epiworld_fast_uint n, epiworld_fast_uint n_exposed, epiworld_double contact_↔rate, epiworld_double transmission_rate, epiworld_double vax_efficacy, epiworld_double vax_reduction↔_recovery_rate, epiworld_double incubation_period, epiworld_double prodromal_period, epiworld_double rash_period, epiworld_double days_undetected, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double prop_vaccinated, epiworld_fast_int quarantine_period, epiworld_↔double quarantine_willingness, epiworld_fast_int isolation_period)

Public Attributes

- std::vector< Agent< TSeq > ∗ > infectious

  Agents infectious for contact.
- bool **system_quarantine_triggered** = false
- std::vector< int > day_flagged

  Either detected or started quarantine.
- std::vector< int > day_rash_onset

  Day of rash onset.

Static Public Attributes

- static constexpr epiworld_fast_uint **SUSCEPTIBLE** = 0u
- static constexpr epiworld_fast_uint **EXPOSED** = 1u
- static constexpr epiworld_fast_uint **PRODROMAL** = 2u
- static constexpr epiworld_fast_uint **RASH** = 3u
- static constexpr epiworld_fast_uint **ISOLATED** = 4u
- static constexpr epiworld_fast_uint **ISOLATED_RECOVERED** = 5u
- static constexpr epiworld_fast_uint **DETECTED_HOSPITALIZED** = 6u
- static constexpr epiworld_fast_uint **QUARANTINED_EXPOSED** = 7u
- static constexpr epiworld_fast_uint **QUARANTINED_SUSCEPTIBLE** = 8u
- static constexpr epiworld_fast_uint **QUARANTINED_PRODROMAL** = 9u
- static constexpr epiworld_fast_uint **QUARANTINED_RECOVERED** = 10u
- static constexpr epiworld_fast_uint **HOSPITALIZED** = 11u
- static constexpr epiworld_fast_uint **RECOVERED** = 12u

Additional Inherited Members

17.32.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelMeaslesSchool< TSeq >

Template for a Measles model with quarantine.

Parameters

TSeq	The type of the sequence to be used.

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 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. Isolated agents then may be moved out of the isolation in isolation↩
_period days.

17.32.2 Constructor & Destructor Documentation

17.32.2.1 ModelMeaslesSchool()

```
template<typename TSeq >
ModelMeaslesSchool< TSeq >::ModelMeaslesSchool (
            ModelMeaslesSchool< TSeq > & model,
            epiworld_fast_uint n,
            epiworld_fast_uint n_exposed,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double vax_efficacy,
            epiworld_double vax_reduction_recovery_rate,
            epiworld_double incubation_period,
            epiworld_double prodromal_period,
            epiworld_double rash_period,
            epiworld_double days_undetected,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double prop_vaccinated,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_fast_int isolation_period )  [inline]
```

Parameters

n	The number of agents in the system.
n_exposed	The number of exposed agents in the system.
contact_rate	The rate of contact between agents.
transmission_rate	The rate of transmission of the virus.
vax_efficacy	The efficacy of the vaccine.
vax_reduction_recovery_rate	The reduction in recovery rate due to the vaccine.
incubation_period	The incubation period of the virus.
prodromal_period	The prodromal period of the virus.
rash_period	The rash period of the virus.
days_undetected	The number of days the virus goes undetected.
hospitalization_rate	The rate of hospitalization.

Parameters

hospitalization_period	The duration of hospitalization.
prop_vaccinated	The proportion of vaccinated agents.
quarantine_period	The number of days for quarantine.
quarantine_willingness	The willingness to be quarantined.
isolation_period	The number of days for isolation.

17.32.3 Member Function Documentation

17.32.3.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelMeaslesSchool< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from Model< TSeq >.

17.32.3.2 quarantine_agents()

```
template<typename TSeq >
void ModelMeaslesSchool< TSeq >::quarantine_agents  [inline]
```

Quarantine agents that are in the system.

The flow should be:

- The function only runs if the quarantine status is active.
- Agents who are in quarantine, isolation, removed, or hospitalized are ignored.
- Agents who are in the RASH state are isolated.
- Vaccinated agents are ignored.
- Susceptible, Exposed, and Prodromal agents are moved to the QUARANTINED_∗ state.
- At the end of the function, the quarantine status is set false.

17.32.3.3 reset()

```
template<typename TSeq >
void ModelMeaslesSchool< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from Model< TSeq >.

The documentation for this class was generated from the following file:

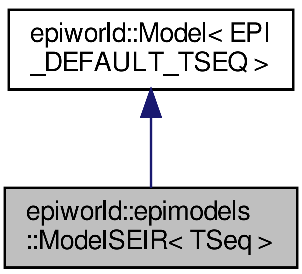
- include/epiworld/models/measlesquarantine.hpp

17.33 epiworld::epimodels::ModelSEIR< TSeq > Class Template Reference

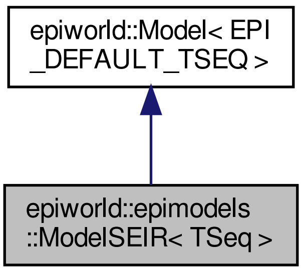
Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

`#include <epiworld.hpp>`

Inheritance diagram for epiworld::epimodels::ModelSEIR< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSEIR< TSeq >:



Public Member Functions

- **ModelSEIR** (ModelSEIR< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate)
- **ModelSEIR** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate)
- ModelSEIR< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

  Set up the initial states of the model.

Public Attributes

- epiworld::UpdateFun< TSeq > **update_exposed_seir**
- epiworld::UpdateFun< TSeq > **update_infected_seir**

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **REMOVED** = 3

Additional Inherited Members

17.33.1 Detailed Description

template< typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelSEIR< TSeq >

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A Model< TSeq > object where to set up the SIR.
vname	std::string Name of the virus
prevalence	epiworld_double Initial prevalence the immune system
transmission_rate	epiworld_double Transmission rate of the virus
avg_incubation_days	epiworld_double Average incubation days of the virus.
recovery_rate	epiworld_double Recovery rate of the virus.

17.33.2 Member Function Documentation

17.33.2.1 initial_states()

```
template<typename TSeq >
ModelSEIR< TSeq > & ModelSEIR< TSeq >::initial_states (
              std::vector< double > proportions_,
              std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set up the initial states of the model.

Parameters

proportions←_	Double vector with the following values: • 0: Proportion of non-infected agents who are removed. • 1: Proportion of exposed agents to be set as infected.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.33.3 Member Data Documentation

17.33.3.1 update_exposed_seir

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
epiworld::UpdateFun<TSeq> epiworld::epimodels::ModelSEIR< TSeq >::update_exposed_seir
```

Initial value:

```
= [](
        epiworld::Agent<TSeq> * p,
        epiworld::Model<TSeq> * m
    ) -> void {

        auto v = p->get_virus();

        if (m->runif() < 1.0/(v->get_incubation(m)))
            p->change_state(m, ModelSEIR<TSeq>::INFECTED);
        return;
    }
```

17.33.3.2 update_infected_seir

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
epiworld::UpdateFun<TSeq> epiworld::epimodels::ModelSEIR< TSeq >::update_infected_seir
```

Initial value:

```
= [](
        epiworld::Agent<TSeq> * p,
        epiworld::Model<TSeq> * m
    ) -> void {

        if (m->runif() < (m->par("Recovery rate")))
            p->rm_virus(m);
        return;
    }
```

The documentation for this class was generated from the following file:

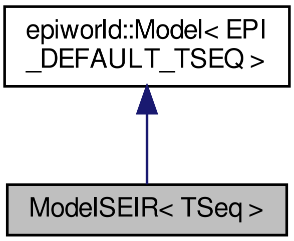
- epiworld.hpp

17.34 ModelSEIR< TSeq > Class Template Reference

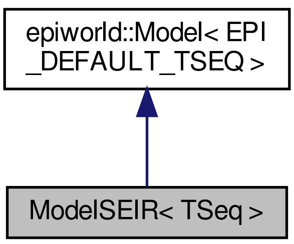
Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

`#include <seir.hpp>`

Inheritance diagram for ModelSEIR< TSeq >:



Collaboration diagram for ModelSEIR< TSeq >:



Public Member Functions

- **ModelSEIR** (ModelSEIR< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_↩ rate)
- **ModelSEIR** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate)
- ModelSEIR< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

  Set up the initial states of the model.

Public Attributes

- epiworld::UpdateFun< TSeq > **update_exposed_seir**
- epiworld::UpdateFun< TSeq > **update_infected_seir**

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **REMOVED** = 3

Additional Inherited Members

17.34.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelSEIR< TSeq >

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	epiworld_double Initial prevalence the immune system
transmission_rate	epiworld_double Transmission rate of the virus
avg_incubation_days	epiworld_double Average incubation days of the virus.
recovery_rate	epiworld_double Recovery rate of the virus.

17.34.2 Member Function Documentation

17.34.2.1 initial_states()

```
template<typename TSeq >
ModelSEIR< TSeq > & ModelSEIR< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set up the initial states of the model.

Parameters

*proportions_*	Double vector with the following values: • 0: Proportion of non-infected agents who are removed. • 1: Proportion of exposed agents to be set as infected.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.34.3 Member Data Documentation

17.34.3.1 update_exposed_seir

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
epiworld::UpdateFun<TSeq> ModelSEIR< TSeq >::update_exposed_seir
```

Initial value:

```
= [](
        epiworld::Agent<TSeq> * p,
        epiworld::Model<TSeq> * m
    ) -> void {

        auto v = p->get_virus();

        if (m->runif() < 1.0/(v->get_incubation(m)))
            p->change_state(m, ModelSEIR<TSeq>::INFECTED);
        return;
    }
```

17.34.3.2 update_infected_seir

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
epiworld::UpdateFun<TSeq> ModelSEIR< TSeq >::update_infected_seir
```

Initial value:

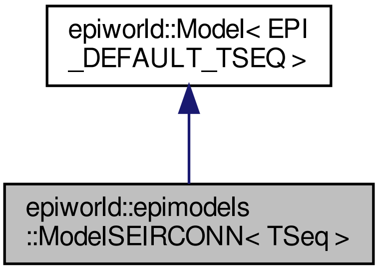
```
= [](
        epiworld::Agent<TSeq> * p,
        epiworld::Model<TSeq> * m
    ) -> void {

        if (m->runif() < (m->par("Recovery rate")))
            p->rm_virus(m);
        return;
    }
```

The documentation for this class was generated from the following file:

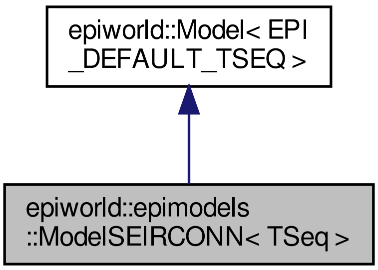
- include/epiworld/models/seir.hpp

17.35 epiworld::epimodels::ModelSEIRCONN< TSeq > Class Template Reference

Inheritance diagram for epiworld::epimodels::ModelSEIRCONN< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSEIRCONN< TSeq >:



Public Member Functions

- ModelSEIRCONN (ModelSEIRCONN< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate)

    Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.
- **ModelSEIRCONN** (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate)
- ModelSEIRCONN< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.

- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- ModelSEIRCONN< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue↩
_={})

    Set the initial states of the model.
- size_t **get_n_infected** () const
- std::vector< double > **generation_time_expected** (int max_days=200, int max_contacts=200) const

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **RECOVERED** = 3

Additional Inherited Members

17.35.1 Constructor & Destructor Documentation

17.35.1.1 ModelSEIRCONN()

```
template<typename TSeq >
ModelSEIRCONN< TSeq >::ModelSEIRCONN (
            ModelSEIRCONN< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate )  [inline]
```

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery

17.35.2 Member Function Documentation

17.35.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSEIRCONN< TSeq >::clone_ptr [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.35.2.2 initial_states()

```
template<typename TSeq >
ModelSEIRCONN< TSeq > & ModelSEIRCONN< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.35.2.3 reset()

```
template<typename TSeq >
void ModelSEIRCONN< TSeq >::reset [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

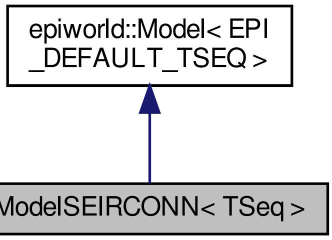
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

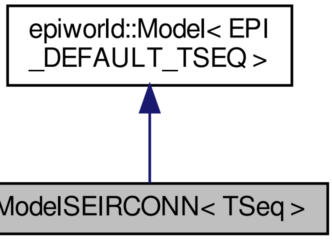
- epiworld.hpp

17.36 ModelSEIRCONN< TSeq > Class Template Reference

Inheritance diagram for ModelSEIRCONN< TSeq >:



Collaboration diagram for ModelSEIRCONN< TSeq >:



Public Member Functions

- ModelSEIRCONN (ModelSEIRCONN< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate)

  Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.
- **ModelSEIRCONN** (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate)
- ModelSEIRCONN< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

  Runs the simulation (after initialization)
- void reset ()

  Reset the model.
- Model< TSeq > $*$ clone_ptr ()

  Advanced usage: Makes a copy of data and returns it as undeleted pointer.

- ModelSEIRCONN< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue←
_={})

    Set the initial states of the model.
- size_t **get_n_infected** () const
- std::vector< double > **generation_time_expected** (int max_days=200, int max_contacts=200) const

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **RECOVERED** = 3

Additional Inherited Members

17.36.1 Constructor & Destructor Documentation

17.36.1.1 ModelSEIRCONN()

```
template<typename TSeq >
ModelSEIRCONN< TSeq >::ModelSEIRCONN (
            ModelSEIRCONN< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate ) [inline]
```

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery

17.36.2 Member Function Documentation

17.36.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSEIRCONN< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.36.2.2 initial_states()

```
template<typename TSeq >
ModelSEIRCONN< TSeq > & ModelSEIRCONN< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.36.2.3 reset()

```
template<typename TSeq >
void ModelSEIRCONN< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

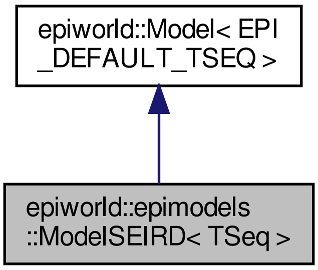
- include/epiworld/models/seirconnected.hpp

17.37 epiworld::epimodels::ModelSEIRD< TSeq > Class Template Reference

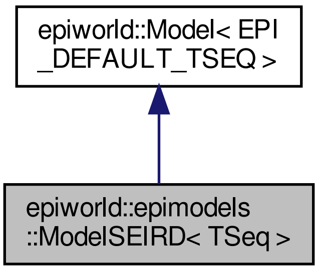
Template for a Susceptible-Exposed-Infected-Removed-Deceased (SEIRD) model.

```
#include <epiworld.hpp>
```

Inheritance diagram for epiworld::epimodels::ModelSEIRD< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSEIRD< TSeq >:



Public Member Functions

- ModelSEIRD (ModelSEIRD< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, epiworld_double death_rate)

    Constructor for the SEIRD model.
- ModelSEIRD (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, epiworld_double death_rate)

    Constructor for the SEIRD model.
- ModelSEIRD< TSeq > & **initial_states** (std::vector< double > proportions_, std::vector< int > queue_={})

Public Attributes

- epiworld::UpdateFun< TSeq > **update_exposed_seir**
- epiworld::UpdateFun< TSeq > **update_infected**

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **REMOVED** = 3
- static const int **DECEASED** = 4

Additional Inherited Members

17.37.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelSEIRD< TSeq >

Template for a Susceptible-Exposed-Infected-Removed-Deceased (SEIRD) model.

17.37.2 Constructor & Destructor Documentation

17.37.2.1 ModelSEIRD() [1/2]

```
template<typename TSeq >
ModelSEIRD< TSeq >::ModelSEIRD (
            ModelSEIRD< TSeq > & model,
            const std::string & vname,
            epiworld_double prevalence,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            epiworld_double death_rate )  [inline]
```

Constructor for the SEIRD model.

Template Parameters

TSeq	Type of the sequence used in the model.

Parameters

model	Reference to the SEIRD model.
vname	Name of the model.

Parameters

prevalence	Prevalence of the disease.
transmission_rate	Transmission rate of the disease.
avg_incubation_days	Average incubation period of the disease.
recovery_rate	Recovery rate of the disease.
death_rate	Death rate of the disease.

17.37.2.2 ModelSEIRD() [2/2]

```
template<typename TSeq >
ModelSEIRD< TSeq >::ModelSEIRD (
            const std::string & vname,
            epiworld_double prevalence,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            epiworld_double death_rate )  [inline]
```

Constructor for the SEIRD model.

Parameters

vname	Name of the model.
prevalence	Initial prevalence of the disease.
transmission_rate	Transmission rate of the disease.
avg_incubation_days	Average incubation period of the disease.
recovery_rate	Recovery rate of the disease.
death_rate	Death rate of the disease.

17.37.3 Member Data Documentation

17.37.3.1 update_exposed_seir

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
epiworld::UpdateFun<TSeq> epiworld::epimodels::ModelSEIRD< TSeq >::update_exposed_seir
```

Initial value:

```
= [](
    epiworld::Agent<TSeq> * p,
    epiworld::Model<TSeq> * m
  ) -> void {

    auto v = p->get_virus();

    if (m->runif() < 1.0/(v->get_incubation(m)))
      p->change_state(m, ModelSEIRD<TSeq>::INFECTED);
    return;
  }
```

The documentation for this class was generated from the following file:

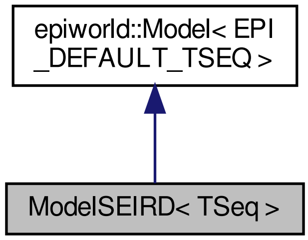
- epiworld.hpp

17.38 ModelSEIRD< TSeq > Class Template Reference

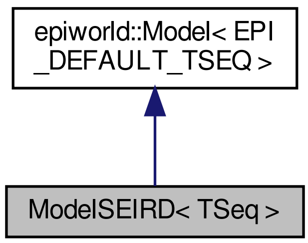
Template for a Susceptible-Exposed-Infected-Removed-Deceased (SEIRD) model.

`#include <seird.hpp>`

Inheritance diagram for ModelSEIRD< TSeq >:



Collaboration diagram for ModelSEIRD< TSeq >:



Public Member Functions

- ModelSEIRD (ModelSEIRD< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, epiworld_double death_rate)

  Constructor for the SEIRD model.
- ModelSEIRD (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, epiworld_double death_rate)

  Constructor for the SEIRD model.
- ModelSEIRD< TSeq > & **initial_states** (std::vector< double > proportions_, std::vector< int > queue_={})

Public Attributes

- epiworld::UpdateFun< TSeq > **update_exposed_seir**
- epiworld::UpdateFun< TSeq > **update_infected**

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **REMOVED** = 3
- static const int **DECEASED** = 4

Additional Inherited Members

17.38.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelSEIRD< TSeq >

Template for a Susceptible-Exposed-Infected-Removed-Deceased (SEIRD) model.

17.38.2 Constructor & Destructor Documentation

17.38.2.1 ModelSEIRD() [1/2]

```
template<typename TSeq >
ModelSEIRD< TSeq >::ModelSEIRD (
            ModelSEIRD< TSeq > & model,
            const std::string & vname,
            epiworld_double prevalence,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            epiworld_double death_rate )  [inline]
```

Constructor for the SEIRD model.

Template Parameters

TSeq	Type of the sequence used in the model.

Parameters

model	Reference to the SEIRD model.
vname	Name of the model.

Parameters

prevalence	Prevalence of the disease.
transmission_rate	Transmission rate of the disease.
avg_incubation_days	Average incubation period of the disease.
recovery_rate	Recovery rate of the disease.
death_rate	Death rate of the disease.

17.38.2.2 ModelSEIRD() [2/2]

```
template<typename TSeq >
ModelSEIRD< TSeq >::ModelSEIRD (
              const std::string & vname,
              epiworld_double prevalence,
              epiworld_double transmission_rate,
              epiworld_double avg_incubation_days,
              epiworld_double recovery_rate,
              epiworld_double death_rate )  [inline]
```

Constructor for the SEIRD model.

Parameters

vname	Name of the model.
prevalence	Initial prevalence of the disease.
transmission_rate	Transmission rate of the disease.
avg_incubation_days	Average incubation period of the disease.
recovery_rate	Recovery rate of the disease.
death_rate	Death rate of the disease.

17.38.3 Member Data Documentation

17.38.3.1 update_exposed_seir

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
epiworld::UpdateFun<TSeq> ModelSEIRD< TSeq >::update_exposed_seir
```

Initial value:

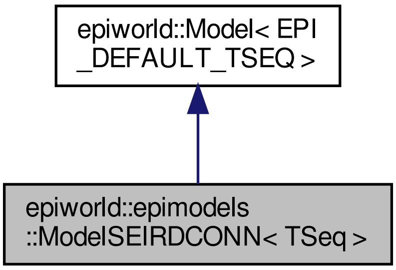
```
= [](
    epiworld::Agent<TSeq> * p,
    epiworld::Model<TSeq> * m
  ) -> void {

    auto v = p->get_virus();

    if (m->runif() < 1.0/(v->get_incubation(m)))
      p->change_state(m, ModelSEIRD<TSeq>::INFECTED);
    return;
  }
```

The documentation for this class was generated from the following file:

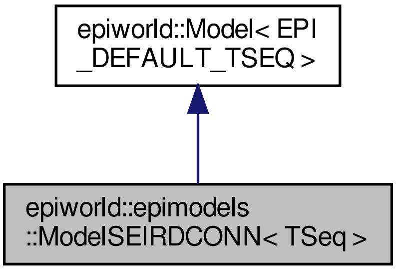
- include/epiworld/models/seird.hpp

17.39 epiworld::epimodels::ModelSEIRDCONN< TSeq > Class Template Reference

Inheritance diagram for epiworld::epimodels::ModelSEIRDCONN< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSEIRDCONN< TSeq >:



Public Member Functions

- ModelSEIRDCONN (ModelSEIRDCONN< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, epiworld_double death_rate)

    Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.
- **ModelSEIRDCONN** (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, epiworld_double death_rate)
- ModelSEIRDCONN< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

  Runs the simulation (after initialization)
- void reset ()

  Reset the model.
- Model< TSeq > * clone_ptr ()

  Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- ModelSEIRDCONN< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

  Set up the initial states of the model.
- size_t **get_n_infected** () const

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **REMOVED** = 3
- static const int **DECEASED** = 4

Additional Inherited Members

17.39.1 Constructor & Destructor Documentation

17.39.1.1 ModelSEIRDCONN()

```
template<typename TSeq >
ModelSEIRDCONN< TSeq >::ModelSEIRDCONN (
            ModelSEIRDCONN< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            epiworld_double death_rate )  [inline]
```

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery
death_rate	Probability of death

17.39.2 Member Function Documentation

17.39.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSEIRDCONN< TSeq >::clone_ptr [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.39.2.2 initial_states()

```
template<typename TSeq >
ModelSEIRDCONN< TSeq > & ModelSEIRDCONN< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set up the initial states of the model.

Parameters

*proportions_*	Double vector with the following values: • 0: Proportion of non-infected agents who are removed. • 1: Proportion of exposed agents to be set as infected.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.39.2.3 reset()

```
template<typename TSeq >
void ModelSEIRDCONN< TSeq >::reset [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

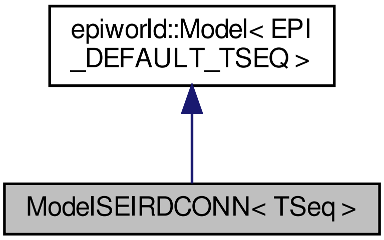
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

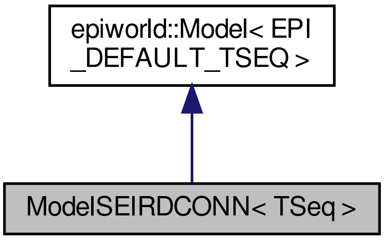
- epiworld.hpp

17.40 ModelSEIRDCONN< TSeq > Class Template Reference

Inheritance diagram for ModelSEIRDCONN< TSeq >:



Collaboration diagram for ModelSEIRDCONN< TSeq >:



Public Member Functions

- ModelSEIRDCONN (ModelSEIRDCONN< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, epiworld_double death_rate)

    Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.
- **ModelSEIRDCONN** (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, epiworld_double death_rate)
- ModelSEIRDCONN< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- ModelSEIRDCONN< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set up the initial states of the model.
- size_t **get_n_infected** () const

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **REMOVED** = 3
- static const int **DECEASED** = 4

Additional Inherited Members

17.40.1 Constructor & Destructor Documentation

17.40.1.1 ModelSEIRDCONN()

```
template<typename TSeq >
ModelSEIRDCONN< TSeq >::ModelSEIRDCONN (
            ModelSEIRDCONN< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            epiworld_double death_rate )  [inline]
```

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery
death_rate	Probability of death

17.40.2 Member Function Documentation

17.40.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSEIRDCONN< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.40.2.2 initial_states()

```
template<typename TSeq >
ModelSEIRDCONN< TSeq > & ModelSEIRDCONN< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set up the initial states of the model.

Parameters

proportions← _	Double vector with the following values: • 0: Proportion of non-infected agents who are removed. • 1: Proportion of exposed agents to be set as infected.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.40.2.3 reset()

```
template<typename TSeq >
void ModelSEIRDCONN< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

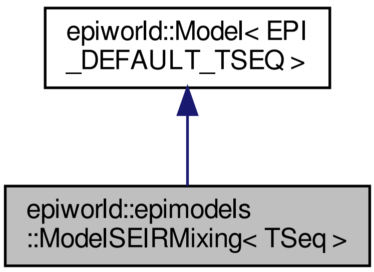
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

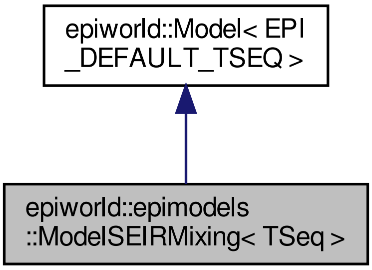
- include/epiworld/models/seirdconnected.hpp

17.41 epiworld::epimodels::ModelSEIRMixing< TSeq > Class Template Reference

Inheritance diagram for epiworld::epimodels::ModelSEIRMixing< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSEIRMixing< TSeq >:



Public Member Functions

- ModelSEIRMixing (ModelSEIRMixing< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, std::vector< double > contact_matrix)

    Constructs a ModelSEIRMixing object.
- ModelSEIRMixing (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, std::vector< double > contact_matrix)

    Constructs a ModelSEIRMixing object.
- ModelSEIRMixing< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- ModelSEIRMixing< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set the initial states of the model.
- void **set_contact_matrix** (std::vector< double > cmat)

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **RECOVERED** = 3

Additional Inherited Members

17.41.1 Constructor & Destructor Documentation

17.41.1.1 ModelSEIRMixing() [1/2]

```
template<typename TSeq >
ModelSEIRMixing< TSeq >::ModelSEIRMixing (
            ModelSEIRMixing< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix )  [inline]
```

Constructs a ModelSEIRMixing object.

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A reference to an existing ModelSEIRMixing object.
vname	The name of the ModelSEIRMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
avg_incubation_days	The average incubation period of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model. Specified in column-major order.
model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery

17.41.1.2 ModelSEIRMixing() [2/2]

```
template<typename TSeq >
ModelSEIRMixing< TSeq >::ModelSEIRMixing (
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix )  [inline]
```

Constructs a ModelSEIRMixing object.

Parameters

vname	The name of the ModelSEIRMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
avg_incubation_days	The average incubation period of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model.

17.41.2 Member Function Documentation

17.41.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSEIRMixing< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.41.2.2 initial_states()

```
template<typename TSeq >
ModelSEIRMixing< TSeq > & ModelSEIRMixing< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.41.2.3 reset()

```
template<typename TSeq >
void ModelSEIRMixing< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

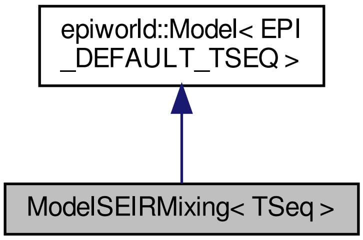
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

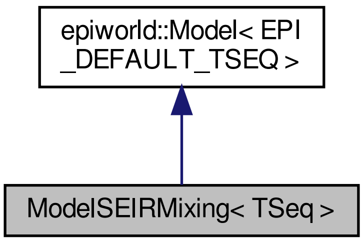
- epiworld.hpp

17.42 ModelSEIRMixing< TSeq > Class Template Reference

Inheritance diagram for ModelSEIRMixing< TSeq >:



Collaboration diagram for ModelSEIRMixing< TSeq >:



Public Member Functions

- ModelSEIRMixing (ModelSEIRMixing< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, std::vector< double > contact_matrix)

    Constructs a ModelSEIRMixing object.
- ModelSEIRMixing (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, std::vector< double > contact_matrix)

    Constructs a ModelSEIRMixing object.
- ModelSEIRMixing< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- ModelSEIRMixing< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set the initial states of the model.
- void **set_contact_matrix** (std::vector< double > cmat)

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **RECOVERED** = 3

Additional Inherited Members

17.42.1 Constructor & Destructor Documentation

17.42.1.1 ModelSEIRMixing() [1/2]

```
template<typename TSeq >
ModelSEIRMixing< TSeq >::ModelSEIRMixing (
            ModelSEIRMixing< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix )  [inline]
```

Constructs a ModelSEIRMixing object.

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A reference to an existing ModelSEIRMixing object.
vname	The name of the ModelSEIRMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
avg_incubation_days	The average incubation period of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model. Specified in column-major order.
model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery

17.42.1.2 ModelSEIRMixing() [2/2]

```
template<typename TSeq >
ModelSEIRMixing< TSeq >::ModelSEIRMixing (
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix )  [inline]
```

Constructs a ModelSEIRMixing object.

Parameters

vname	The name of the ModelSEIRMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
avg_incubation_days	The average incubation period of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model.

17.42.2 Member Function Documentation

17.42.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSEIRMixing< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.42.2.2 initial_states()

```
template<typename TSeq >
ModelSEIRMixing< TSeq > & ModelSEIRMixing< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.42.2.3 reset()

```
template<typename TSeq >
void ModelSEIRMixing< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

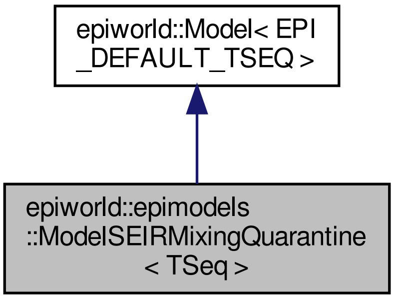
- include/epiworld/models/seirmixing.hpp

17.43 epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq > Class Template Reference

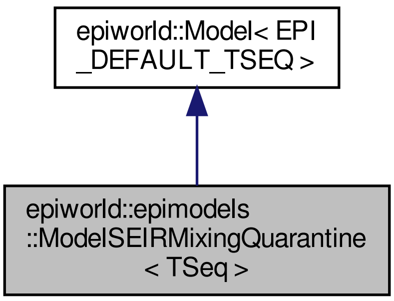
SEIR model with mixing, quarantine, and contact tracing.

`#include <epiworld.hpp>`

Inheritance diagram for epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >:



Public Member Functions

- ModelSEIRMixingQuarantine (ModelSEIRMixingQuarantine< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, std::vector< double > contact_matrix, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double days_undetected, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_double isolation_willingness, epiworld_fast_int isolation_period, epiworld_double contact_tracing_success_rate=1.0, epiworld_fast_uint contact_tracing_days_prior=4u)

Constructs a ModelSEIRMixingQuarantine object.

- ModelSEIRMixingQuarantine (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, std::vector< double > contact_matrix, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double days_undetected, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_double isolation_willingness, epiworld_fast_int isolation_period, epiworld_double contact_tracing_success_rate=1.0, epiworld_fast_uint contact_tracing_days_prior=4u)

  Constructs a ModelSEIRMixingQuarantine object.
- ModelSEIRMixingQuarantine< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

  Run the model simulation.
- void reset ()

  Reset the model to initial state.
- Model< TSeq > * clone_ptr ()

  Create a clone of this model.
- ModelSEIRMixingQuarantine< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

  Set the initial states of the model.
- void set_contact_matrix (std::vector< double > cmat)

  Set the contact matrix for population mixing.
- std::vector< double > get_contact_matrix () const

  Get the current contact matrix.
- std::vector< size_t > get_agent_quarantine_triggered () const

  Get the quarantine trigger status for all agents.
- std::vector< bool > get_quarantine_willingness () const

  Get the quarantine willingness for all agents.
- std::vector< bool > get_isolation_willingness () const

  Get the isolation willingness for all agents.

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **ISOLATED** = 3
- static const int **DETECTED_HOSPITALIZED** = 4
- static const int **QUARANTINED_SUSCEPTIBLE** = 5
- static const int **QUARANTINED_EXPOSED** = 6
- static const int **ISOLATED_RECOVERED** = 7
- static const int **HOSPITALIZED** = 8
- static const int **RECOVERED** = 9
- static const size_t **QUARANTINE_PROCESS_INACTIVE** = 0u
- static const size_t **QUARANTINE_PROCESS_ACTIVE** = 1u
- static const size_t **QUARANTINE_PROCESS_DONE** = 2u

Additional Inherited Members

17.43.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >

SEIR model with mixing, quarantine, and contact tracing.

This class implements a Susceptible-Exposed-Infected-Removed (SEIR) epidemiological model with additional features including:

- Population mixing based on contact matrices
- Quarantine measures for exposed contacts
- Isolation policies for detected infected individuals
- Contact tracing with configurable success rates
- Hospitalization of severe cases
- Individual willingness to comply with public health measures

The model supports 10 distinct states:

- Susceptible: Individuals who can become infected
- Exposed: Infected but not yet infectious (incubation period)
- Infected: Infectious individuals in the community
- Isolated: Detected infected individuals in self-isolation
- Detected Hospitalized: Hospitalized individuals who were contact-traced
- Quarantined Susceptible: Susceptible individuals in quarantine due to contact tracing
- Quarantined Exposed: Exposed individuals in quarantine due to contact tracing
- Isolated Recovered: Recovered individuals still in isolation
- Hospitalized: Individuals requiring hospital care
- Recovered: Individuals who have recovered and gained immunity

Template Parameters

TSeq	Type for genetic sequences (default: EPI_DEFAULT_TSEQ)

17.43.2 Constructor & Destructor Documentation

17.43.2.1 ModelSEIRMixingQuarantine() [1/2]

```
template<typename TSeq >
ModelSEIRMixingQuarantine< TSeq >::ModelSEIRMixingQuarantine (
            ModelSEIRMixingQuarantine< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double days_undetected,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_double isolation_willingness,
            epiworld_fast_int isolation_period,
            epiworld_double contact_tracing_success_rate = 1.0,
            epiworld_fast_uint contact_tracing_days_prior = 4u )  [inline]
```

Constructs a ModelSEIRMixingQuarantine object.

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model with mixing, quarantine, and contact tracing.

Parameters

model	A reference to an existing ModelSEIRMixingQuarantine object.
vname	The name of the ModelSEIRMixingQuarantine object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
avg_incubation_days	The average incubation period of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model. Specified in column-major order.
hospitalization_rate	The rate at which infected individuals are hospitalized.
hospitalization_period	The average duration of hospitalization in days.
days_undetected	The average number of days an infected individual remains undetected.
quarantine_period	The duration of quarantine in days for exposed contacts.
quarantine_willingness	The proportion of individuals willing to comply with quarantine measures.
isolation_willingness	The proportion of individuals willing to self-isolate when detected.
isolation_period	The duration of isolation in days for detected infected individuals.
contact_tracing_success_rate	The probability of successfully identifying and tracing contacts (default: 1.0).
contact_tracing_days_prior	The number of days prior to detection for which contacts are traced (default: 4).
model	A ModelSEIRMixingQuarantine<TSeq> object where to set up the SEIR model.
vname	Name of the virus
n	Number of agents in the population
prevalence	Initial prevalence (proportion of infected individuals)

Parameters

contact_rate	Average number of contacts (interactions) per step
transmission_rate	Probability of transmission per contact
avg_incubation_days	Average incubation period in days
recovery_rate	Probability of recovery per day
contact_matrix	Contact matrix specifying mixing patterns between population groups
hospitalization_rate	Rate at which infected individuals are hospitalized
hospitalization_period	Average duration of hospitalization in days
days_undetected	Average number of days an infected individual remains undetected
quarantine_period	Duration of quarantine in days for exposed contacts
quarantine_willingness	Proportion of individuals willing to comply with quarantine
isolation_willingness	Proportion of individuals willing to self-isolate when detected
isolation_period	Duration of isolation in days for detected infected individuals
contact_tracing_success_rate	Probability of successfully identifying contacts during tracing
contact_tracing_days_prior	Number of days prior to detection for contact tracing

17.43.2.2 ModelSEIRMixingQuarantine() [2/2]

```
template<typename TSeq >
ModelSEIRMixingQuarantine< TSeq >::ModelSEIRMixingQuarantine (
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double days_undetected,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_double isolation_willingness,
            epiworld_fast_int isolation_period,
            epiworld_double contact_tracing_success_rate = 1.0,
            epiworld_fast_uint contact_tracing_days_prior = 4u )  [inline]
```

Constructs a ModelSEIRMixingQuarantine object.

Parameters

vname	The name of the ModelSEIRMixingQuarantine object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
avg_incubation_days	The average incubation period of the disease in the model.

Parameters

recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model.
hospitalization_rate	The rate at which infected individuals are hospitalized.
hospitalization_period	The average duration of hospitalization in days.
days_undetected	The average number of days an infected individual remains undetected.
quarantine_period	The duration of quarantine in days for exposed contacts.
quarantine_willingness	The proportion of individuals willing to comply with quarantine measures.
isolation_willingness	The proportion of individuals willing to self-isolate when detected.
isolation_period	The duration of isolation in days for detected infected individuals.
contact_tracing_success_rate	The probability of successfully identifying and tracing contacts (default: 1.0).
contact_tracing_days_prior	The number of days prior to detection for which contacts are traced (default: 4).

17.43.3 Member Function Documentation

17.43.3.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSEIRMixingQuarantine< TSeq >::clone_ptr  [inline], [virtual]
```

Create a clone of this model.

Returns

Pointer to a new model instance with the same configuration

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.43.3.2 get_agent_quarantine_triggered()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< size_t > epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >::get_agent_↩
quarantine_triggered ( ) const  [inline]
```

Get the quarantine trigger status for all agents.

Returns

Vector indicating quarantine process status for each agent

17.43.3.3 get_contact_matrix()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< double > epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >::get_contact_↩
matrix ( ) const [inline]
```

Get the current contact matrix.

Returns

Vector representing the contact matrix

17.43.3.4 get_isolation_willingness()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< bool > epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >::get_isolation_↩
willingness ( ) const [inline]
```

Get the isolation willingness for all agents.

Returns

Vector of boolean values indicating each agent's willingness to self-isolate

17.43.3.5 get_quarantine_willingness()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< bool > epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >::get_quarantine_↩
willingness ( ) const [inline]
```

Get the quarantine willingness for all agents.

Returns

Vector of boolean values indicating each agent's willingness to quarantine

17.43.3.6 initial_states()

```
template<typename TSeq >
ModelSEIRMixingQuarantine< TSeq > & ModelSEIRMixingQuarantine< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set the initial states of the model.

Parameters

proportions←↩ _	Double vector with two elements: • [0]: The proportion of initially infected individuals who start in the exposed state. • [1]: The proportion of initially non-infected individuals who have recovered (immune).
*queue_*	Optional vector for queuing specifications (default: empty).

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.43.3.7 run()

```
template<typename TSeq >
ModelSEIRMixingQuarantine< TSeq > & ModelSEIRMixingQuarantine< TSeq >::run (
            epiworld_fast_uint ndays,
            int seed = -1 ) [inline], [virtual]
```

Run the model simulation.

Parameters

ndays	Number of days to simulate
seed	Random seed for reproducibility (default: -1 for random seed)

Returns

Reference to this model instance

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.43.3.8 set_contact_matrix()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
void epiworld::epimodels::ModelSEIRMixingQuarantine< TSeq >::set_contact_matrix (
            std::vector< double > cmat ) [inline]
```

Set the contact matrix for population mixing.

Parameters

cmat	Contact matrix specifying interaction rates between groups

The documentation for this class was generated from the following file:

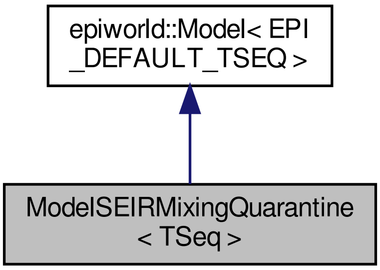
- epiworld.hpp

17.44 ModelSEIRMixingQuarantine< TSeq > Class Template Reference

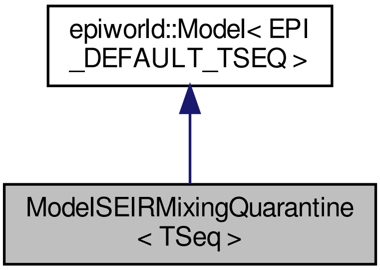
SEIR model with mixing, quarantine, and contact tracing.

`#include <seirmixingquarantine.hpp>`

Inheritance diagram for ModelSEIRMixingQuarantine< TSeq >:



Collaboration diagram for ModelSEIRMixingQuarantine< TSeq >:



Public Member Functions

- ModelSEIRMixingQuarantine (ModelSEIRMixingQuarantine< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, std::vector< double > contact_matrix, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double days_undetected, epiworld_fast_int quarantine_period, epiworld_double quarantine_willingness, epiworld_double isolation_willingness, epiworld_fast_int isolation_period, epiworld_double contact_tracing_success_rate=1.0, epiworld_fast_uint contact_tracing_days_prior=4u)

    Constructs a ModelSEIRMixingQuarantine object.

- ModelSEIRMixingQuarantine (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double avg_incubation_days, epiworld_double recovery_rate, std::vector< double > contact_matrix, epiworld_double hospitalization_rate, epiworld_double hospitalization_period, epiworld_double days_undetected, epiworld_fast_int quarantine↩_period, epiworld_double quarantine_willingness, epiworld_double isolation_willingness, epiworld_fast_int isolation_period, epiworld_double contact_tracing_success_rate=1.0, epiworld_fast_uint contact_tracing_↩days_prior=4u)

    Constructs a ModelSEIRMixingQuarantine object.
- ModelSEIRMixingQuarantine< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Run the model simulation.
- void reset ()

    Reset the model to initial state.
- Model< TSeq > * clone_ptr ()

    Create a clone of this model.
- ModelSEIRMixingQuarantine< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set the initial states of the model.
- void set_contact_matrix (std::vector< double > cmat)

    Set the contact matrix for population mixing.
- std::vector< double > get_contact_matrix () const

    Get the current contact matrix.
- std::vector< size_t > get_agent_quarantine_triggered () const

    Get the quarantine trigger status for all agents.
- std::vector< bool > get_quarantine_willingness () const

    Get the quarantine willingness for all agents.
- std::vector< bool > get_isolation_willingness () const

    Get the isolation willingness for all agents.

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **ISOLATED** = 3
- static const int **DETECTED_HOSPITALIZED** = 4
- static const int **QUARANTINED_SUSCEPTIBLE** = 5
- static const int **QUARANTINED_EXPOSED** = 6
- static const int **ISOLATED_RECOVERED** = 7
- static const int **HOSPITALIZED** = 8
- static const int **RECOVERED** = 9
- static const size_t **QUARANTINE_PROCESS_INACTIVE** = 0u
- static const size_t **QUARANTINE_PROCESS_ACTIVE** = 1u
- static const size_t **QUARANTINE_PROCESS_DONE** = 2u

Additional Inherited Members

17.44.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelSEIRMixingQuarantine< TSeq >

SEIR model with mixing, quarantine, and contact tracing.

This class implements a Susceptible-Exposed-Infected-Removed (SEIR) epidemiological model with additional features including:

- Population mixing based on contact matrices
- Quarantine measures for exposed contacts
- Isolation policies for detected infected individuals
- Contact tracing with configurable success rates
- Hospitalization of severe cases
- Individual willingness to comply with public health measures

The model supports 10 distinct states:

- Susceptible: Individuals who can become infected
- Exposed: Infected but not yet infectious (incubation period)
- Infected: Infectious individuals in the community
- Isolated: Detected infected individuals in self-isolation
- Detected Hospitalized: Hospitalized individuals who were contact-traced
- Quarantined Susceptible: Susceptible individuals in quarantine due to contact tracing
- Quarantined Exposed: Exposed individuals in quarantine due to contact tracing
- Isolated Recovered: Recovered individuals still in isolation
- Hospitalized: Individuals requiring hospital care
- Recovered: Individuals who have recovered and gained immunity

Template Parameters

TSeq	Type for genetic sequences (default: EPI_DEFAULT_TSEQ)

17.44.2 Constructor & Destructor Documentation

17.44.2.1 ModelSEIRMixingQuarantine() [1/2]

```
template<typename TSeq >
ModelSEIRMixingQuarantine< TSeq >::ModelSEIRMixingQuarantine (
            ModelSEIRMixingQuarantine< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double days_undetected,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_double isolation_willingness,
            epiworld_fast_int isolation_period,
            epiworld_double contact_tracing_success_rate = 1.0,
            epiworld_fast_uint contact_tracing_days_prior = 4u )  [inline]
```

Constructs a ModelSEIRMixingQuarantine object.

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model with mixing, quarantine, and contact tracing.

Parameters

model	A reference to an existing ModelSEIRMixingQuarantine object.
vname	The name of the ModelSEIRMixingQuarantine object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
avg_incubation_days	The average incubation period of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model. Specified in column-major order.
hospitalization_rate	The rate at which infected individuals are hospitalized.
hospitalization_period	The average duration of hospitalization in days.
days_undetected	The average number of days an infected individual remains undetected.
quarantine_period	The duration of quarantine in days for exposed contacts.
quarantine_willingness	The proportion of individuals willing to comply with quarantine measures.
isolation_willingness	The proportion of individuals willing to self-isolate when detected.
isolation_period	The duration of isolation in days for detected infected individuals.
contact_tracing_success_rate	The probability of successfully identifying and tracing contacts (default: 1.0).
contact_tracing_days_prior	The number of days prior to detection for which contacts are traced (default: 4).
model	A ModelSEIRMixingQuarantine<TSeq> object where to set up the SEIR model.
vname	Name of the virus
n	Number of agents in the population
prevalence	Initial prevalence (proportion of infected individuals)

Parameters

contact_rate	Average number of contacts (interactions) per step
transmission_rate	Probability of transmission per contact
avg_incubation_days	Average incubation period in days
recovery_rate	Probability of recovery per day
contact_matrix	Contact matrix specifying mixing patterns between population groups
hospitalization_rate	Rate at which infected individuals are hospitalized
hospitalization_period	Average duration of hospitalization in days
days_undetected	Average number of days an infected individual remains undetected
quarantine_period	Duration of quarantine in days for exposed contacts
quarantine_willingness	Proportion of individuals willing to comply with quarantine
isolation_willingness	Proportion of individuals willing to self-isolate when detected
isolation_period	Duration of isolation in days for detected infected individuals
contact_tracing_success_rate	Probability of successfully identifying contacts during tracing
contact_tracing_days_prior	Number of days prior to detection for contact tracing

17.44.2.2 ModelSEIRMixingQuarantine() [2/2]

```
template<typename TSeq >
ModelSEIRMixingQuarantine< TSeq >::ModelSEIRMixingQuarantine (
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double avg_incubation_days,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix,
            epiworld_double hospitalization_rate,
            epiworld_double hospitalization_period,
            epiworld_double days_undetected,
            epiworld_fast_int quarantine_period,
            epiworld_double quarantine_willingness,
            epiworld_double isolation_willingness,
            epiworld_fast_int isolation_period,
            epiworld_double contact_tracing_success_rate = 1.0,
            epiworld_fast_uint contact_tracing_days_prior = 4u ) [inline]
```

Constructs a ModelSEIRMixingQuarantine object.

Parameters

vname	The name of the ModelSEIRMixingQuarantine object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
avg_incubation_days	The average incubation period of the disease in the model.

Parameters

recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model.
hospitalization_rate	The rate at which infected individuals are hospitalized.
hospitalization_period	The average duration of hospitalization in days.
days_undetected	The average number of days an infected individual remains undetected.
quarantine_period	The duration of quarantine in days for exposed contacts.
quarantine_willingness	The proportion of individuals willing to comply with quarantine measures.
isolation_willingness	The proportion of individuals willing to self-isolate when detected.
isolation_period	The duration of isolation in days for detected infected individuals.
contact_tracing_success_rate	The probability of successfully identifying and tracing contacts (default: 1.0).
contact_tracing_days_prior	The number of days prior to detection for which contacts are traced (default: 4).

17.44.3 Member Function Documentation

17.44.3.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSEIRMixingQuarantine< TSeq >::clone_ptr  [inline], [virtual]
```

Create a clone of this model.

Returns

Pointer to a new model instance with the same configuration

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.44.3.2 get_agent_quarantine_triggered()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< size_t > ModelSEIRMixingQuarantine< TSeq >::get_agent_quarantine_triggered ( )
const  [inline]
```

Get the quarantine trigger status for all agents.

Returns

Vector indicating quarantine process status for each agent

17.44.3.3 get_contact_matrix()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< double > ModelSEIRMixingQuarantine< TSeq >::get_contact_matrix ( ) const [inline]
```

Get the current contact matrix.

Returns

Vector representing the contact matrix

17.44.3.4 get_isolation_willingness()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< bool > ModelSEIRMixingQuarantine< TSeq >::get_isolation_willingness ( ) const
[inline]
```

Get the isolation willingness for all agents.

Returns

Vector of boolean values indicating each agent's willingness to self-isolate

17.44.3.5 get_quarantine_willingness()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
std::vector< bool > ModelSEIRMixingQuarantine< TSeq >::get_quarantine_willingness ( ) const
[inline]
```

Get the quarantine willingness for all agents.

Returns

Vector of boolean values indicating each agent's willingness to quarantine

17.44.3.6 initial_states()

```
template<typename TSeq >
ModelSEIRMixingQuarantine< TSeq > & ModelSEIRMixingQuarantine< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set the initial states of the model.

Parameters

proportions←→_	Double vector with two elements: • [0]: The proportion of initially infected individuals who start in the exposed state. • [1]: The proportion of initially non-infected individuals who have recovered (immune).
*queue_*	Optional vector for queuing specifications (default: empty).

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.44.3.7 run()

```
template<typename TSeq >
ModelSEIRMixingQuarantine< TSeq > & ModelSEIRMixingQuarantine< TSeq >::run (
            epiworld_fast_uint ndays,
            int seed = -1 ) [inline], [virtual]
```

Run the model simulation.

Parameters

ndays	Number of days to simulate
seed	Random seed for reproducibility (default: -1 for random seed)

Returns

Reference to this model instance

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.44.3.8 set_contact_matrix()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
void ModelSEIRMixingQuarantine< TSeq >::set_contact_matrix (
            std::vector< double > cmat ) [inline]
```

Set the contact matrix for population mixing.

Parameters

cmat	Contact matrix specifying interaction rates between groups

The documentation for this class was generated from the following file:

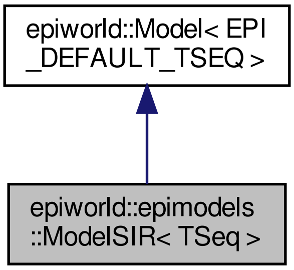
- include/epiworld/models/seirmixingquarantine.hpp

17.45 epiworld::epimodels::ModelSIR< TSeq > Class Template Reference

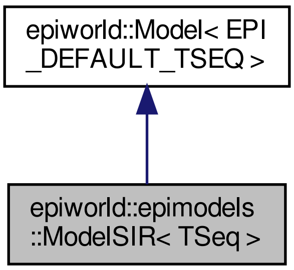
Template for a Susceptible-Infected-Removed (SIR) model.

```
#include <epiworld.hpp>
```

Inheritance diagram for epiworld::epimodels::ModelSIR< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSIR< TSeq >:



Public Member Functions

- **ModelSIR** (ModelSIR< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate)
- **ModelSIR** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate)
- ModelSIR< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

  Set the initial states of the model.

Additional Inherited Members

17.45.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelSIR< TSeq >

Template for a Susceptible-Infected-Removed (SIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
initial_prevalence	epiworld_double Initial prevalence
initial_efficacy	epiworld_double Initial susceptibility_reduction of the immune system
initial_recovery	epiworld_double Initial recovery_rate rate of the immune system

17.45.2 Member Function Documentation

17.45.2.1 initial_states()

```
template<typename TSeq >
ModelSIR< TSeq > & ModelSIR< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set the initial states of the model.

Parameters

proportions← _	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

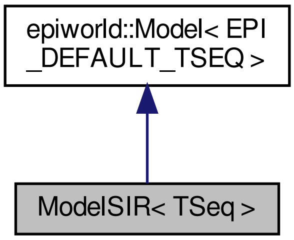
- epiworld.hpp

17.46 ModelSIR< TSeq > Class Template Reference

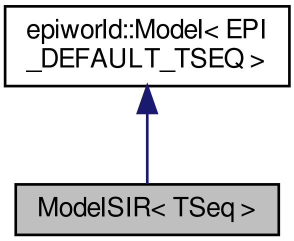
Template for a Susceptible-Infected-Removed (SIR) model.

```
#include <sir.hpp>
```

Inheritance diagram for ModelSIR< TSeq >:



Collaboration diagram for ModelSIR< TSeq >:



Public Member Functions

- **ModelSIR** (ModelSIR< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld↩_double transmission_rate, epiworld_double recovery_rate)
- **ModelSIR** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate)
- ModelSIR< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

  Set the initial states of the model.

Additional Inherited Members

17.46.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelSIR< TSeq >

Template for a Susceptible-Infected-Removed (SIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
initial_prevalence	epiworld_double Initial prevalence
initial_efficacy	epiworld_double Initial susceptibility_reduction of the immune system
initial_recovery	epiworld_double Initial recovery_rate rate of the immune system

17.46.2 Member Function Documentation

17.46.2.1 initial_states()

```
template<typename TSeq >
ModelSIR< TSeq > & ModelSIR< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set the initial states of the model.

Parameters

proportions←→_	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

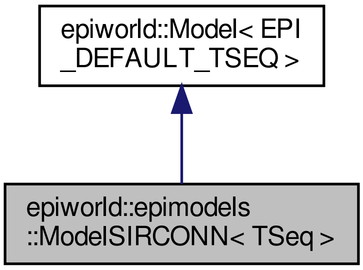
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

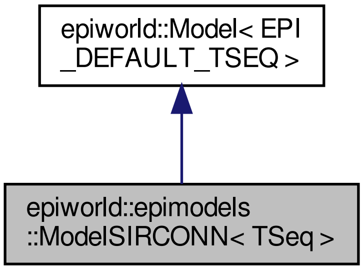
- include/epiworld/models/sir.hpp

17.47 epiworld::epimodels::ModelSIRCONN< TSeq > Class Template Reference

Inheritance diagram for epiworld::epimodels::ModelSIRCONN< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSIRCONN< TSeq >:



Public Member Functions

- ModelSIRCONN (ModelSIRCONN< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate)

  Template for a Susceptible-Infected-Removed (SIR) model.
- **ModelSIRCONN** (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate)
- ModelSIRCONN< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

  Runs the simulation (after initialization)
- void reset ()

  Reset the model.
- Model< TSeq > * clone_ptr ()

Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- ModelSIRCONN< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue↩_={})

  Set the initial states of the model.
- size_t get_n_infected () const

  Get the infected individuals.
- std::vector< double > **generation_time_expected** (int max_days=200, int max_contacts=200) const

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **INFECTED** = 1
- static const int **RECOVERED** = 2

Additional Inherited Members

17.47.1 Constructor & Destructor Documentation

17.47.1.1 ModelSIRCONN()

```
template<typename TSeq >
ModelSIRCONN< TSeq >::ModelSIRCONN (
            ModelSIRCONN< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate )  [inline]
```

Template for a Susceptible-Infected-Removed (SIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery

17.47.2 Member Function Documentation

17.47.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSIRCONN< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.47.2.2 get_n_infected()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
size_t epiworld::epimodels::ModelSIRCONN< TSeq >::get_n_infected ( ) const  [inline]
```

Get the infected individuals.

Returns

std::vector< epiworld::Agent<TSeq> * >

17.47.2.3 initial_states()

```
template<typename TSeq >
ModelSIRCONN< TSeq > & ModelSIRCONN< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.47.2.4 reset()

```
template<typename TSeq >
void ModelSIRCONN< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

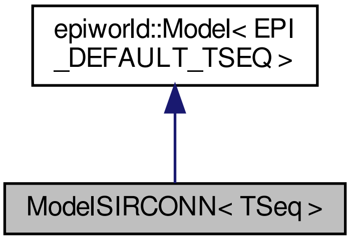
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

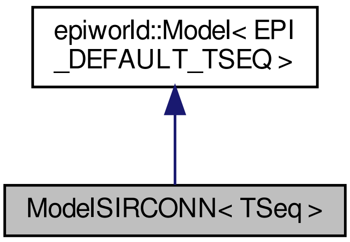
- epiworld.hpp

17.48 ModelSIRCONN< TSeq > Class Template Reference

Inheritance diagram for ModelSIRCONN< TSeq >:



Collaboration diagram for ModelSIRCONN< TSeq >:



Public Member Functions

- ModelSIRCONN (ModelSIRCONN< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate)

    Template for a Susceptible-Infected-Removed (SIR) model.
- **ModelSIRCONN** (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate)
- ModelSIRCONN< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- ModelSIRCONN< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set the initial states of the model.
- size_t get_n_infected () const

    Get the infected individuals.
- std::vector< double > **generation_time_expected** (int max_days=200, int max_contacts=200) const

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **INFECTED** = 1
- static const int **RECOVERED** = 2

Additional Inherited Members

17.48.1 Constructor & Destructor Documentation

17.48.1.1 ModelSIRCONN()

```
template<typename TSeq >
ModelSIRCONN< TSeq >::ModelSIRCONN (
            ModelSIRCONN< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate )  [inline]
```

Template for a Susceptible-Infected-Removed (SIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery

17.48.2 Member Function Documentation

17.48.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSIRCONN< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.48.2.2 get_n_infected()

```
template<typename TSeq = EPI_DEFAULT_TSEQ>
size_t ModelSIRCONN< TSeq >::get_n_infected ( ) const  [inline]
```

Get the infected individuals.

Returns

std::vector< epiworld::Agent<TSeq> * >

17.48.2.3 initial_states()

```
template<typename TSeq >
ModelSIRCONN< TSeq > & ModelSIRCONN< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.48.2.4 reset()

```
template<typename TSeq >
void ModelSIRCONN< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

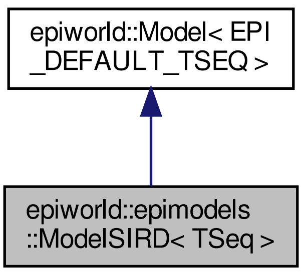
- include/epiworld/models/sirconnected.hpp

17.49 epiworld::epimodels::ModelSIRD< TSeq > Class Template Reference

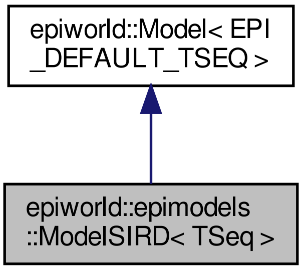
Template for a Susceptible-Infected-Removed-Deceased (SIRD) model.

`#include <epiworld.hpp>`

Inheritance diagram for epiworld::epimodels::ModelSIRD< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSIRD< TSeq >:



Public Member Functions

- ModelSIRD< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set the initial states of the model.

- ModelSIRD (ModelSIRD< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)

    Constructs a new SIRD model with the given parameters.
- **ModelSIRD** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)

Additional Inherited Members

17.49.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelSIRD< TSeq >

Template for a Susceptible-Infected-Removed-Deceased (SIRD) model.

17.49.2 Constructor & Destructor Documentation

17.49.2.1 ModelSIRD()

```
template<typename TSeq >
ModelSIRD< TSeq >::ModelSIRD (
            ModelSIRD< TSeq > & model,
            const std::string & vname,
            epiworld_double prevalence,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            epiworld_double death_rate )  [inline]
```

Constructs a new SIRD model with the given parameters.

Parameters

model	The SIRD model to copy from.
vname	The name of the vertex associated with this model.
prevalence	The initial prevalence of the disease in the population.
transmission_rate	The rate at which the disease spreads from infected to susceptible individuals.
recovery_rate	The rate at which infected individuals recover and become immune.
death_rate	The rate at which infected individuals die.

17.49.3 Member Function Documentation

17.49.3.1 initial_states()

```
template<typename TSeq >
ModelSIRD< TSeq > & ModelSIRD< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set the initial states of the model.

Parameters

proportions↩ _	Double vector with two elements: • The proportion of non-infected individuals who have recovered. • The proportion of non-infected individuals who have died.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

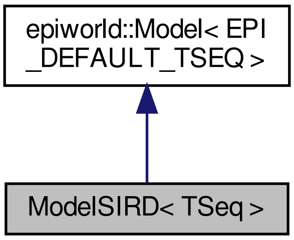
- epiworld.hpp

17.50 ModelSIRD< TSeq > Class Template Reference

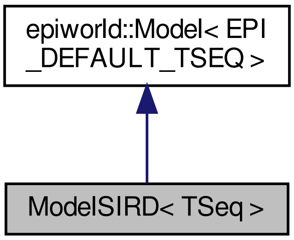
Template for a Susceptible-Infected-Removed-Deceased (SIRD) model.

```
#include <sird.hpp>
```

Inheritance diagram for ModelSIRD< TSeq >:



Collaboration diagram for ModelSIRD< TSeq >:



Public Member Functions

- ModelSIRD< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set the initial states of the model.

- ModelSIRD (ModelSIRD< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)

    Constructs a new SIRD model with the given parameters.
- **ModelSIRD** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)

Additional Inherited Members

17.50.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelSIRD< TSeq >

Template for a Susceptible-Infected-Removed-Deceased (SIRD) model.

17.50.2 Constructor & Destructor Documentation

17.50.2.1 ModelSIRD()

```
template<typename TSeq >
ModelSIRD< TSeq >::ModelSIRD (
            ModelSIRD< TSeq > & model,
            const std::string & vname,
            epiworld_double prevalence,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            epiworld_double death_rate ) [inline]
```

Constructs a new SIRD model with the given parameters.

Parameters

model	The SIRD model to copy from.
vname	The name of the vertex associated with this model.
prevalence	The initial prevalence of the disease in the population.
transmission_rate	The rate at which the disease spreads from infected to susceptible individuals.
recovery_rate	The rate at which infected individuals recover and become immune.
death_rate	The rate at which infected individuals die.

17.50.3 Member Function Documentation

17.50.3.1 initial_states()

```
template<typename TSeq >
ModelSIRD< TSeq > & ModelSIRD< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with two elements: • The proportion of non-infected individuals who have recovered. • The proportion of non-infected individuals who have died.

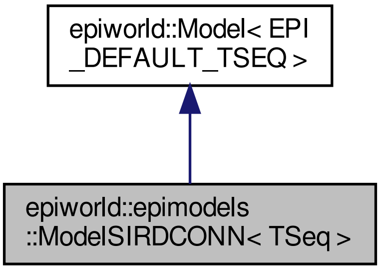
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

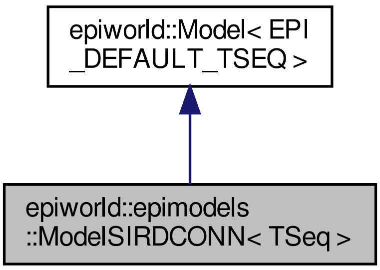
- include/epiworld/models/sird.hpp

17.51 epiworld::epimodels::ModelSIRDCONN< TSeq > Class Template Reference

Inheritance diagram for epiworld::epimodels::ModelSIRDCONN< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSIRDCONN< TSeq >:



Public Member Functions

- ModelSIRDCONN (ModelSIRDCONN< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)

    Template for a Susceptible-Infected-Removed (SIR) model.

- **ModelSIRDCONN** (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld↩_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)
- ModelSIRDCONN< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **INFECTED** = 1
- static const int **RECOVERED** = 2
- static const int **DECEASED** = 3

Additional Inherited Members

17.51.1 Constructor & Destructor Documentation

17.51.1.1 ModelSIRDCONN()

```
template<typename TSeq >
ModelSIRDCONN< TSeq >::ModelSIRDCONN (
            ModelSIRDCONN< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            epiworld_double death_rate )  [inline]
```

Template for a Susceptible-Infected-Removed (SIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery
death_rate	Probability of death

17.51.2 Member Function Documentation

17.51.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSIRDCONN< TSeq >::clone_ptr [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.51.2.2 reset()

```
template<typename TSeq >
void ModelSIRDCONN< TSeq >::reset [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

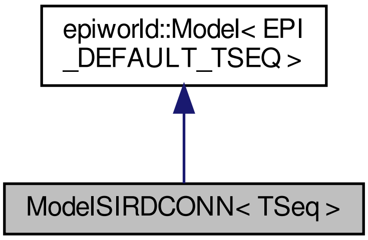
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

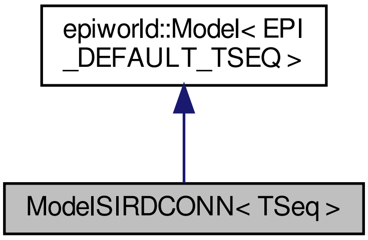
- epiworld.hpp

17.52 ModelSIRDCONN< TSeq > Class Template Reference

Inheritance diagram for ModelSIRDCONN< TSeq >:



Collaboration diagram for ModelSIRDCONN< TSeq >:



Public Member Functions

- ModelSIRDCONN (ModelSIRDCONN< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)

    Template for a Susceptible-Infected-Removed (SIR) model.
- **ModelSIRDCONN** (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)
- ModelSIRDCONN< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **INFECTED** = 1
- static const int **RECOVERED** = 2
- static const int **DECEASED** = 3

Additional Inherited Members

17.52.1 Constructor & Destructor Documentation

17.52.1.1 ModelSIRDCONN()

```
template<typename TSeq >
ModelSIRDCONN< TSeq >::ModelSIRDCONN (
            ModelSIRDCONN< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            epiworld_double death_rate )  [inline]
```

Template for a Susceptible-Infected-Removed (SIR) model.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery
death_rate	Probability of death

17.52.2 Member Function Documentation

17.52.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSIRDCONN< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.52.2.2 reset()

```
template<typename TSeq >
void ModelSIRDCONN< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

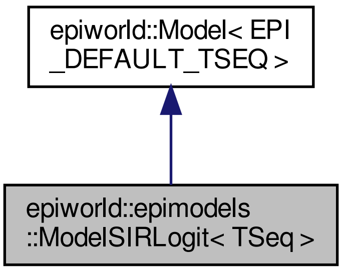
- include/epiworld/models/sirdconnected.hpp

17.53 epiworld::epimodels::ModelSIRLogit< TSeq > Class Template Reference

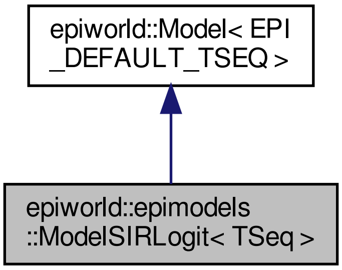
Template for a Susceptible-Infected-Removed (SIR) model.

`#include <epiworld.hpp>`

Inheritance diagram for epiworld::epimodels::ModelSIRLogit< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSIRLogit< TSeq >:



Public Member Functions

- ModelSIRLogit (ModelSIRLogit< TSeq > &model, const std::string &vname, double *data, size_t ncols, std::vector< double > coefs_infect, std::vector< double > coefs_recover, std::vector< size_t > coef_infect_cols, std::vector< size_t > coef_recover_cols, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double prevalence)

    Template for a Susceptible-Infected-Removed (SIR) model.
- **ModelSIRLogit** (const std::string &vname, double *data, size_t ncols, std::vector< double > coefs_infect, std::vector< double > coefs_recover, std::vector< size_t > coef_infect_cols, std::vector< size_t > coef_recover_cols, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double prevalence)
- ModelSIRLogit< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- void reset ()

    Reset the model.

Public Attributes

- std::vector< double > **coefs_infect**
- std::vector< double > **coefs_recover**
- std::vector< size_t > **coef_infect_cols**
- std::vector< size_t > **coef_recover_cols**

Additional Inherited Members

17.53.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelSIRLogit< TSeq >

Template for a Susceptible-Infected-Removed (SIR) model.

In this model, infection and recoveru probabilities are computed using a logit model. Particularly, the probability of infection is computed as:

$$\frac{1}{1 + \exp\left(-\left(\beta_0 E_i + \sum_{i=1}^{n} \beta_i x_i\right)\right)}$$

where β_0 is the exposure coefficient and E_i is the exposure number, β_i are the coefficients for the features x_i of the agents, and n is the number of features. The probability of recovery is computed as:

$$\frac{1}{1 + \exp\left(-\left(\sum_{i=1}^{n} \beta_i x_i\right)\right)}$$

where β_i are the coefficients for the features x_i of the agents, and n is the number of features.

Parameters

TSeq	Type of the sequence (e.g. std::vector, std::deque)

17.53.2 Constructor & Destructor Documentation

17.53.2.1 ModelSIRLogit()

```
template<typename TSeq >
ModelSIRLogit< TSeq >::ModelSIRLogit (
            ModelSIRLogit< TSeq > & model,
            const std::string & vname,
            double * data,
            size_t ncols,
            std::vector< double > coefs_infect,
            std::vector< double > coefs_recover,
            std::vector< size_t > coef_infect_cols,
            std::vector< size_t > coef_recover_cols,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            epiworld_double prevalence )  [inline]
```

Template for a Susceptible-Infected-Removed (SIR) model.

Parameters

vname	Name of the virus.
coefs_infect	Double ptr. Infection coefficients.
coefs_recover	Double ptr. Recovery coefficients.
ncoef_infect	Unsigned int. Number of infection coefficients.
ncoef_recover	Unsigned int. Number of recovery coefficients.
coef_infect_cols	Vector<unsigned int>. Ids of infection vars.
coef_recover_cols	Vector<unsigned int>. Ids of recover vars.

Parameters

model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
prob_transmission	Probability of transmission
prob_recovery	Probability of recovery

17.53.3 Member Function Documentation

17.53.3.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSIRLogit< TSeq >::clone_ptr [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.53.3.2 reset()

```
template<typename TSeq >
void ModelSIRLogit< TSeq >::reset [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

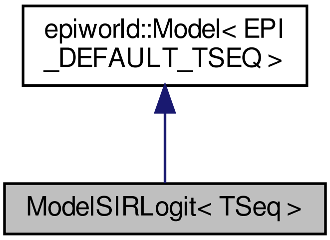
- epiworld.hpp

17.54 ModelSIRLogit< TSeq > Class Template Reference

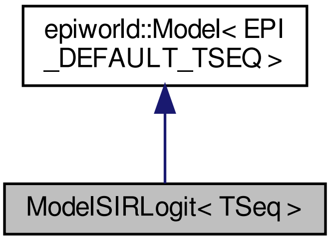
Template for a Susceptible-Infected-Removed (SIR) model.

```
#include <sirlogit.hpp>
```

Inheritance diagram for ModelSIRLogit< TSeq >:



Collaboration diagram for ModelSIRLogit< TSeq >:



Public Member Functions

- ModelSIRLogit (ModelSIRLogit< TSeq > &model, const std::string &vname, double ∗data, size_t ncols, std::vector< double > coefs_infect, std::vector< double > coefs_recover, std::vector< size_t > coef_infect_cols, std::vector< size_t > coef_recover_cols, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double prevalence)

    Template for a Susceptible-Infected-Removed (SIR) model.
- **ModelSIRLogit** (const std::string &vname, double ∗data, size_t ncols, std::vector< double > coefs_infect, std::vector< double > coefs_recover, std::vector< size_t > coef_infect_cols, std::vector< size_t > coef_recover_cols, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double prevalence)
- ModelSIRLogit< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- Model< TSeq > ∗ clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- void reset ()

    Reset the model.

Public Attributes

- std::vector< double > **coefs_infect**
- std::vector< double > **coefs_recover**
- std::vector< size_t > **coef_infect_cols**
- std::vector< size_t > **coef_recover_cols**

Additional Inherited Members

17.54.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelSIRLogit< TSeq >

Template for a Susceptible-Infected-Removed (SIR) model.

In this model, infection and recoveru probabilities are computed using a logit model. Particularly, the probability of infection is computed as:

$$\frac{1}{1 + \exp\left(-\left(\beta_0 E_i + \sum_{i=1}^{n} \beta_i x_i\right)\right)}$$

where β_0 is the exposure coefficient and E_i is the exposure number, β_i are the coefficients for the features x_i of the agents, and n is the number of features. The probability of recovery is computed as:

$$\frac{1}{1 + \exp\left(-\left(\sum_{i=1}^{n} \beta_i x_i\right)\right)}$$

where β_i are the coefficients for the features x_i of the agents, and n is the number of features.

Parameters

TSeq	Type of the sequence (e.g. std::vector, std::deque)

17.54.2 Constructor & Destructor Documentation

17.54.2.1 ModelSIRLogit()

```
template<typename TSeq >
ModelSIRLogit< TSeq >::ModelSIRLogit (
            ModelSIRLogit< TSeq > & model,
            const std::string & vname,
            double * data,
            size_t ncols,
```

```
std::vector< double > coefs_infect,
std::vector< double > coefs_recover,
std::vector< size_t > coef_infect_cols,
std::vector< size_t > coef_recover_cols,
epiworld_double transmission_rate,
epiworld_double recovery_rate,
epiworld_double prevalence )  [inline]
```

Template for a Susceptible-Infected-Removed (SIR) model.

Parameters

vname	Name of the virus.
coefs_infect	Double ptr. Infection coefficients.
coefs_recover	Double ptr. Recovery coefficients.
ncoef_infect	Unsigned int. Number of infection coefficients.
ncoef_recover	Unsigned int. Number of recovery coefficients.
coef_infect_cols	Vector<unsigned int>. Ids of infection vars.
coef_recover_cols	Vector<unsigned int>. Ids of recover vars.
model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
prob_transmission	Probability of transmission
prob_recovery	Probability of recovery

17.54.3 Member Function Documentation

17.54.3.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSIRLogit< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.54.3.2 reset()

```
template<typename TSeq >
void ModelSIRLogit< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

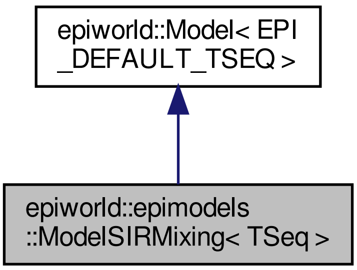
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

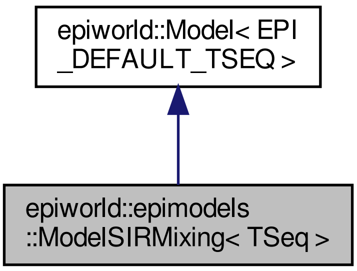
- include/epiworld/models/sirlogit.hpp

17.55 epiworld::epimodels::ModelSIRMixing< TSeq > Class Template Reference

Inheritance diagram for epiworld::epimodels::ModelSIRMixing< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSIRMixing< TSeq >:



Public Member Functions

- ModelSIRMixing (ModelSIRMixing< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate, std::vector< double > contact_matrix)

    Constructs a ModelSIRMixing object.
- ModelSIRMixing (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate, std::vector< double > contact_matrix)

    Constructs a ModelSIRMixing object.
- ModelSIRMixing< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.
- ModelSIRMixing< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue_={})

    Set the initial states of the model.
- size_t **get_n_infected** (size_t group) const
- void **set_contact_matrix** (std::vector< double > cmat)

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **INFECTED** = 1
- static const int **RECOVERED** = 2

Additional Inherited Members

17.55.1 Constructor & Destructor Documentation

17.55.1.1 ModelSIRMixing() [1/2]

```
template<typename TSeq >
ModelSIRMixing< TSeq >::ModelSIRMixing (
            ModelSIRMixing< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix ) [inline]
```

Constructs a ModelSIRMixing object.

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A reference to an existing ModelSIRMixing object.
vname	The name of the ModelSIRMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model.
model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery

17.55.1.2 ModelSIRMixing() [2/2]

```
template<typename TSeq >
ModelSIRMixing< TSeq >::ModelSIRMixing (
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix )  [inline]
```

Constructs a ModelSIRMixing object.

Parameters

vname	The name of the ModelSIRMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model.

17.55.2 Member Function Documentation

17.55.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSIRMixing< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.55.2.2 initial_states()

```
template<typename TSeq >
ModelSIRMixing< TSeq > & ModelSIRMixing< TSeq >::initial_states (
            std::vector< double > proportions_,
            std::vector< int > queue_ = {} )  [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.55.2.3 reset()

```
template<typename TSeq >
void ModelSIRMixing< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

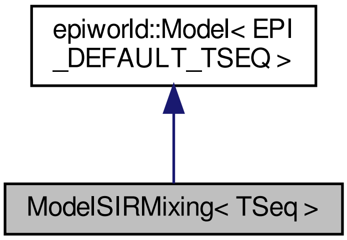
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

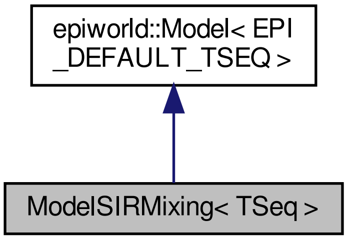
- epiworld.hpp

17.56 ModelSIRMixing< TSeq > Class Template Reference

Inheritance diagram for ModelSIRMixing< TSeq >:



Collaboration diagram for ModelSIRMixing< TSeq >:



Public Member Functions

- ModelSIRMixing (ModelSIRMixing< TSeq > &model, const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate, std::vector< double > contact_matrix)

    Constructs a ModelSIRMixing object.
- ModelSIRMixing (const std::string &vname, epiworld_fast_uint n, epiworld_double prevalence, epiworld_double contact_rate, epiworld_double transmission_rate, epiworld_double recovery_rate, std::vector< double > contact_matrix)

    Constructs a ModelSIRMixing object.
- ModelSIRMixing< TSeq > & run (epiworld_fast_uint ndays, int seed=-1)

    Runs the simulation (after initialization)
- void reset ()

    Reset the model.
- Model< TSeq > * clone_ptr ()

    Advanced usage: Makes a copy of data and returns it as undeleted pointer.

- ModelSIRMixing< TSeq > & initial_states (std::vector< double > proportions_, std::vector< int > queue↩_={})

    Set the initial states of the model.
- size_t **get_n_infected** (size_t group) const
- void **set_contact_matrix** (std::vector< double > cmat)

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **INFECTED** = 1
- static const int **RECOVERED** = 2

Additional Inherited Members

17.56.1 Constructor & Destructor Documentation

17.56.1.1 ModelSIRMixing() [1/2]

```
template<typename TSeq >
ModelSIRMixing< TSeq >::ModelSIRMixing (
            ModelSIRMixing< TSeq > & model,
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix )  [inline]
```

Constructs a ModelSIRMixing object.

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

Parameters

model	A reference to an existing ModelSIRMixing object.
vname	The name of the ModelSIRMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model.
model	A Model<TSeq> object where to set up the SIR.
vname	std::string Name of the virus
prevalence	Initial prevalence (proportion)
contact_rate	Average number of contacts (interactions) per step.
transmission_rate	Probability of transmission
recovery_rate	Probability of recovery

17.56.1.2 ModelSIRMixing() [2/2]

```
template<typename TSeq >
ModelSIRMixing< TSeq >::ModelSIRMixing (
            const std::string & vname,
            epiworld_fast_uint n,
            epiworld_double prevalence,
            epiworld_double contact_rate,
            epiworld_double transmission_rate,
            epiworld_double recovery_rate,
            std::vector< double > contact_matrix )  [inline]
```

Constructs a ModelSIRMixing object.

Parameters

vname	The name of the ModelSIRMixing object.
n	The number of entities in the model.
prevalence	The initial prevalence of the disease in the model.
contact_rate	The contact rate between entities in the model.
transmission_rate	The transmission rate of the disease in the model.
recovery_rate	The recovery rate of the disease in the model.
contact_matrix	The contact matrix between entities in the model.

17.56.2 Member Function Documentation

17.56.2.1 clone_ptr()

```
template<typename TSeq >
Model< TSeq > * ModelSIRMixing< TSeq >::clone_ptr  [inline], [virtual]
```

Advanced usage: Makes a copy of data and returns it as undeleted pointer.

Parameters

copy	

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.56.2.2 initial_states()

```
template<typename TSeq >
ModelSIRMixing< TSeq > & ModelSIRMixing< TSeq >::initial_states (
```

```
std::vector< double > proportions_,
std::vector< int > queue_ = {} ) [inline], [virtual]
```

Set the initial states of the model.

Parameters

*proportions_*	Double vector with a single element: • The proportion of non-infected individuals who have recovered.

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

17.56.2.3 reset()

```
template<typename TSeq >
void ModelSIRMixing< TSeq >::reset [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

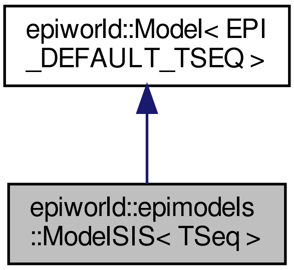
- include/epiworld/models/sirmixing.hpp

17.57 epiworld::epimodels::ModelSIS< TSeq > Class Template Reference

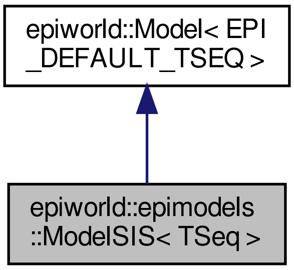
Template for a Susceptible-Infected-Susceptible (SIS) model.

```
#include <epiworld.hpp>
```

Inheritance diagram for epiworld::epimodels::ModelSIS< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSIS< TSeq >:



Public Member Functions

- **ModelSIS** (ModelSIS< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate)
- **ModelSIS** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate)

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **INFECTED** = 1

Additional Inherited Members

17.57.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelSIS< TSeq >

Template for a Susceptible-Infected-Susceptible (SIS) model.

Parameters

vname	std::string Name of the virus
initial_prevalence	epiworld_double Initial prevalence
initial_efficacy	epiworld_double Initial susceptibility_reduction of the immune system
initial_recovery	epiworld_double Initial recovery_rate rate of the immune system

The documentation for this class was generated from the following file:

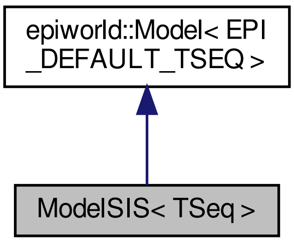
- epiworld.hpp

17.58 ModelSIS< TSeq > Class Template Reference

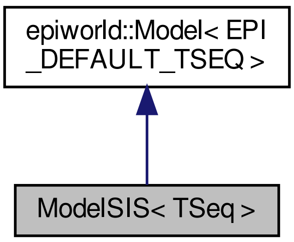
Template for a Susceptible-Infected-Susceptible (SIS) model.

`#include <sis.hpp>`

Inheritance diagram for ModelSIS< TSeq >:



Collaboration diagram for ModelSIS< TSeq >:



Public Member Functions

- **ModelSIS** (ModelSIS< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate)
- **ModelSIS** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate)

Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **INFECTED** = 1

Additional Inherited Members

17.58.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelSIS< TSeq >

Template for a Susceptible-Infected-Susceptible (SIS) model.

Parameters

vname	std::string Name of the virus
initial_prevalence	epiworld_double Initial prevalence
initial_efficacy	epiworld_double Initial susceptibility_reduction of the immune system
initial_recovery	epiworld_double Initial recovery_rate rate of the immune system

The documentation for this class was generated from the following file:

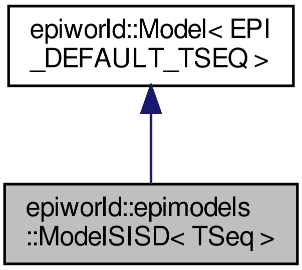
- include/epiworld/models/sis.hpp

17.59 epiworld::epimodels::ModelSISD< TSeq > Class Template Reference

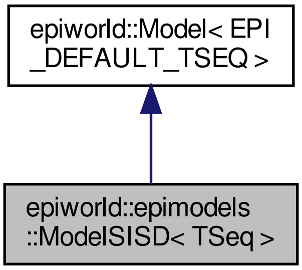
Template for a Susceptible-Infected-Susceptible-Deceased (SISD) model.

```
#include <epiworld.hpp>
```

Inheritance diagram for epiworld::epimodels::ModelSISD< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSISD< TSeq >:



Public Member Functions

- **ModelSISD** (ModelSISD< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)
- **ModelSISD** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)

Additional Inherited Members

17.59.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class epiworld::epimodels::ModelSISD< TSeq >

Template for a Susceptible-Infected-Susceptible-Deceased (SISD) model.

Parameters

vname	std::string Name of the virus
initial_prevalence	epiworld_double Initial prevalence
initial_efficacy	epiworld_double Initial susceptibility_reduction of the immune system
initial_recovery	epiworld_double Initial recovery_rate rate of the immune system
inital_death	epiworld_double Initial death_rate of the immune system

The documentation for this class was generated from the following file:

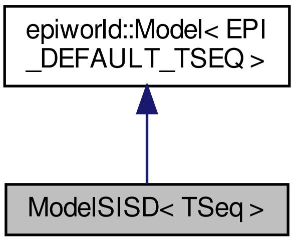
- epiworld.hpp

17.60 ModelSISD< TSeq > Class Template Reference

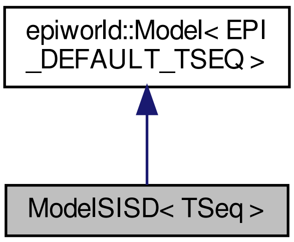
Template for a Susceptible-Infected-Susceptible-Deceased (SISD) model.

```
#include <sisd.hpp>
```

Inheritance diagram for ModelSISD< TSeq >:



Collaboration diagram for ModelSISD< TSeq >:



Public Member Functions

- **ModelSISD** (ModelSISD< TSeq > &model, const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)
- **ModelSISD** (const std::string &vname, epiworld_double prevalence, epiworld_double transmission_rate, epiworld_double recovery_rate, epiworld_double death_rate)

Additional Inherited Members

17.60.1 Detailed Description

template<typename TSeq = EPI_DEFAULT_TSEQ>
class ModelSISD< TSeq >

Template for a Susceptible-Infected-Susceptible-Deceased (SISD) model.

Parameters

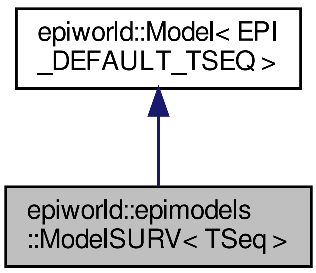
vname	std::string Name of the virus
initial_prevalence	epiworld_double Initial prevalence
initial_efficacy	epiworld_double Initial susceptibility_reduction of the immune system
initial_recovery	epiworld_double Initial recovery_rate rate of the immune system
inital_death	epiworld_double Initial death_rate of the immune system

The documentation for this class was generated from the following file:

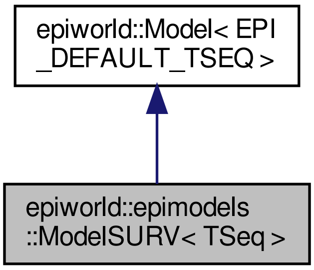
- include/epiworld/models/sisd.hpp

17.61 epiworld::epimodels::ModelSURV< TSeq > Class Template Reference

Inheritance diagram for epiworld::epimodels::ModelSURV< TSeq >:



Collaboration diagram for epiworld::epimodels::ModelSURV< TSeq >:



Public Member Functions

- void reset ()

  Reset the model.

Construct a new ModelSURV object

The ModelSURV class simulates a survaillence model where agents can be isolated, even if asyptomatic.

Parameters

vname	*String. Name of the virus*
prevalence	*Integer. Number of initial cases of the virus.*
efficacy_vax	*Double. Efficacy of the vaccine (1 - P(acquire the disease)).*
latent_period	*Double. Shape parameter of a `Gamma(latent_period, 1)` distribution. This coincides with the expected number of latent days.*
infect_period	*Double. Shape parameter of a `Gamma(infected_period, 1)` distribution. This coincides with the expected number of infectious days.*
prob_symptoms	*Double. Probability of generating symptoms.*
prop_vaccinated	*Double. Probability of vaccination. Coincides with the initial prevalence of vaccinated individuals.*
prop_vax_redux_transm	*Double. Factor by which the vaccine reduces transmissibility.*
prop_vax_redux_infect	*Double. Factor by which the vaccine reduces the chances of becoming infected.*
surveillance_prob	*Double. Probability of testing an agent.*
prob_transmission	*Double. Raw transmission probability.*
prob_death	*Double. Raw probability of death for symptomatic individuals.*
prob_noreinfect	*Double. Probability of no re-infection.*

This model features the following states:

- *Susceptible*
- *Latent*
- *Symptomatic*
- *Symptomatic isolated*

- *Asymptomatic*
- *Asymptomatic isolated*
- *Recovered*
- *Removed*

Returns

An object of class `epiworld_surv`

- **ModelSURV** ()
- **ModelSURV** (ModelSURV< TSeq > &model, const std::string &vname, epiworld_fast_uint prevalence=50, epiworld_double efficacy_vax=0.9, epiworld_double latent_period=3u, epiworld_double infect_period=6u, epiworld_double prob_symptoms=0.6, epiworld_double prop_vaccinated=0.25, epiworld_double prop_vax_redux_transm=0.5, epiworld_double prop_vax_redux_infect=0.5, epiworld_double surveillance_prob=0.001, epiworld_double prob_transmission=1.0, epiworld_double prob_death=0.001, epiworld_double prob_noreinfect=0.9)
- **ModelSURV** (const std::string &vname, epiworld_fast_uint prevalence=50, epiworld_double efficacy_vax=0.9, epiworld_double latent_period=3u, epiworld_double infect_period=6u, epiworld_double prob_symptoms=0.6, epiworld_double prop_vaccinated=0.25, epiworld_double prop_vax_redux_transm=0.5, epiworld_double prop_vax_redux_infect=0.5, epiworld_double surveillance_prob=0.001, epiworld_double prob_transmission=1.0, epiworld_double prob_death=0.001, epiworld_double prob_noreinfect=0.9)

Public Attributes

- std::vector< epiworld_double > days_latent_and_infectious

  Vector of days spent in latent and infectious states A row-major matrix.

Additional Inherited Members

17.61.1 Member Function Documentation

17.61.1.1 reset()

```
template<typename TSeq >
void ModelSURV< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

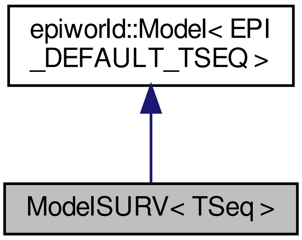
Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

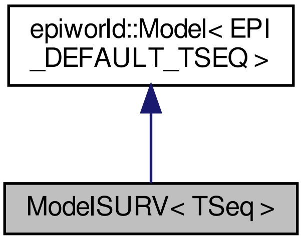
- epiworld.hpp

17.62 ModelSURV< TSeq > Class Template Reference

Inheritance diagram for ModelSURV< TSeq >:



Collaboration diagram for ModelSURV< TSeq >:



Public Member Functions

- void reset ()

  Reset the model.

Construct a new ModelSURV object

The ModelSURV class simulates a survaillence model where agents can be isolated, even if asyptomatic.

Parameters

vname	*String. Name of the virus*
prevalence	*Integer. Number of initial cases of the virus.*
efficacy_vax	*Double. Efficacy of the vaccine (1 - P(acquire the disease)).*
latent_period	*Double. Shape parameter of a* `Gamma(latent_period, 1)` *distribution. This coincides with the expected number of latent days.*

Parameters

infect_period	*Double. Shape parameter of a* `Gamma(infected_period, 1)` *distribution. This coincides with the expected number of infectious days.*
prob_symptoms	*Double. Probability of generating symptoms.*
prop_vaccinated	*Double. Probability of vaccination. Coincides with the initial prevalence of vaccinated individuals.*
prop_vax_redux_transm	*Double. Factor by which the vaccine reduces transmissibility.*
prop_vax_redux_infect	*Double. Factor by which the vaccine reduces the chances of becoming infected.*
surveillance_prob	*Double. Probability of testing an agent.*
prob_transmission	*Double. Raw transmission probability.*
prob_death	*Double. Raw probability of death for symptomatic individuals.*
prob_noreinfect	*Double. Probability of no re-infection.*

This model features the following states:

- *Susceptible*
- *Latent*
- *Symptomatic*
- *Symptomatic isolated*
- *Asymptomatic*
- *Asymptomatic isolated*
- *Recovered*
- *Removed*

Returns

An object of class `epiworld_surv`

- **ModelSURV** ()
- **ModelSURV** (ModelSURV< TSeq > &model, const std::string &vname, epiworld_fast_uint prevalence=50, epiworld_double efficacy_vax=0.9, epiworld_double latent_period=3u, epiworld_double infect_period=6u, epiworld_double prob_symptoms=0.6, epiworld_double prop_vaccinated=0.25, epiworld_double prop_vax_redux_transm=0.5, epiworld_double prop_vax_redux_infect=0.5, epiworld_double surveillance_prob=0.001, epiworld_double prob_transmission=1.0, epiworld_double prob_death=0.001, epiworld_double prob_noreinfect=0.9)
- **ModelSURV** (const std::string &vname, epiworld_fast_uint prevalence=50, epiworld_double efficacy_vax=0.9, epiworld_double latent_period=3u, epiworld_double infect_period=6u, epiworld_double prob_symptoms=0.6, epiworld_double prop_vaccinated=0.25, epiworld_double prop_vax_redux_transm=0.5, epiworld_double prop_vax_redux_infect=0.5, epiworld_double surveillance_prob=0.001, epiworld_double prob_transmission=1.0, epiworld_double prob_death=0.001, epiworld_double prob_noreinfect=0.9)

Public Attributes

- std::vector< epiworld_double > days_latent_and_infectious

  Vector of days spent in latent and infectious states A row-major matrix.

Additional Inherited Members

17.62.1 Member Function Documentation

17.62.1.1 reset()

```
template<typename TSeq >
void ModelSURV< TSeq >::reset  [inline], [virtual]
```

Reset the model.

Resetting the model will:

- clear the database
- restore the population (if `set_backup()` was called before)
- re-distribute tools
- re-distribute viruses
- set the date to 0

Reimplemented from epiworld::Model< EPI_DEFAULT_TSEQ >.

The documentation for this class was generated from the following file:

- include/epiworld/models/surveillance.hpp

17.63 Network< Nettype, Nodetype, Edgetype > Class Template Reference

Public Member Functions

- **NType** ()
- Edgetype **operator()** (int i, int j)
- bool **is_directed** () const
- size_t **vcount** () const
- size_t **ecount** () const
- void **add_edge** (int i, int j)
- void **rm_edge** (int i, int j)

The documentation for this class was generated from the following file:

- include/epiworld/network-bones.hpp

17.64 epiworld::PersonTools< TSeq > Class Template Reference

The documentation for this class was generated from the following file:

- epiworld.hpp

17.65 PersonTools< TSeq > Class Template Reference

The documentation for this class was generated from the following file:

- include/epiworld/config.hpp

17.66 epiworld::Progress Class Reference

A simple progress bar.

`#include <epiworld.hpp>`

Public Member Functions

- **Progress** (int n_, int width_)
- void **start** ()
- void **next** ()
- void **end** ()

17.66.1 Detailed Description

A simple progress bar.

The documentation for this class was generated from the following file:

- epiworld.hpp

17.67 Progress Class Reference

A simple progress bar.

`#include <progress.hpp>`

Public Member Functions

- **Progress** (int n_, int width_)
- void **start** ()
- void **next** ()
- void **end** ()

17.67.1 Detailed Description

A simple progress bar.

The documentation for this class was generated from the following file:

- include/epiworld/progress.hpp

17.68 epiworld::Queue< TSeq > Class Template Reference

Controls which agents are verified at each step.

`#include <epiworld.hpp>`

Public Member Functions

- void **operator+=** (Agent< TSeq > *p)
- void **operator-=** (Agent< TSeq > *p)
- epiworld_fast_int & **operator[ ]** (epiworld_fast_uint i)
- void **reset** ()
- bool **operator==** (const Queue< TSeq > &other) const
- bool **operator!=** (const Queue< TSeq > &other) const

Static Public Attributes

- static const int **NoOne** = 0
- static const int **OnlySelf** = 1
- static const int **Everyone** = 2

Friends

- class **Model**< **TSeq** >

17.68.1 Detailed Description

template<typename TSeq>
class epiworld::Queue< TSeq >

Controls which agents are verified at each step.

The idea is that only agents who are either in an infected state or have an infected neighbor should be checked. Otherwise it makes no sense (no chance to recover or capture the disease).

Template Parameters

TSeq	

The documentation for this class was generated from the following file:

- epiworld.hpp

17.69 Queue< TSeq > Class Template Reference

Controls which agents are verified at each step.

`#include <queue-bones.hpp>`

Public Member Functions

- void **operator+=** (Agent< TSeq > *p)
- void **operator-=** (Agent< TSeq > *p)
- epiworld_fast_int & **operator[ ]** (epiworld_fast_uint i)
- void **reset** ()
- bool **operator==** (const Queue< TSeq > &other) const
- bool **operator!=** (const Queue< TSeq > &other) const

Static Public Attributes

- static const int **NoOne** = 0
- static const int **OnlySelf** = 1
- static const int **Everyone** = 2

Friends

- class **Model**< **TSeq** >

17.69.1 Detailed Description

template<typename TSeq>
class Queue< TSeq >

Controls which agents are verified at each step.

The idea is that only agents who are either in an infected state or have an infected neighbor should be checked. Otherwise it makes no sense (no chance to recover or capture the disease).

Template Parameters

TSeq	

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/queue-bones.hpp

17.70 RandGraph Class Reference

Public Member Functions

- **RandGraph** (int N_)
- void **init** (int s)
- void **set_rand_engine** (std::shared_ptr< std::mt19937 > &e)
- epiworld_double **runif** ()

The documentation for this class was generated from the following file:

- include/epiworld/random_graph.hpp

17.71 epiworld::SAMPLETYPE Class Reference

Static Public Attributes

- static const int **MODEL** = 0
- static const int **ENTITY** = 1
- static const int **AGENT** = 2

The documentation for this class was generated from the following file:

- epiworld.hpp

17.72 SAMPLETYPE Class Reference

Static Public Attributes

- static const int **MODEL** = 0
- static const int **ENTITY** = 1
- static const int **AGENT** = 2

The documentation for this class was generated from the following file:

- include/epiworld/agentssample-bones.hpp

17.73 epiworld::Tool< TSeq > Class Template Reference

Tools for defending the agent against the virus.

```
#include <epiworld.hpp>
```

Public Member Functions

- **Tool** (std::string name="unknown tool")
- **Tool** (std::string name, epiworld_double prevalence, bool as_proportion)
- void **set_sequence** (TSeq d)
- void **set_sequence** (std::shared_ptr< TSeq > d)
- **EPI_TYPENAME_TRAITS** (TSeq, int) get_sequence()
- void **set_name** (std::string name)
- std::string **get_name** () const
- Agent< TSeq > * **get_agent** ()
- int **get_id** () const
- void **set_id** (int id)
- void **set_date** (int d)
- int **get_date** () const
- void **set_state** (epiworld_fast_int init, epiworld_fast_int post)
- void **set_queue** (epiworld_fast_int init, epiworld_fast_int post)
- void **get_state** (epiworld_fast_int *init, epiworld_fast_int *post)
- void **get_queue** (epiworld_fast_int *init, epiworld_fast_int *post)
- bool **operator==** (const Tool< TSeq > &other) const
- bool **operator!=** (const Tool< TSeq > &other) const
- void **print** () const
- void **distribute** (Model< TSeq > *model)
- void **set_distribution** (ToolToAgentFun< TSeq > fun)

Get and set the tool functions

Parameters

v	*The virus over which to operate*
fun	*the function to be used*

Returns

epiworld_double

- epiworld_double **get_susceptibility_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_transmission_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_recovery_enhancer** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_death_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- void **set_susceptibility_reduction_fun** (ToolFun< TSeq > fun)
- void **set_transmission_reduction_fun** (ToolFun< TSeq > fun)
- void **set_recovery_enhancer_fun** (ToolFun< TSeq > fun)
- void **set_death_reduction_fun** (ToolFun< TSeq > fun)
- void **set_susceptibility_reduction** (epiworld_double *prob)
- void **set_transmission_reduction** (epiworld_double *prob)
- void **set_recovery_enhancer** (epiworld_double *prob)
- void **set_death_reduction** (epiworld_double *prob)
- void **set_susceptibility_reduction** (epiworld_double prob)
- void **set_transmission_reduction** (epiworld_double prob)
- void **set_recovery_enhancer** (epiworld_double prob)
- void **set_death_reduction** (epiworld_double prob)

Friends

- class **Agent**< **TSeq** >
- class **Model**< **TSeq** >
- void **default_add_tool** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_tool** (Event< TSeq > &a, Model< TSeq > *m)

17.73.1 Detailed Description

template<typename TSeq>
class epiworld::Tool< TSeq >

Tools for defending the agent against the virus.

Template Parameters

TSeq	Type of sequence

The documentation for this class was generated from the following file:

- epiworld.hpp

17.74 Tool< TSeq > Class Template Reference

Tools for defending the agent against the virus.

```
#include <tool-bones.hpp>
```

Public Member Functions

- **Tool** (std::string name="unknown tool")
- **Tool** (std::string name, epiworld_double prevalence, bool as_proportion)
- void **set_sequence** (TSeq d)
- void **set_sequence** (std::shared_ptr< TSeq > d)
- **EPI_TYPENAME_TRAITS** (TSeq, int) get_sequence()
- void **set_name** (std::string name)
- std::string **get_name** () const
- Agent< TSeq > * **get_agent** ()
- int **get_id** () const
- void **set_id** (int id)
- void **set_date** (int d)
- int **get_date** () const
- void **set_state** (epiworld_fast_int init, epiworld_fast_int post)
- void **set_queue** (epiworld_fast_int init, epiworld_fast_int post)
- void **get_state** (epiworld_fast_int *init, epiworld_fast_int *post)
- void **get_queue** (epiworld_fast_int *init, epiworld_fast_int *post)
- bool **operator==** (const Tool< TSeq > &other) const
- bool **operator!=** (const Tool< TSeq > &other) const
- void **print** () const
- void **distribute** (Model< TSeq > *model)
- void **set_distribution** (ToolToAgentFun< TSeq > fun)
- void **set_sequence** (int d)
- bool **operator==** (const Tool< std::vector< int >> &other) const
- void **set_sequence** (int d)
- bool **operator==** (const Tool< std::vector< int >> &other) const

Get and set the tool functions

Parameters

v	*The virus over which to operate*
fun	*the function to be used*

Returns

epiworld_double

- epiworld_double **get_susceptibility_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_transmission_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_recovery_enhancer** (VirusPtr< TSeq > v, Model< TSeq > *model)
- epiworld_double **get_death_reduction** (VirusPtr< TSeq > v, Model< TSeq > *model)
- void **set_susceptibility_reduction_fun** (ToolFun< TSeq > fun)
- void **set_transmission_reduction_fun** (ToolFun< TSeq > fun)
- void **set_recovery_enhancer_fun** (ToolFun< TSeq > fun)
- void **set_death_reduction_fun** (ToolFun< TSeq > fun)
- void **set_susceptibility_reduction** (epiworld_double *prob)
- void **set_transmission_reduction** (epiworld_double *prob)
- void **set_recovery_enhancer** (epiworld_double *prob)
- void **set_death_reduction** (epiworld_double *prob)
- void **set_susceptibility_reduction** (epiworld_double prob)
- void **set_transmission_reduction** (epiworld_double prob)
- void **set_recovery_enhancer** (epiworld_double prob)
- void **set_death_reduction** (epiworld_double prob)

Friends

- class **Agent**< **TSeq** >
- class **Model**< **TSeq** >
- void **default_add_tool** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_tool** (Event< TSeq > &a, Model< TSeq > *m)

17.74.1 Detailed Description

template<typename TSeq>
class Tool< TSeq >

Tools for defending the agent against the virus.

Template Parameters

TSeq	Type of sequence

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/tool-bones.hpp
- include/epiworld/tool-meat.hpp

17.75 epiworld::ToolFunctions< TSeq > Class Template Reference

Helper class to store the functions avoiding multiple shared_pointers (we have only one for the four of these)

```
#include <epiworld.hpp>
```

Public Attributes

- ToolFun< TSeq > **susceptibility_reduction** = nullptr
- ToolFun< TSeq > **transmission_reduction** = nullptr
- ToolFun< TSeq > **recovery_enhancer** = nullptr
- ToolFun< TSeq > **death_reduction** = nullptr
- ToolToAgentFun< TSeq > **dist** = nullptr

17.75.1 Detailed Description

template<typename TSeq>
class epiworld::ToolFunctions< TSeq >

Helper class to store the functions avoiding multiple shared_pointers (we have only one for the four of these)

The documentation for this class was generated from the following file:

- epiworld.hpp

17.76 ToolFunctions< TSeq > Class Template Reference

Helper class to store the functions avoiding multiple shared_pointers (we have only one for the four of these)

`#include <tool-bones.hpp>`

Public Attributes

- ToolFun< TSeq > **susceptibility_reduction** = nullptr
- ToolFun< TSeq > **transmission_reduction** = nullptr
- ToolFun< TSeq > **recovery_enhancer** = nullptr
- ToolFun< TSeq > **death_reduction** = nullptr
- ToolToAgentFun< TSeq > **dist** = nullptr

17.76.1 Detailed Description

template<typename TSeq>
class ToolFunctions< TSeq >

Helper class to store the functions avoiding multiple shared_pointers (we have only one for the four of these)

The documentation for this class was generated from the following file:

- include/epiworld/tool-bones.hpp

17.77 epiworld::Tools< TSeq > Class Template Reference

Set of tools (useful for building iterators)

`#include <epiworld.hpp>`

Public Member Functions

- **Tools** (Agent< TSeq > &p)
- std::vector< ToolPtr< TSeq > >::iterator **begin** ()
- std::vector< ToolPtr< TSeq > >::iterator **end** ()
- ToolPtr< TSeq > & **operator()** (size_t i)
- ToolPtr< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- void **print** () const noexcept

Friends

- class **Tool< TSeq >**
- class **Agent< TSeq >**

17.77.1 Detailed Description

template<typename TSeq>
class epiworld::Tools< TSeq >

Set of tools (useful for building iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following file:

- epiworld.hpp

17.78 Tools< TSeq > Class Template Reference

Set of tools (useful for building iterators)

```
#include <tools-bones.hpp>
```

Public Member Functions

- **Tools** (Agent< TSeq > &p)
- std::vector< ToolPtr< TSeq > >::iterator **begin** ()
- std::vector< ToolPtr< TSeq > >::iterator **end** ()
- ToolPtr< TSeq > & **operator()** (size_t i)
- ToolPtr< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- void **print** () const noexcept

Friends

- class **Tool**< **TSeq** >
- class **Agent**< **TSeq** >

17.78.1 Detailed Description

template< typename TSeq >
class Tools< TSeq >

Set of tools (useful for building iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/tools-bones.hpp

17.79 epiworld::Tools_const< TSeq > Class Template Reference

Set of Tools (const) (useful for iterators)

```
#include <epiworld.hpp>
```

Public Member Functions

- **Tools_const** (const Agent< TSeq > &p)
- std::vector< ToolPtr< TSeq > >::const_iterator **begin** () const
- std::vector< ToolPtr< TSeq > >::const_iterator **end** () const
- const ToolPtr< TSeq > & **operator()** (size_t i)
- const ToolPtr< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- void **print** () const noexcept

Friends

- class **Tool**< **TSeq** >
- class **Agent**< **TSeq** >

17.79.1 Detailed Description

template<typename TSeq>
class epiworld::Tools_const< TSeq >

Set of Tools (const) (useful for iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following file:

- epiworld.hpp

17.80 Tools_const< TSeq > Class Template Reference

Set of Tools (const) (useful for iterators)

```
#include <tools-bones.hpp>
```

Public Member Functions

- **Tools_const** (const Agent< TSeq > &p)
- std::vector< ToolPtr< TSeq > >::const_iterator **begin** () const
- std::vector< ToolPtr< TSeq > >::const_iterator **end** () const
- const ToolPtr< TSeq > & **operator()** (size_t i)
- const ToolPtr< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- void **print** () const noexcept

Friends

- class **Tool**< **TSeq** >
- class **Agent**< **TSeq** >

17.80.1 Detailed Description

template<typename TSeq>
class Tools_const< TSeq >

Set of Tools (const) (useful for iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/tools-bones.hpp

17.81 epiworld::UserData< TSeq > Class Template Reference

Personalized data by the user.

```
#include <epiworld.hpp>
```

Public Member Functions

- **UserData** (Model< TSeq > &m)
- **UserData** (Model< TSeq > *m)
- UserData (std::vector< std::string > names)

  Construct a new User Data object.
- std::vector< std::string > & **get_names** ()
- std::vector< int > & **get_dates** ()
- std::vector< epiworld_double > & **get_data** ()

- void **get_all** (std::vector< std::string > *names=nullptr, std::vector< int > *date=nullptr, std::vector< epiworld_double > *data=nullptr)
- epiworld_fast_uint **nrow** () const
- epiworld_fast_uint **ncol** () const
- void **write** (std::string fn)
- void **print** () const

Append data

Parameters

x	*A vector of length `ncol()` (if vector), otherwise a `epiworld_double`.*
j	*Index of the data point, from 0 to `ncol() - 1`.*

- void **add** (std::vector< epiworld_double > x)
- void **add** (epiworld_fast_uint j, epiworld_double x)

Access data

Parameters

i	*Row (0 through ndays - 1.)*
j	*Column (0 through `ncols()`).*

Returns

epiworld_double&

- epiworld_double & **operator()** (epiworld_fast_uint i, epiworld_fast_uint j)
- epiworld_double & **operator()** (epiworld_fast_uint i, std::string name)

Friends

- class **Model**< **TSeq** >
- class **DataBase**< **TSeq** >

17.81.1 Detailed Description

template<typename TSeq>
class epiworld::UserData< TSeq >

Personalized data by the user.

Template Parameters

TSeq	

17.81.2 Constructor & Destructor Documentation

17.81.2.1 UserData()

```
template<typename TSeq >
UserData< TSeq >::UserData (
            std::vector< std::string > names )  [inline]
```

Construct a new User Data object.

Parameters

names	A vector of names. The length of the vector sets the number of columns to record.

The documentation for this class was generated from the following file:

- epiworld.hpp

17.82 UserData< TSeq > Class Template Reference

Personalized data by the user.

```
#include <userdata-bones.hpp>
```

Public Member Functions

- **UserData** (Model< TSeq > &m)
- **UserData** (Model< TSeq > *m)
- UserData (std::vector< std::string > names)

    Construct a new User Data object.
- std::vector< std::string > & **get_names** ()
- std::vector< int > & **get_dates** ()
- std::vector< epiworld_double > & **get_data** ()
- void **get_all** (std::vector< std::string > *names=nullptr, std::vector< int > *date=nullptr, std::vector< epiworld_double > *data=nullptr)
- epiworld_fast_uint **nrow** () const
- epiworld_fast_uint **ncol** () const
- void **write** (std::string fn)
- void **print** () const

Append data

Parameters

x	*A vector of length `ncol()` (if vector), otherwise a `epiworld_double`.*
j	*Index of the data point, from 0 to `ncol() - 1`.*

- void **add** (std::vector< epiworld_double > x)
- void **add** (epiworld_fast_uint j, epiworld_double x)

Access data

Parameters

i	*Row (0 through ndays - 1.)*
j	*Column (0 through `ncols()`).*

Returns

epiworld_double&

- epiworld_double & **operator()** (epiworld_fast_uint i, epiworld_fast_uint j)
- epiworld_double & **operator()** (epiworld_fast_uint i, std::string name)

Friends

- class **Model**< **TSeq** >
- class **DataBase**< **TSeq** >

17.82.1 Detailed Description

template<typename TSeq>
class UserData< TSeq >

Personalized data by the user.

Template Parameters

TSeq	

17.82.2 Constructor & Destructor Documentation

17.82.2.1 UserData()

```
template<typename TSeq >
UserData< TSeq >::UserData (
            std::vector< std::string > names )  [inline]
```

Construct a new User Data object.

Parameters

names	A vector of names. The length of the vector sets the number of columns to record.

The documentation for this class was generated from the following files:

- include/epiworld/database-bones.hpp
- include/epiworld/userdata-bones.hpp
- include/epiworld/userdata-meat.hpp

17.83 epiworld::vecHasher< T > Struct Template Reference

Vector hasher.

`#include <epiworld.hpp>`

Public Member Functions

- std::size_t **operator()** (std::vector< T > const &dat) const noexcept

17.83.1 Detailed Description

template<typename T>
struct epiworld::vecHasher< T >

Vector hasher.

Template Parameters

T	

The documentation for this struct was generated from the following file:

- epiworld.hpp

17.84 vecHasher< T > Struct Template Reference

Vector hasher.

`#include <misc.hpp>`

Public Member Functions

- std::size_t **operator()** (std::vector< T > const &dat) const noexcept

17.84.1 Detailed Description

template<typename T>
struct vecHasher< T >

Vector hasher.

Template Parameters

T	

The documentation for this struct was generated from the following file:

- include/epiworld/misc.hpp

17.85 epiworld::Virus< TSeq > Class Template Reference

Virus.

```
#include <epiworld.hpp>
```

Public Member Functions

- **Virus** (std::string name="unknown virus")
- **Virus** (std::string name, epiworld_double prevalence, bool as_proportion)
- void **mutate** (Model< TSeq > *model)
- void **set_mutation** (MutFun< TSeq > fun)
- **EPI_TYPENAME_TRAITS** (TSeq, int) get_sequence()
- void **set_sequence** (TSeq sequence)
- Agent< TSeq > * **get_agent** ()
- void **set_agent** (Agent< TSeq > *p)
- void **set_date** (int d)
- int **get_date** () const
- void **set_id** (int idx)
- int **get_id** () const
- void **set_name** (std::string name)
- std::string **get_name** () const
- bool **operator==** (const Virus< TSeq > &other) const
- bool **operator!=** (const Virus< TSeq > &other) const
- void **print** () const

Get and set the tool functions

Parameters

v	*The virus over which to operate*
fun	*the function to be used*

Returns

epiworld_double

- epiworld_double **get_prob_infecting** (Model< TSeq > *model)
- epiworld_double **get_prob_recovery** (Model< TSeq > *model)
- epiworld_double **get_prob_death** (Model< TSeq > *model)
- epiworld_double **get_incubation** (Model< TSeq > *model)
- void **post_recovery** (Model< TSeq > *model)

- void **set_post_recovery** (PostRecoveryFun< TSeq > fun)
- void **set_post_immunity** (epiworld_double prob)
- void **set_post_immunity** (epiworld_double *prob)
- void **set_prob_infecting_fun** (VirusFun< TSeq > fun)
- void **set_prob_recovery_fun** (VirusFun< TSeq > fun)
- void **set_prob_death_fun** (VirusFun< TSeq > fun)
- void **set_incubation_fun** (VirusFun< TSeq > fun)
- void **set_prob_infecting** (const epiworld_double *prob)
- void **set_prob_recovery** (const epiworld_double *prob)
- void **set_prob_death** (const epiworld_double *prob)
- void **set_incubation** (const epiworld_double *prob)
- void **set_prob_infecting** (epiworld_double prob)
- void **set_prob_recovery** (epiworld_double prob)
- void **set_prob_death** (epiworld_double prob)
- void **set_incubation** (epiworld_double prob)

Get and set the state and queue

After applied, viruses can change the state and affect the queue of agents. These function sets the default values, which are retrieved when adding or removing a virus does not specify a change in state or in queue.

Parameters

init	*After the virus/tool is added to the agent.*
end	*After the virus/tool is removed.*
removed	*After the agent (Agent) is removed.*

- void **set_state** (epiworld_fast_int init, epiworld_fast_int end, epiworld_fast_int removed=-99)
- void **set_queue** (epiworld_fast_int init, epiworld_fast_int end, epiworld_fast_int removed=-99)
- void **get_state** (epiworld_fast_int *init, epiworld_fast_int *end, epiworld_fast_int *removed=nullptr)
- void **get_queue** (epiworld_fast_int *init, epiworld_fast_int *end, epiworld_fast_int *removed=nullptr)

- void distribute (Model< TSeq > *model)

  Get information about the prevalence of the virus.
- void **set_distribution** (VirusToAgentFun< TSeq > fun)

Friends

- class **Agent< TSeq >**
- class **Model< TSeq >**
- class **DataBase< TSeq >**
- void **default_add_virus** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_virus** (Event< TSeq > &a, Model< TSeq > *m)

17.85.1 Detailed Description

template<typename TSeq>
class epiworld::Virus< TSeq >

Virus.

Template Parameters

TSeq	

Raw transmisibility of a virus should be a function of its genetic sequence. Nonetheless, transmisibility can be reduced as a result of having one or more tools to fight the virus. Because of this, transmisibility should be a function of the agent.

The documentation for this class was generated from the following file:

- epiworld.hpp

17.86 Virus< TSeq > Class Template Reference

Virus.

```
#include <virus-bones.hpp>
```

Public Member Functions

- **Virus** (std::string name="unknown virus")
- **Virus** (std::string name, epiworld_double prevalence, bool as_proportion)
- void **mutate** (Model< TSeq > *model)
- void **set_mutation** (MutFun< TSeq > fun)
- **EPI_TYPENAME_TRAITS** (TSeq, int) get_sequence()
- void **set_sequence** (TSeq sequence)
- Agent< TSeq > * **get_agent** ()
- void **set_agent** (Agent< TSeq > *p)
- void **set_date** (int d)
- int **get_date** () const
- void **set_id** (int idx)
- int **get_id** () const
- void **set_name** (std::string name)
- std::string **get_name** () const
- bool **operator==** (const Virus< TSeq > &other) const
- bool **operator!=** (const Virus< TSeq > &other) const
- void **print** () const
- void **set_sequence** (int sequence)
- bool **operator==** (const Virus< std::vector< int >> &other) const
- void **set_sequence** (int sequence)
- bool **operator==** (const Virus< std::vector< int >> &other) const

Get and set the tool functions

Parameters

v	*The virus over which to operate*
fun	*the function to be used*

Returns

epiworld_double

- epiworld_double **get_prob_infecting** (Model< TSeq > *model)
- epiworld_double **get_prob_recovery** (Model< TSeq > *model)
- epiworld_double **get_prob_death** (Model< TSeq > *model)
- epiworld_double **get_incubation** (Model< TSeq > *model)
- void **post_recovery** (Model< TSeq > *model)
- void **set_post_recovery** (PostRecoveryFun< TSeq > fun)
- void **set_post_immunity** (epiworld_double prob)
- void **set_post_immunity** (epiworld_double *prob)
- void **set_prob_infecting_fun** (VirusFun< TSeq > fun)
- void **set_prob_recovery_fun** (VirusFun< TSeq > fun)
- void **set_prob_death_fun** (VirusFun< TSeq > fun)
- void **set_incubation_fun** (VirusFun< TSeq > fun)
- void **set_prob_infecting** (const epiworld_double *prob)
- void **set_prob_recovery** (const epiworld_double *prob)
- void **set_prob_death** (const epiworld_double *prob)
- void **set_incubation** (const epiworld_double *prob)
- void **set_prob_infecting** (epiworld_double prob)
- void **set_prob_recovery** (epiworld_double prob)
- void **set_prob_death** (epiworld_double prob)
- void **set_incubation** (epiworld_double prob)

Get and set the state and queue

After applied, viruses can change the state and affect the queue of agents. These function sets the default values, which are retrieved when adding or removing a virus does not specify a change in state or in queue.

Parameters

init	*After the virus/tool is added to the agent.*
end	*After the virus/tool is removed.*
removed	*After the agent (Agent) is removed.*

- void **set_state** (epiworld_fast_int init, epiworld_fast_int end, epiworld_fast_int removed=-99)
- void **set_queue** (epiworld_fast_int init, epiworld_fast_int end, epiworld_fast_int removed=-99)
- void **get_state** (epiworld_fast_int *init, epiworld_fast_int *end, epiworld_fast_int *removed=nullptr)
- void **get_queue** (epiworld_fast_int *init, epiworld_fast_int *end, epiworld_fast_int *removed=nullptr)

- void distribute (Model< TSeq > *model)

  Get information about the prevalence of the virus.
- void **set_distribution** (VirusToAgentFun< TSeq > fun)

Friends

- class **Agent**< **TSeq** >
- class **Model**< **TSeq** >
- class **DataBase**< **TSeq** >
- void **default_add_virus** (Event< TSeq > &a, Model< TSeq > *m)
- void **default_rm_virus** (Event< TSeq > &a, Model< TSeq > *m)

17.86.1 Detailed Description

template<typename TSeq>
class Virus< TSeq >

Virus.

Template Parameters

TSeq	

Raw transmisibility of a virus should be a function of its genetic sequence. Nonetheless, transmisibility can be reduced as a result of having one or more tools to fight the virus. Because of this, transmisibility should be a function of the agent.

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/virus-bones.hpp
- include/epiworld/virus-meat.hpp

17.87 epiworld::Viruses< TSeq > Class Template Reference

Set of viruses (useful for building iterators)

```
#include <epiworld.hpp>
```

Public Member Functions

- **Viruses** (Agent< TSeq > &p)
- std::vector< VirusPtr< TSeq > >::iterator **begin** ()
- std::vector< VirusPtr< TSeq > >::iterator **end** ()
- VirusPtr< TSeq > & **operator()** (size_t i)
- VirusPtr< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- void **print** () const noexcept

Friends

- class **Virus< TSeq >**
- class **Agent< TSeq >**

17.87.1 Detailed Description

template<typename TSeq>
class epiworld::Viruses< TSeq >

Set of viruses (useful for building iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following file:

- epiworld.hpp

17.88 Viruses< TSeq > Class Template Reference

Set of viruses (useful for building iterators)

```
#include <viruses-bones.hpp>
```

Public Member Functions

- **Viruses** (Agent< TSeq > &p)
- std::vector< VirusPtr< TSeq > >::iterator **begin** ()
- std::vector< VirusPtr< TSeq > >::iterator **end** ()
- VirusPtr< TSeq > & **operator()** (size_t i)
- VirusPtr< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- void **print** () const noexcept

Friends

- class **Virus**< **TSeq** >
- class **Agent**< **TSeq** >

17.88.1 Detailed Description

template<typename TSeq>
class Viruses< TSeq >

Set of viruses (useful for building iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/viruses-bones.hpp

17.89 epiworld::Viruses_const< TSeq > Class Template Reference

Set of Viruses (const) (useful for iterators)

```
#include <epiworld.hpp>
```

Public Member Functions

- **Viruses_const** (const Agent< TSeq > &p)
- std::vector< VirusPtr< TSeq > >::const_iterator **begin** () const
- std::vector< VirusPtr< TSeq > >::const_iterator **end** () const
- const VirusPtr< TSeq > & **operator()** (size_t i)
- const VirusPtr< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- void **print** () const noexcept

Friends

- class **Virus**< **TSeq** >
- class **Agent**< **TSeq** >

17.89.1 Detailed Description

template<typename TSeq>
class epiworld::Viruses_const< TSeq >

Set of Viruses (const) (useful for iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following file:

- epiworld.hpp

17.90 Viruses_const< TSeq > Class Template Reference

Set of Viruses (const) (useful for iterators)

```
#include <viruses-bones.hpp>
```

Public Member Functions

- **Viruses_const** (const Agent< TSeq > &p)
- std::vector< VirusPtr< TSeq > >::const_iterator **begin** () const
- std::vector< VirusPtr< TSeq > >::const_iterator **end** () const
- const VirusPtr< TSeq > & **operator()** (size_t i)
- const VirusPtr< TSeq > & **operator[ ]** (size_t i)
- size_t **size** () const noexcept
- void **print** () const noexcept

Friends

- class **Virus**< **TSeq** >
- class **Agent**< **TSeq** >

17.90.1 Detailed Description

template<typename TSeq>
class Viruses_const< TSeq >

Set of Viruses (const) (useful for iterators)

Template Parameters

TSeq	

The documentation for this class was generated from the following files:

- include/epiworld/agent-bones.hpp
- include/epiworld/viruses-bones.hpp

17.91 epiworld::VirusFunctions< TSeq > Class Template Reference

Public Attributes

- MutFun< TSeq > **mutation** = nullptr
- PostRecoveryFun< TSeq > **post_recovery** = nullptr
- VirusFun< TSeq > **probability_of_infecting** = nullptr
- VirusFun< TSeq > **probability_of_recovery** = nullptr
- VirusFun< TSeq > **probability_of_death** = nullptr
- VirusFun< TSeq > **incubation** = nullptr
- VirusToAgentFun< TSeq > **dist** = nullptr

The documentation for this class was generated from the following file:

- epiworld.hpp

17.92 VirusFunctions< TSeq > Class Template Reference

Public Attributes

- MutFun< TSeq > **mutation** = nullptr
- PostRecoveryFun< TSeq > **post_recovery** = nullptr
- VirusFun< TSeq > **probability_of_infecting** = nullptr
- VirusFun< TSeq > **probability_of_recovery** = nullptr
- VirusFun< TSeq > **probability_of_death** = nullptr
- VirusFun< TSeq > **incubation** = nullptr
- VirusToAgentFun< TSeq > **dist** = nullptr

The documentation for this class was generated from the following file:

- include/epiworld/virus-bones.hpp

Chapter 18

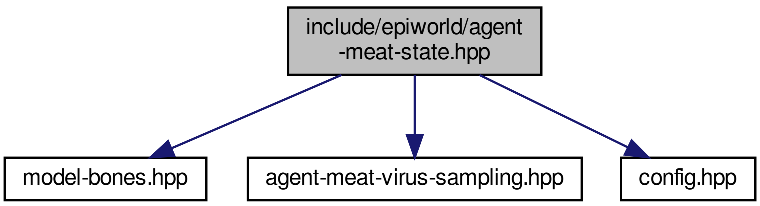
File Documentation

18.1 include/epiworld/agent-meat-state.hpp File Reference

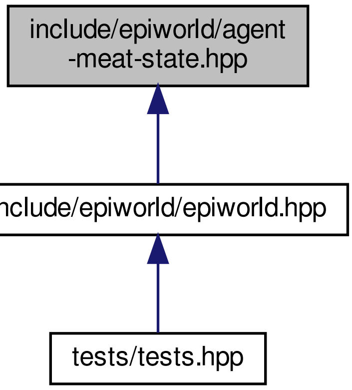
Sampling functions are getting big, so we keep them in a separate file.

```
#include "model-bones.hpp"
#include "agent-meat-virus-sampling.hpp"
#include "config.hpp"
```

Include dependency graph for agent-meat-state.hpp:



This graph shows which files directly or indirectly include this file:



Functions

- template<typename TSeq = EPI_DEFAULT_TSEQ>
  void **default_update_susceptible** (Agent< TSeq > *p, Model< TSeq > *m)
- template<typename TSeq = EPI_DEFAULT_TSEQ>
  void **default_update_exposed** (Agent< TSeq > *p, Model< TSeq > *m)

18.1.1 Detailed Description

Sampling functions are getting big, so we keep them in a separate file.

Author

George G. Vega Yon (g.vegayon en gmail)

Version

0.1

Date

2022-06-15

Copyright

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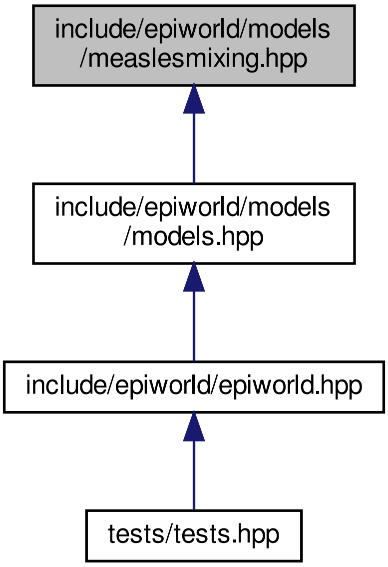
18.2 include/epiworld/models/measlesmixing.hpp File Reference

Template for a Measles model with population mixing, quarantine, and contact tracing.

This graph shows which files directly or indirectly include this file:



Classes

- class ModelMeaslesMixing< TSeq >

  Measles model with population mixing, quarantine, and contact tracing.

Macros

- #define **MM**(i, j, n) $j * n + i$
- #define **GET_MODEL**(model, output)
- #define **SAMPLE_FROM_PROBS**(n, ans)

18.2.1 Detailed Description

Template for a Measles model with population mixing, quarantine, and contact tracing.

18.2.2 Macro Definition Documentation

18.2.2.1 GET_MODEL

```
#define GET_MODEL(
            model,
            output )
```

Value:

```
auto * output = dynamic_cast< ModelMeaslesMixing<TSeq> * >( (model) ); \
assert((output) != nullptr);
```

18.2.2.2 SAMPLE_FROM_PROBS

```
#define SAMPLE_FROM_PROBS(
            n,
            ans )
```

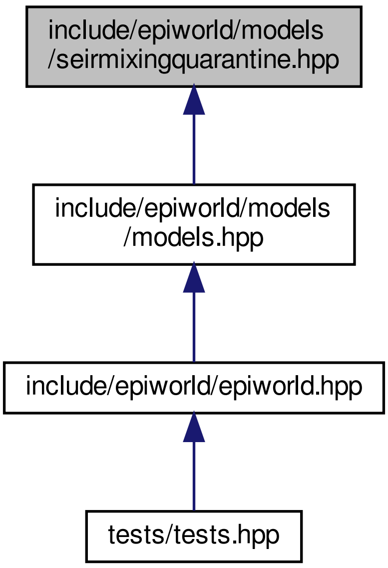
Value:

```
size_t ans; \
epiworld_double p_total = m->runif(); \
for (ans = 0u; ans < n; ++ans) \
{ \
    if (p_total < m->array_double_tmp[ans]) \
        break; \
    m->array_double_tmp[ans + 1] += m->array_double_tmp[ans]; \
}
```

18.3 include/epiworld/models/seirmixingquarantine.hpp File Reference

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model with mixing, quarantine, and contact tracing.

This graph shows which files directly or indirectly include this file:



Classes

- class ModelSEIRMixingQuarantine< TSeq >

  SEIR model with mixing, quarantine, and contact tracing.

Macros

- #define **MM**(i, j, n) j ∗ n + i
- #define **GET_MODEL**(model, output)
- #define **SAMPLE_FROM_PROBS**(n, ans)

18.3.1 Detailed Description

Template for a Susceptible-Exposed-Infected-Removed (SEIR) model with mixing, quarantine, and contact tracing.

18.3.2 Macro Definition Documentation

18.3.2.1 GET_MODEL

```
#define GET_MODEL(
                model,
                output )
```

Value:

```
        auto * output = dynamic_cast< ModelSEIRMixingQuarantine<TSeq> * >( (model) ); \
        assert((output) != nullptr);
```

18.3.2.2 SAMPLE_FROM_PROBS

```
#define SAMPLE_FROM_PROBS(
                n,
                ans )
```

Value:

```
    size_t ans; \
    epiworld_double p_total = m->runif(); \
    for (ans = 0u; ans < n; ++ans) \
    { \
        if (p_total < m->array_double_tmp[ans]) \
            break; \
        m->array_double_tmp[ans + 1] += m->array_double_tmp[ans]; \
    }
```

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