

epiworld

0.0-1

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# Chapter 1

## Example: 00-hello-world

### Output from the program:

Running the model...

```
||||| done.
[epiworld-debug] DEBUGGING ON (compiled with EPI_DEBUG defined)

SIMULATION STUDY
Population size      : 10000
Number of entitites : 0
Days (duration)     : 100 (of 100)
Number of variants  : 1
Last run elapsed t   : 40.00ms
Rewiring             : off
Virus(es):
- covid 19 (baseline prevalence: 50 seeds)
Tool(s):
- vaccine (baseline prevalence: 50.00%)
- Immunity (covid 19) (originated in the model...)
Model parameters:
(none)
Distribution of the population at time 100:
- (0) Susceptible : 9950 -> 70
- (1) Exposed     : 50 -> 70
- (2) Recovered   : 0 -> 9271
- (3) Removed     : 0 -> 589
Transition Probabilities:
- Susceptible 0.95 0.05 0.00 0.00
- Exposed      0.00 0.85 0.14 0.01
- Recovered    0.00 0.00 1.00 0.00
- Removed      0.00 0.00 0.00 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.

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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

# epiworld c++ template library

### 4.1 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.

### 4.2 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 statuses (arbitrary number of them).

## Run

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

Along update:

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

## 4.3 Hello world (C++)

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

    // Creating a tool
    epiworld::Tool<> vax("vaccine");
    vax.set_contagion_reduction(.95);
    // Creating a model
    epiworld::Model<> model;
    // Adding the tool and virus
    model.add_virus(covid19, .01);
    model.add_tool(vax, .5);
    // 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;
}
```

## 4.4 Surveillance simulation

- Incubation time of the disease  $\sim \text{Gamma}(3, 1)$
- Duration of the disease  $\sim \text{Gamma}(12, 1)$
- 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.



### 4.4.1 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
## - Surveillance prob. : 1.0e-04
## - Vax efficacy       : 0.9000
## - Vax redux transmission : 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
## - Surveillance prob. : 0.0020
## - Vax efficacy       : 0.9000
## - Vax redux transmission : 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 = status, linetype=sim)) +
  geom_line() +
  # scale_y_log10() +
  labs(y = "Counts (log)")
```

#### 4.4.2 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_asymp),
    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_asymp),
    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 5

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## Chapter 6

### 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 efficacy 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

```  $P(i \text{ gets the disease from } j \mid \text{their states}) = C(k) * (1 - E(i, k)) * (1 - E(j, k))$  ```

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:  

$$\Pr(h \rightarrow s | i, t, k, u) \sim \sum(g \in \{u, v\}) (N(i, t-1, s, k | g) + \sum(j \neq i) F(i, j) * N(j, t-1, s, k | g)) * C(k) / (N(i) + \sum(j \neq i) N(j))$$
  - b. Vaccinated individuals can become sick of variant  $k$  with probability:  $\Pr(v \rightarrow s | i, t, k, v) \sim \Pr(h \rightarrow s | i, t, k) * (1 - E(v, k))$ .
  - b. Recovered individuals can become sick of variant  $k$  with probability:  $\Pr(v \rightarrow s | i, t, k, r) \sim \Pr(h \rightarrow s | i, t, k) * (1 - E(r, k))$ .
  - 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  $P(u \rightarrow v) \sim V(A(i, t), B(i))$ .
  - e. The country vaccine supply changes.

## Chapter 7

# EPI Simulator

### 7.1 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.

### 7.2 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.

### 7.3 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.

### 7.4 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

## 7.5 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:

$$\begin{aligned} P(\text{Variant } k | \text{at most 1}) &= P(\text{at most 1} | \text{Variant } k) * P(\text{Variant } k) / P(\text{at most 1}) \\ &= P(\text{only variant } k) / P(\text{variant } k) * P(\text{Variant } k) / P(\text{at most 1}) \\ &= P(\text{only variant } k) / P(\text{at most 1}) \end{aligned}$$

Where

$$\begin{aligned} P(\text{only variant } k) &= P(k) * \text{Prod}(m \neq v) (1 - P(m)) \\ P(\text{at most 1}) &= P(\text{None}) + \text{Sum}(v \text{ in variants}) P(v) * \text{Prod}(m \neq v) (1 - P(m)) \\ P(\text{None}) &= \text{Prod}(v \text{ in variants}) (1 - P(v)) \end{aligned}$$

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

### 7.5.1 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](#) changes can be a function of an ERGM. Apply K steps throughout time.
- Add progress bar.



## Chapter 8

# Namespace Index

### 8.1 Namespace List

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

<a href="#">epiworld::sampler</a>	Functions for sampling viruses . . . . .	<a href="#">27</a>
<a href="#">sampler</a>	Functions for sampling viruses . . . . .	<a href="#">30</a>



## Chapter 9

# Hierarchical Index

### 9.1 Class Hierarchy

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

Action< TSeq > . . . . .	35
epiworld::Action< TSeq > . . . . .	37
AdjList . . . . .	38
epiworld::AdjList . . . . .	40
Agent< TSeq > . . . . .	41
epiworld::Agent< TSeq > . . . . .	44
AgentsSample< TSeq > . . . . .	47
epiworld::AgentsSample< TSeq > . . . . .	49
DataBase< TSeq > . . . . .	50
epiworld::DataBase< TSeq > . . . . .	53
Entities< TSeq > . . . . .	56
epiworld::Entities< TSeq > . . . . .	56
Entities_const< TSeq > . . . . .	57
epiworld::Entities_const< TSeq > . . . . .	58
Entity< TSeq > . . . . .	59
epiworld::Entity< TSeq > . . . . .	59
epiworld::LFMCMC< TData > . . . . .	60
LFMCMC< TData > . . . . .	61
epiworld::Model< TSeq > . . . . .	63
Model< TSeq > . . . . .	72
epiworld::Model< EPI_DEFAULT_TSEQ > . . . . .	63
ModelSEIRCONN< TSeq > . . . . .	87
ModelSEIRCONNLogit< TSeq > . . . . .	89
ModelSIRCONN< TSeq > . . . . .	95
ModelSURV< TSeq > . . . . .	102
epiworld::epimodels::ModelSEIRCONN< TSeq > . . . . .	85
epiworld::epimodels::ModelSIRCONN< TSeq > . . . . .	93
epiworld::epimodels::ModelSURV< TSeq > . . . . .	100
epiworld::Model< int > . . . . .	63
ModelSEIR< TSeq > . . . . .	83
ModelSIR< TSeq > . . . . .	92
ModelSIS< TSeq > . . . . .	99
epiworld::epimodels::ModelSEIR< TSeq > . . . . .	81
epiworld::epimodels::ModelSIR< TSeq > . . . . .	90
epiworld::epimodels::ModelSIS< TSeq > . . . . .	97

Network< Nettype, Nodetype, Edgetype > . . . . .	104
epiworld::PersonTools< TSeq > . . . . .	104
PersonTools< TSeq > . . . . .	105
epiworld::Progress . . . . .	105
Progress . . . . .	105
epiworld::Queue< TSeq > . . . . .	106
Queue< TSeq > . . . . .	106
epiworld::QueueValues . . . . .	107
QueueValues . . . . .	107
RandGraph . . . . .	108
epiworld::SAMPLETYPE . . . . .	108
SAMPLETYPE . . . . .	108
epiworld::Tool< TSeq > . . . . .	108
Tool< TSeq > . . . . .	111
epiworld::Tools< TSeq > . . . . .	112
Tools< TSeq > . . . . .	113
epiworld::Tools_const< TSeq > . . . . .	114
Tools_const< TSeq > . . . . .	115
epiworld::UserData< TSeq > . . . . .	115
UserData< TSeq > . . . . .	117
epiworld::vecHasher< T > . . . . .	119
vecHasher< T > . . . . .	119
epiworld::Virus< TSeq > . . . . .	120
Virus< TSeq > . . . . .	122
epiworld::Viruses< TSeq > . . . . .	124
Viruses< TSeq > . . . . .	124
epiworld::Viruses_const< TSeq > . . . . .	125
Viruses_const< TSeq > . . . . .	126

## Chapter 10

# Class Index

### 10.1 Class List

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

<a href="#">Action&lt; TSeq &gt;</a>	
Action data for update an agent	35
<a href="#">epiworld::Action&lt; TSeq &gt;</a>	
Action data for update an agent	37
<a href="#">AdjList</a>	38
<a href="#">epiworld::AdjList</a>	40
<a href="#">Agent&lt; TSeq &gt;</a>	
Agent (agents)	41
<a href="#">epiworld::Agent&lt; TSeq &gt;</a>	
Agent (agents)	44
<a href="#">AgentsSample&lt; TSeq &gt;</a>	
Sample of agents	47
<a href="#">epiworld::AgentsSample&lt; TSeq &gt;</a>	
Sample of agents	49
<a href="#">DataBase&lt; TSeq &gt;</a>	
Statistical data about the process	50
<a href="#">epiworld::DataBase&lt; TSeq &gt;</a>	
Statistical data about the process	53
<a href="#">Entities&lt; TSeq &gt;</a>	
Set of <a href="#">Entities</a> (useful for building iterators)	56
<a href="#">epiworld::Entities&lt; TSeq &gt;</a>	
Set of <a href="#">Entities</a> (useful for building iterators)	56
<a href="#">Entities_const&lt; TSeq &gt;</a>	
Set of <a href="#">Entities</a> (const) (useful for iterators)	57
<a href="#">epiworld::Entities_const&lt; TSeq &gt;</a>	
Set of <a href="#">Entities</a> (const) (useful for iterators)	58
<a href="#">Entity&lt; TSeq &gt;</a>	59
<a href="#">epiworld::Entity&lt; TSeq &gt;</a>	59
<a href="#">epiworld::LFMCMC&lt; TData &gt;</a>	
Likelihood-Free Markov Chain Monte Carlo	60
<a href="#">LFMCMC&lt; TData &gt;</a>	
Likelihood-Free Markov Chain Monte Carlo	61
<a href="#">epiworld::Model&lt; TSeq &gt;</a>	
Core class of epiworld	63
<a href="#">Model&lt; TSeq &gt;</a>	
Core class of epiworld	72

<a href="#">epiworld::epimodels::ModelSEIR&lt; TSeq &gt;</a>	
Template for a Susceptible-Exposed-Infected-Removed (SEIR) model	81
<a href="#">ModelSEIR&lt; TSeq &gt;</a>	
Template for a Susceptible-Exposed-Infected-Removed (SEIR) model	83
<a href="#">epiworld::epimodels::ModelSEIRCONN&lt; TSeq &gt;</a>	85
<a href="#">ModelSEIRCONN&lt; TSeq &gt;</a>	87
<a href="#">ModelSEIRCONNLogit&lt; TSeq &gt;</a>	89
<a href="#">epiworld::epimodels::ModelSIR&lt; TSeq &gt;</a>	
Template for a Susceptible-Infected-Removed (SIR) model	90
<a href="#">ModelSIR&lt; TSeq &gt;</a>	
Template for a Susceptible-Infected-Removed (SIR) model	92
<a href="#">epiworld::epimodels::ModelSIRCONN&lt; TSeq &gt;</a>	93
<a href="#">ModelSIRCONN&lt; TSeq &gt;</a>	95
<a href="#">epiworld::epimodels::ModelSIS&lt; TSeq &gt;</a>	
Template for a Susceptible-Infected-Susceptible (SIS) model	97
<a href="#">ModelSIS&lt; TSeq &gt;</a>	
Template for a Susceptible-Infected-Susceptible (SIS) model	99
<a href="#">epiworld::epimodels::ModelSURV&lt; TSeq &gt;</a>	100
<a href="#">ModelSURV&lt; TSeq &gt;</a>	102
<a href="#">Network&lt; Nettype, Nodetype, Edgetype &gt;</a>	104
<a href="#">epiworld::PersonTools&lt; TSeq &gt;</a>	104
<a href="#">PersonTools&lt; TSeq &gt;</a>	105
<a href="#">epiworld::Progress</a>	
A simple progress bar	105
<a href="#">Progress</a>	
A simple progress bar	105
<a href="#">epiworld::Queue&lt; TSeq &gt;</a>	
Controls which agents are verified at each step	106
<a href="#">Queue&lt; TSeq &gt;</a>	
Controls which agents are verified at each step	106
<a href="#">epiworld::QueueValues</a>	107
<a href="#">QueueValues</a>	107
<a href="#">RandGraph</a>	108
<a href="#">epiworld::SAMPLETYPE</a>	108
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<a href="#">epiworld::Tool&lt; TSeq &gt;</a>	
Tools for defending the agent against the virus	108
<a href="#">Tool&lt; TSeq &gt;</a>	
Tools for defending the agent against the virus	111
<a href="#">epiworld::Tools&lt; TSeq &gt;</a>	
Set of tools (useful for building iterators)	112
<a href="#">Tools&lt; TSeq &gt;</a>	
Set of tools (useful for building iterators)	113
<a href="#">epiworld::Tools_const&lt; TSeq &gt;</a>	
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<a href="#">epiworld::UserData&lt; TSeq &gt;</a>	
Personalized data by the user	115
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<a href="#">epiworld::vecHasher&lt; T &gt;</a>	
Vector hasher	119
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Vector hasher	119
<a href="#">epiworld::Virus&lt; TSeq &gt;</a>	
Virus	120

<a href="#">Virus&lt; TSeq &gt;</a>	
<a href="#">Virus</a> . . . . .	122
<a href="#">epiworld::Viruses&lt; TSeq &gt;</a>	
Set of viruses (useful for building iterators) . . . . .	124
<a href="#">Viruses&lt; TSeq &gt;</a>	
Set of viruses (useful for building iterators) . . . . .	124
<a href="#">epiworld::Viruses_const&lt; TSeq &gt;</a>	
Set of <a href="#">Viruses</a> (const) (useful for iterators) . . . . .	125
<a href="#">Viruses_const&lt; TSeq &gt;</a>	
Set of <a href="#">Viruses</a> (const) (useful for iterators) . . . . .	126





# Chapter 11

## File Index

### 11.1 File List

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

<b>epiworld.hpp</b>	??
include/epiworld/ <b>adjlist-bones.hpp</b>	??
include/epiworld/ <b>adjlist-meat.hpp</b>	??
include/epiworld/ <b>agent-actions-meat.hpp</b>	??
include/epiworld/ <b>agent-bones.hpp</b>	??
include/epiworld/ <b>agent-meat-status.hpp</b>	
Sampling functions are getting big, so we keep them in a separate file	127
include/epiworld/ <b>agent-meat-virus-sampling.hpp</b>	??
include/epiworld/ <b>agent-meat.hpp</b>	??
include/epiworld/ <b>agentssample-bones.hpp</b>	??
include/epiworld/ <b>config.hpp</b>	??
include/epiworld/ <b>database-bones.hpp</b>	??
include/epiworld/ <b>database-meat.hpp</b>	??
include/epiworld/ <b>entities-bones.hpp</b>	??
include/epiworld/ <b>entity-bones.hpp</b>	??
include/epiworld/ <b>entity-meat.hpp</b>	??
include/epiworld/ <b>epiworld-macros.hpp</b>	??
include/epiworld/ <b>epiworld.hpp</b>	??
include/epiworld/ <b>misc.hpp</b>	??
include/epiworld/ <b>model-bones.hpp</b>	??
include/epiworld/ <b>model-meat-print.hpp</b>	??
include/epiworld/ <b>model-meat.hpp</b>	??
include/epiworld/ <b>network-bones.hpp</b>	??
include/epiworld/ <b>progress.hpp</b>	??
include/epiworld/ <b>queue-bones.hpp</b>	??
include/epiworld/ <b>randgraph.hpp</b>	??
include/epiworld/ <b>random_graph.hpp</b>	??
include/epiworld/ <b>seq_processing.hpp</b>	??
include/epiworld/ <b>tool-bones.hpp</b>	??
include/epiworld/ <b>tool-meat.hpp</b>	??
include/epiworld/ <b>tools-bones.hpp</b>	??
include/epiworld/ <b>userdata-bones.hpp</b>	??
include/epiworld/ <b>userdata-meat.hpp</b>	??
include/epiworld/ <b>virus-bones.hpp</b>	??
include/epiworld/ <b>virus-meat.hpp</b>	??

include/epiworld/ <b>viruses-bones.hpp</b>	??
include/epiworld/math/ <b>lfmcmc.hpp</b>	??
include/epiworld/math/lfmcmc/ <b>lfmcmc-bones.hpp</b>	??
include/epiworld/math/lfmcmc/ <b>lfmcmc-meat-print.hpp</b>	??
include/epiworld/math/lfmcmc/ <b>lfmcmc-meat.hpp</b>	??
include/epiworld/models/ <b>models.hpp</b>	??
include/epiworld/models/ <b>seir.hpp</b>	??
include/epiworld/models/ <b>seirconnected.hpp</b>	??
include/epiworld/models/ <b>seirconnected_logit.hpp</b>	??
include/epiworld/models/ <b>sir.hpp</b>	??
include/epiworld/models/ <b>sirconnected.hpp</b>	??
include/epiworld/models/ <b>sis.hpp</b>	??
include/epiworld/models/ <b>surveillance.hpp</b>	??
tests/ <b>tests.hpp</b>	??

## Chapter 12

# Namespace Documentation

### 12.1 epiworld::sampler Namespace Reference

Functions for sampling viruses.

#### Functions

- `template<typename 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 = int>`  
`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 = int>`  
`Virus< TSeq > * sample\_virus\_single (Agent< TSeq > *p, Model< TSeq > *m)`  
*Sample from neighbors pool of viruses (at most one)*

#### 12.1.1 Detailed Description

Functions for sampling viruses.

#### 12.1.2 Function Documentation

##### 12.1.2.1 `make_sample_virus_neighbors()`

```
template<typename TSeq = int>
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

<i>TSeq</i>	
-------------	--

## Parameters

<i>exclude</i>	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;

**12.1.2.2 make\_update\_susceptible()**

```
template<typename 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

<i>TSeq</i>	
-------------	--

## Parameters

<i>exclude</i>	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;

**12.1.2.3 sample\_virus\_single()**

```
template<typename TSeq = int>
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

<i>TSeq</i>	
-------------	--

## Parameters

<i>p</i>	Pointer to person
<i>m</i>	Pointer to the model

## Returns

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

## 12.2 sampler Namespace Reference

Functions for sampling viruses.

### Functions

- `template<typename 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 = int> 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 = int> Virus< TSeq > * sample\_virus\_single (Agent< TSeq > *p, Model< TSeq > *m)`  
*Sample from neighbors pool of viruses (at most one)*

### 12.2.1 Detailed Description

Functions for sampling viruses.

### 12.2.2 Function Documentation

#### 12.2.2.1 [make\\_sample\\_virus\\_neighbors\(\)](#)

```
template<typename TSeq = int>
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

<i>TSeq</i>	
-------------	--

## Parameters

<i>exclude</i>	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;

## 12.2.2.2 make\_update\_susceptible()

```
template<typename 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

<i>TSeq</i>	
-------------	--

## Parameters

<i>exclude</i>	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;

## 12.2.2.3 sample\_virus\_single()

```
template<typename TSeq = int>
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

<i>TSeq</i>	
-------------	--

## Parameters

<i>p</i>	Pointer to person
<i>m</i>	Pointer to the model

## Returns

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



# Chapter 13

## Class Documentation

### 13.1 Action< TSeq > Struct Template Reference

Action data for update an agent.

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

#### Public Member Functions

- Action (Agent< TSeq > \*agent\_, VirusPtr< TSeq > virus\_, ToolPtr< TSeq > tool\_, Entity< TSeq > \*entity\_, epiworld\_fast\_int new\_status\_, epiworld\_fast\_int queue\_, ActionFun< TSeq > call\_, int idx\_agent←\_, int idx\_object\_)

Construct a new Action object.

#### Public Attributes

- Agent< TSeq > \* agent
- VirusPtr< TSeq > virus
- ToolPtr< TSeq > tool
- Entity< TSeq > \* entity
- epiworld\_fast\_int new\_status
- epiworld\_fast\_int queue
- ActionFun< TSeq > call
- int idx\_agent
- int idx\_object

#### 13.1.1 Detailed Description

```
template<typename TSeq>  
struct Action< TSeq >
```

Action data for update an agent.

## Template Parameters

<i>TSeq</i>	
-------------	--

## 13.1.2 Constructor &amp; Destructor Documentation

## 13.1.2.1 Action()

```
template<typename TSeq >
Action< TSeq >::Action (
    Agent< TSeq > * agent_,
    VirusPtr< TSeq > virus_,
    ToolPtr< TSeq > tool_,
    Entity< TSeq > * entity_,
    epiworld_fast_int new_status_,
    epiworld_fast_int queue_,
    ActionFun< TSeq > call_,
    int idx_agent_,
    int idx_object_ ) [inline]
```

Construct a new [Action](#) object.

All the parameters are rather optional.

## Parameters

<i>agent_</i>	<a href="#">Agent</a> over who the action will happen
<i>virus_</i>	<a href="#">Virus</a> to add
<i>tool_</i>	<a href="#">Tool</a> to add
<i>virus_idx</i>	Index of virus to be removed (if needed)
<i>tool_idx</i>	Index of tool to be removed (if needed)
<i>new_status_↔</i>	Next status
<i>queue_</i>	Efect on the queue
<i>call_</i>	The action call (if needed)
<i>idx_agent_↔</i>	Location of agent in object.
<i>idx_object_↔</i>	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

## 13.2 epiworld::Action< TSeq > Struct Template Reference

[Action](#) data for update an agent.

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

### Public Member Functions

- [Action](#) ([Agent](#)< TSeq > \*agent\_, [VirusPtr](#)< TSeq > virus\_, [ToolPtr](#)< TSeq > tool\_, [Entity](#)< TSeq > \*entity\_, epiworld\_fast\_int new\_status\_, epiworld\_fast\_int queue\_, [ActionFun](#)< TSeq > call\_, int idx\_agent\_, int idx\_object\_)  
Construct a new [Action](#) object.

### Public Attributes

- [Agent](#)< TSeq > \* **agent**
- [VirusPtr](#)< TSeq > **virus**
- [ToolPtr](#)< TSeq > **tool**
- [Entity](#)< TSeq > \* **entity**
- epiworld\_fast\_int **new\_status**
- epiworld\_fast\_int **queue**
- [ActionFun](#)< TSeq > **call**
- int **idx\_agent**
- int **idx\_object**

### 13.2.1 Detailed Description

```
template<typename TSeq>
struct epiworld::Action< TSeq >
```

[Action](#) data for update an agent.

Template Parameters

<a href="#">TSeq</a>	
----------------------	--

### 13.2.2 Constructor & Destructor Documentation

#### 13.2.2.1 Action()

```
template<typename TSeq >
epiworld::Action< TSeq >::Action (
    Agent< TSeq > * agent_,
```

```

VirusPtr< TSeq > virus_,
ToolPtr< TSeq > tool_,
Entity< TSeq > * entity_,
epiworld_fast_int new_status_,
epiworld_fast_int queue_,
ActionFun< TSeq > call_,
int idx_agent_,
int idx_object_ ) [inline]

```

Construct a new [Action](#) object.

All the parameters are rather optional.

#### Parameters

<i>agent_</i>	<a href="#">Agent</a> over who the action will happen
<i>virus_</i>	<a href="#">Virus</a> to add
<i>tool_</i>	<a href="#">Tool</a> to add
<i>virus_idx</i>	Index of virus to be removed (if needed)
<i>tool_idx</i>	Index of tool to be removed (if needed)
<i>new_↔ status_</i>	Next status
<i>queue_</i>	Efect on the queue
<i>call_</i>	The action call (if needed)
<i>idx_agent_↔ _</i>	Location of agent in object.
<i>idx_object_↔ _</i>	Location of object in agent.

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

- epiworld.hpp

## 13.3 AdjList Class Reference

### Public Member Functions

- [AdjList](#) (const std::vector< epiworld\_fast\_uint > &source, const std::vector< epiworld\_fast\_uint > &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< epiworld\_fast\_uint, epiworld\_fast\_uint > **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< epiworld\_fast\_uint, epiworld\_fast\_uint > > & **get\_dat** ()
- bool [is\\_directed](#) () const  
*true if the network is directed.*

### 13.3.1 Constructor & Destructor Documentation

#### 13.3.1.1 AdjList()

```
AdjList::AdjList (
    const std::vector< epiworld_fast_uint > & source,
    const std::vector< epiworld_fast_uint > & 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

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

### 13.3.2 Member Function Documentation

#### 13.3.2.1 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

<i>fn</i>	Path to the file
<i>skip</i>	Number of lines to skip (e.g., 1 if there's a header)
<i>directed</i>	true if the network is directed
<i>size</i>	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

## 13.4 epiworld::AdjList Class Reference

### Public Member Functions

- [AdjList](#) (const std::vector< epiworld\_fast\_uint > &source, const std::vector< epiworld\_fast\_uint > &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< epiworld\_fast\_uint, epiworld\_fast\_uint > **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< epiworld\_fast\_uint, epiworld\_fast\_uint > > & **get\_dat** ()
- bool [is\\_directed](#) () const  
*true if the network is directed.*

### 13.4.1 Constructor & Destructor Documentation

#### 13.4.1.1 AdjList()

```
AdjList::AdjList (
    const std::vector< epiworld_fast_uint > & source,
    const std::vector< epiworld_fast_uint > & 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

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



## 13.4.2 Member Function Documentation

### 13.4.2.1 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

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

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

- `epiworld.hpp`

## 13.5 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** (int i)
- [Viruses](#)< TSeq > **get\_viruses** ()
- const [Viruses\\_const](#)< TSeq > **get\_viruses** () const
- size\_t **get\_n\_viruses** () const noexcept
- 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\_variant** ()
- void **add\_neighbor** ([Agent](#)< TSeq > \*p, bool check\_source=true, bool check\_target=true)
- std::vector< [Agent](#)< TSeq > \* > & **get\_neighbors** ()
- void **change\_status** ([Model](#)< TSeq > \*model, epiworld\_fast\_uint new\_status, epiworld\_fast\_int queue=0)
- const epiworld\_fast\_uint & **get\_status** () const
- void **reset** ()
- bool **has\_tool** (epiworld\_fast\_uint t) const
- bool **has\_tool** (std::string name) const
- bool **has\_virus** (epiworld\_fast\_uint t) const
- bool **has\_virus** (std::string name) const
- void **print** ([Model](#)< TSeq > \*model, bool compressed=false) const
- [Entities](#)< TSeq > **get\_entities** ()  
*Access the j-th column of the agent.*
- const [Entities\\_const](#)< TSeq > **get\_entities** () const

### Add/Remove Virus/Tool

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

#### Parameters

tool	<a href="#">Tool</a> to add
virus	<a href="#">Virus</a> to add
status_new	Status after the change
queue	

- void **add\_tool** ([ToolPtr](#)< TSeq > tool, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **add\_tool** ([Tool](#)< TSeq > tool, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **add\_virus** ([VirusPtr](#)< TSeq > virus, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **add\_virus** ([Virus](#)< TSeq > virus, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **add\_entity** ([Entity](#)< TSeq > &entity, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_tool** (epiworld\_fast\_uint tool\_idx, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_tool** ([ToolPtr](#)< TSeq > &tool, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_virus** (epiworld\_fast\_uint virus\_idx, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_virus** ([VirusPtr](#)< TSeq > &virus, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_entity** (epiworld\_fast\_uint entity\_idx, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_entity** ([Entity](#)< TSeq > &entity, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_agent\_by\_virus** (epiworld\_fast\_uint virus\_idx, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)  
*[Agent](#) removed by virus.*
- void **rm\_agent\_by\_virus** ([VirusPtr](#)< TSeq > &virus, [Model](#)< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)  
*[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)

**Friends**

- class **Model**< TSeq >
- class **Virus**< TSeq >
- class **Viruses**< TSeq >
- class **Viruses\_const**< TSeq >
- class **Tool**< TSeq >
- class **Tools**< TSeq >
- class **Tools\_const**< TSeq >
- class **Queue**< TSeq >
- class **Entities**< TSeq >
- class **AgentsSample**< TSeq >
- void **default\_add\_virus** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_add\_tool** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_add\_entity** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_virus** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_tool** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_entity** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)

**13.5.1 Detailed Description**

```
template<typename TSeq>
class Agent< TSeq >
```

[Agent](#) (agents)*Template Parameters*

<i>TSeq</i>	Sequence type (should match TSeq across the model)
-------------	----------------------------------------------------

**13.5.2 Member Function Documentation**

### 13.5.2.1 get\_entities()

```
template<typename TSeq >
Entities< TSeq > Agent< TSeq >::get_entities [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

<i>j</i>	
----------	--

#### Returns

double&

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

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

## 13.6 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** (int i)
- [Viruses](#)< TSeq > **get\_viruses** ()
- const [Viruses\\_const](#)< TSeq > **get\_viruses** () const
- size\_t **get\_n\_viruses** () const noexcept
- 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\_variant** ()
- void **add\_neighbor** ([Agent](#)< TSeq > \*p, bool check\_source=true, bool check\_target=true)
- std::vector< [Agent](#)< TSeq > \* > & **get\_neighbors** ()

- void **change\_status** (Model< TSeq > \*model, epiworld\_fast\_uint new\_status, epiworld\_fast\_int queue=0)
- const epiworld\_fast\_uint & **get\_status** () const
- void **reset** ()
- bool **has\_tool** (epiworld\_fast\_uint t) const
- bool **has\_tool** (std::string name) const
- bool **has\_virus** (epiworld\_fast\_uint t) const
- bool **has\_virus** (std::string name) const
- void **print** (Model< TSeq > \*model, bool compressed=false) const
- Entities< TSeq > **get\_entities** ()  
*Access the j-th column of the agent.*
- const Entities\_const< TSeq > **get\_entities** () const

### Add/Remove Virus/Tool

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

#### Parameters

tool	<i>Tool to add</i>
virus	<i>Virus to add</i>
status_new	<i>Status after the change</i>
queue	

- void **add\_tool** (ToolPtr< TSeq > tool, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **add\_tool** (Tool< TSeq > tool, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **add\_virus** (VirusPtr< TSeq > virus, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **add\_virus** (Virus< TSeq > virus, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **add\_entity** (Entity< TSeq > &entity, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_tool** (epiworld\_fast\_uint tool\_idx, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_tool** (ToolPtr< TSeq > &tool, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_virus** (epiworld\_fast\_uint virus\_idx, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_virus** (VirusPtr< TSeq > &virus, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_entity** (epiworld\_fast\_uint entity\_idx, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_entity** (Entity< TSeq > &entity, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)
- void **rm\_agent\_by\_virus** (epiworld\_fast\_uint virus\_idx, Model< TSeq > \*model, epiworld\_fast\_int status\_new=-99, epiworld\_fast\_int queue=-99)  
*Agent removed by virus.*
- void **rm\_agent\_by\_virus** (VirusPtr< TSeq > &virus, Model< TSeq > \*model, epiworld\_fast\_int status←\_new=-99, epiworld\_fast\_int queue=-99)  
*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)

**Friends**

- class **Model**< TSeq >
- class **Virus**< TSeq >
- class **Viruses**< TSeq >
- class **Viruses\_const**< TSeq >
- class **Tool**< TSeq >
- class **Tools**< TSeq >
- class **Tools\_const**< TSeq >
- class **Queue**< TSeq >
- class **Entities**< TSeq >
- class **AgentsSample**< TSeq >
- void **default\_add\_virus** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_add\_tool** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_add\_entity** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_virus** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_tool** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_entity** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)

**13.6.1 Detailed Description**

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

[Agent](#) (agents)**Template Parameters**

<i>TSeq</i>	Sequence type (should match TSeq across the model)
-------------	----------------------------------------------------

**13.6.2 Member Function Documentation**

### 13.6.2.1 get\_entities()

```
template<typename TSeq >
Entities< TSeq > Agent< TSeq >::get_entities [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

<i>j</i>	
----------	--

#### Returns

double&

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

- epiworld.hpp

## 13.7 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, bool truncate=false)`
- `AgentsSample(Model< TSeq > *model, Entity< TSeq > &entity_, size_t n, bool truncate=false)`
- `AgentsSample(Model< TSeq > *model, Agent< TSeq > &agent_, size_t n, 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`

### 13.7.1 Detailed Description

```
template<typename TSeq>
class AgentsSample< TSeq >
```

Sample of agents.

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

Template Parameters

<i>TSeq</i>	
-------------	--

### 13.7.2 Constructor & Destructor Documentation

#### 13.7.2.1 AgentsSample()

```
template<typename TSeq >
AgentsSample< TSeq >::AgentsSample (
    Model< TSeq > * model,
    Agent< TSeq > & agent_,
    size_t n,
    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

<i>TSeq</i>	
-------------	--

Parameters

<i>agent_</i>	
<i>n</i>	Sample size
<i>truncate</i>	If the agent has fewer than <i>n</i> connections, then <i>truncate</i> = 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



## 13.8 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, bool truncate=false)
- [AgentsSample](#) ([Model](#)< TSeq > \*model, [Entity](#)< TSeq > &entity\_, size\_t n, bool truncate=false)
- [AgentsSample](#) ([Model](#)< TSeq > \*model, [Agent](#)< TSeq > &agent\_, size\_t n, 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

### 13.8.1 Detailed Description

```
template<typename TSeq>
class epiworld::AgentsSample< TSeq >
```

Sample of agents.

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

#### Template Parameters

<i>TSeq</i>	
-------------	--

### 13.8.2 Constructor & Destructor Documentation

#### 13.8.2.1 AgentsSample()

```
template<typename TSeq >
AgentsSample< TSeq >::AgentsSample (
    Model< TSeq > * model,
```

```

Agent< TSeq > & agent_,
size_t n,
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

<i>TSeq</i>	
-------------	--

#### Parameters

<i>agent</i> ↔	
—	
<i>n</i>	Sample size
<i>truncate</i>	If the agent has fewer than <i>n</i> connections, then <i>truncate</i> = 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

## 13.9 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\_variant** (*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 **set\_model** (*Model*< TSeq > &m)
- *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\_variant\_info, std::string fn\_variant\_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) const
- void **record\_transmission** (int i, int j, int variant, int i\_expo\_date)
- size\_t **get\_n\_variants** () const

- `size_t get_n_tools ()` const
- `void reset ()`
- `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 > transition_probability (bool print=true)` const

*Calculates the transition probabilities.*

### Get recorded information from the model

#### Parameters

what	<i>std::string, The status, e.g., 0, 1, 2, ...</i>
------	----------------------------------------------------

#### Returns

*In get\_today\_total, the current counts of what.*

*In get\_today\_variant, the current counts of what for each variant.*

*In get\_hist\_total, the time series of what*

*In get\_hist\_variant, the time series of what for each variant.*

*In get\_hist\_total\_date and get\_hist\_variant\_date the corresponding dates*

- `int get_today_total (std::string what)` const
  - `int get_today_total (epiworld_fast_uint what)` const
  - `void get_today_total (std::vector< std::string > *status=nullptr, std::vector< int > *counts=nullptr)` const
  - `void get_today_variant (std::vector< std::string > &status, std::vector< int > &id, std::vector< int > &counts)` const
  - `void get_hist_total (std::vector< int > *date, std::vector< std::string > *status, std::vector< int > *counts)` const
  - `void get_hist_variant (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &status, std::vector< int > &counts)` const
- 
- `MapVec_type< int, int > reproductive_number ()` const
- Computes the reproductive number of each case.*
- `void reproductive_number (std::string fn)` const

### Friends

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

## 13.9.1 Detailed Description

```
template<typename TSeq>
class DataBase< TSeq >
```

Statistical data about the process.

## Template Parameters

<i>TSeq</i>	
-------------	--

## 13.9.2 Member Function Documentation

### 13.9.2.1 record\_variant()

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

Registering a new variant.

## Parameters

<i>v</i>	Pointer to the new variant. Since variants are originated in the agent, the numbers simply move around. From the parent variant to the new variant. And the total number of infected does not change.
----------	-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

### 13.9.2.2 reproductive\_number()

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

Computes the reproductive number of each case.

By definition, whereas it computes  $R_0$  (basic reproductive number) or  $R_t/R$  (the effective reproductive number) will depend on whether the virus is allowed to circulate naïvely or not, respectively.

## Parameters

<i>fn</i>	File where to write out the reproductive number.
-----------	--------------------------------------------------

### 13.9.2.3 transition\_probability()

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

Calculates the transition probabilities.

## Returns

std::vector< epiworld\_double >

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

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

## 13.10 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\_variant** ([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 **set\_model** ([Model](#)< TSeq > &m)
- [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\_variant\_info, std::string fn\_variant\_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) const
- void **record\_transmission** (int i, int j, int variant, int i\_expo\_date)
- size\_t **get\_n\_variants** () const
- size\_t **get\_n\_tools** () const
- void **reset** ()
- 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 > **transition\_probability** (bool print=true) const  
*Calculates the transition probabilities.*

### Get recorded information from the model

#### Parameters

what	std::string, The status, e.g., 0, 1, 2, ...
------	---------------------------------------------

**Returns**

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

*In `get_today_variant`, the current counts of what for each variant.*

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

*In `get_hist_variant`, the time series of what for each variant.*

*In `get_hist_total_date` and `get_hist_variant_date` the corresponding dates*

- int **get\_today\_total** (std::string what) const
  - int **get\_today\_total** (epiworld\_fast\_uint what) const
  - void **get\_today\_total** (std::vector< std::string > \*status=nullptr, std::vector< int > \*counts=nullptr) const
  - void **get\_today\_variant** (std::vector< std::string > &status, std::vector< int > &id, std::vector< int > &counts) const
  - void **get\_hist\_total** (std::vector< int > \*date, std::vector< std::string > \*status, std::vector< int > \*counts) const
  - void **get\_hist\_variant** (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &status, std::vector< int > &counts) const
- 
- MapVec\_type< int, int > **reproductive\_number** () const  
*Computes the reproductive number of each case.*
  - void **reproductive\_number** (std::string fn) const

**Friends**

- class **Model**< TSeq >
- void **default\_add\_virus** (Action< TSeq > &a, Model< TSeq > \*m)
- void **default\_add\_tool** (Action< TSeq > &a, Model< TSeq > \*m)
- void **default\_rm\_virus** (Action< TSeq > &a, Model< TSeq > \*m)
- void **default\_rm\_tool** (Action< TSeq > &a, Model< TSeq > \*m)

**13.10.1 Detailed Description**

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

Statistical data about the process.

**Template Parameters**

<i>TSeq</i>	
-------------	--

**13.10.2 Member Function Documentation**

### 13.10.2.1 record\_variant()

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

Registering a new variant.

#### Parameters

<i>v</i>	Pointer to the new variant. Since variants are originated in the agent, the numbers simply move around. From the parent variant to the new variant. And the total number of infected does not change.
----------	-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

### 13.10.2.2 reproductive\_number()

```
template<typename TSeq >
MapVec_type< int, int > DataBase< TSeq >::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

<i>fn</i>	File where to write out the reproductive number.
-----------	--------------------------------------------------

### 13.10.2.3 transition\_probability()

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

Calculates the transition probabilities.

#### Returns

`std::vector< epiworld_double >`

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

- epiworld.hpp

## 13.11 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

### Friends

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

#### 13.11.1 Detailed Description

```
template<typename TSeq>
class Entities< TSeq >
```

Set of [Entities](#) (useful for building iterators)

Template Parameters

<i>TSeq</i>	
-------------	--

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

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

## 13.12 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



## Friends

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

### 13.12.1 Detailed Description

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

Set of [Entities](#) (useful for building iterators)

Template Parameters

<i>TSeq</i>	
-------------	--

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

- epiworld.hpp

## 13.13 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

## Friends

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

### 13.13.1 Detailed Description

```
template<typename TSeq>
class Entities_const< TSeq >
```

Set of [Entities](#) (const) (useful for iterators)

## Template Parameters

<i>TSeq</i>	
-------------	--

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

- include/epiworld/entities-bones.hpp

## 13.14 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

### Friends

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

#### 13.14.1 Detailed Description

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

Set of [Entities](#) (const) (useful for iterators)

## Template Parameters

<i>TSeq</i>	
-------------	--

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

- epiworld.hpp

## 13.15 Entity< TSeq > Class Template Reference

### Public Member Functions

- **Entity** (std::string name)
- void **add\_agent** ([Agent](#)< TSeq > &p, [Model](#)< TSeq > \*model)
- void **add\_agent** ([Agent](#)< TSeq > \*p, [Model](#)< TSeq > \*model)
- void **rm\_agent** (size\_t idx)
- size\_t **size** () const noexcept
- void **set\_location** (std::vector< epiworld\_double > loc)
- std::vector< epiworld\_double > & **get\_location** ()
- std::vector< [Agent](#)< TSeq > \* >::iterator **begin** ()
- std::vector< [Agent](#)< TSeq > \* >::iterator **end** ()
- std::vector< [Agent](#)< TSeq > \* >::const\_iterator **begin** () const
- std::vector< [Agent](#)< TSeq > \* >::const\_iterator **end** () const
- [Agent](#)< TSeq > \* **operator[]** (size\_t i)
- int **get\_id** () const noexcept
- const std::string & **get\_name** () const noexcept
- void **set\_status** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **set\_queue** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **get\_status** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)
- void **get\_queue** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)

### Friends

- class **Agent**< TSeq >
- class **AgentsSample**< TSeq >
- class **Model**< TSeq >
- void **default\_add\_entity** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_entity** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)

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

## 13.16 epiworld::Entity< TSeq > Class Template Reference

### Public Member Functions

- **Entity** (std::string name)
- void **add\_agent** ([Agent](#)< TSeq > &p, [Model](#)< TSeq > \*model)
- void **add\_agent** ([Agent](#)< TSeq > \*p, [Model](#)< TSeq > \*model)
- void **rm\_agent** (size\_t idx)
- size\_t **size** () const noexcept
- void **set\_location** (std::vector< epiworld\_double > loc)
- std::vector< epiworld\_double > & **get\_location** ()
- std::vector< [Agent](#)< TSeq > \* >::iterator **begin** ()
- std::vector< [Agent](#)< TSeq > \* >::iterator **end** ()

- `std::vector< Agent< TSeq > * >::const_iterator begin () const`
- `std::vector< Agent< TSeq > * >::const_iterator end () const`
- `Agent< TSeq > * operator[] (size_t i)`
- `int get_id () const noexcept`
- `const std::string & get_name () const noexcept`
- `void set_status (epiworld_fast_int init, epiworld_fast_int post)`
- `void set_queue (epiworld_fast_int init, epiworld_fast_int post)`
- `void get_status (epiworld_fast_int *init, epiworld_fast_int *post)`
- `void get_queue (epiworld_fast_int *init, epiworld_fast_int *post)`

## Friends

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

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

- `epiworld.hpp`

## 13.17 epiworld::LFMCMC< TData > Class Template Reference

Likelihood-Free Markov Chain Monte Carlo.

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

### Public Member Functions

- `void run (std::vector< epiworld_double > param_init, size_t n_samples_, epiworld_double epsilon_)`
- `LFMCMC (TData &observed_data_)`
- `void set_observed_data (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)`
- `size_t get_n_samples () const`
- `size_t get_n_statistics () const`
- `size_t get_n_parameters () const`
- `epiworld_double get_epsilon () const`
- `const std::vector< epiworld_double > & get_params_now ()`
- `const std::vector< epiworld_double > & get_params_prev ()`
- `const std::vector< epiworld_double > & get_params_init ()`
- `const std::vector< epiworld_double > & get_statistics_obs ()`
- `const std::vector< epiworld_double > & get_statistics_hist ()`
- `const std::vector< bool > & get_statistics_accepted ()`
- `const std::vector< epiworld_double > & get_posterior_if_prob ()`
- `const std::vector< epiworld_double > & get_drawn_prob ()`
- `std::vector< TData > * get_sampled_data ()`
- `void set_par_names (std::vector< std::string > names)`
- `void set_stats_names (std::vector< std::string > names)`
- `std::vector< epiworld_double > get_params_mean ()`
- `std::vector< epiworld_double > get_stats_mean ()`
- `void print ()`

### Random number generation

*Parameters*

eng	
-----	--

- void **set\_rand\_engine** (std::mt19937 &eng)
- std::mt19937 \* **get\_rand\_engine** ()
- 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)

**13.17.1 Detailed Description**

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

Likelihood-Free Markov Chain Monte Carlo.

*Template Parameters*

<i>TData</i>	Type of data that is generated
--------------	--------------------------------

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

- epiworld.hpp

**13.18 LFMCMC< TData > Class Template Reference**

Likelihood-Free Markov Chain Monte Carlo.

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

**Public Member Functions**

- void **run** (std::vector< epiworld\_double > param\_init, size\_t n\_samples\_, epiworld\_double epsilon\_)
- **LFMCMC** (TData &observed\_data\_)
- void **set\_observed\_data** (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)
- size\_t **get\_n\_samples** () const
- size\_t **get\_n\_statistics** () const
- size\_t **get\_n\_parameters** () const
- epiworld\_double **get\_epsilon** () const

- `const std::vector< epiworld_double > & get_params_now ()`
- `const std::vector< epiworld_double > & get_params_prev ()`
- `const std::vector< epiworld_double > & get_params_init ()`
- `const std::vector< epiworld_double > & get_statistics_obs ()`
- `const std::vector< epiworld_double > & get_statistics_hist ()`
- `const std::vector< bool > & get_statistics_accepted ()`
- `const std::vector< epiworld_double > & get_posterior_if_prob ()`
- `const std::vector< epiworld_double > & get_drawn_prob ()`
- `std::vector< TData > * get_sampled_data ()`
- `void set_par_names (std::vector< std::string > names)`
- `void set_stats_names (std::vector< std::string > names)`
- `std::vector< epiworld_double > get_params_mean ()`
- `std::vector< epiworld_double > get_stats_mean ()`
- `void print ()`

### Random number generation

#### Parameters

eng	
-----	--

- `void set_rand_engine (std::mt19937 &eng)`
- `std::mt19937 * get_rand_engine ()`
- `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)`

## 13.18.1 Detailed Description

```
template<typename TData>
class LFMCMC< TData >
```

Likelihood-Free Markov Chain Monte Carlo.

#### Template Parameters

<i>TData</i>	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`

## 13.19 epiworld::Model< TSeq > Class Template Reference

Core class of epiworld.

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

### Public Member Functions

- [DataBase](#)< TSeq > & **get\_db** ()
- 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.*
- size\_t **get\_n\_variants** () const
- size\_t **get\_n\_tools** () const
- epiworld\_fast\_uint **get\_ndays** () const
- epiworld\_fast\_uint **get\_n\_replicates** () const
- void **set\_ndays** (epiworld\_fast\_uint ndays)
- bool **get\_verbose** () const
- void **verbose\_off** ()
- void **verbose\_on** ()
- int [today](#) () const  
*The current time of the model.*
- void [write\\_data](#) (std::string fn\_variant\_info, std::string fn\_variant\_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) const  
*Wrapper of DataBase::write\_data*
- std::map< std::string, epiworld\_double > & **params** ()
- void [reset](#) ()  
*Reset the model.*
- void **print** () const
- [Model](#)< TSeq > && **clone** () 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\\_global\\_action](#) (std::function< void([Model](#)< TSeq > \*)> fun, int date=-99)  
*Set a global action.*
- void **run\_global\_actions** ()
- void **clear\_status\_set** ()
- const std::vector< VirusPtr< TSeq > > & **get\_viruses** () const
- const std::vector< ToolPtr< TSeq > > & **get\_tools** () const
- void [set\\_agents\\_data](#) (double \*data\_, size\_t ncols\_)  
*Set the agents data object.*
- void [set\\_name](#) (std::string name)  
*Set the name object.*
- std::string **get\_name** () const

### 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** ()
- void **restore\_backup** ()

### Random number generation

*Parameters*

eng	<i>Random number generator</i>
s	<i>Seed</i>

- void **set\_rand\_engine** (std::mt19937 &eng)
- std::mt19937 \* **get\_rand\_engine** ()
- void **seed** (epiworld\_fast\_uint 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)
- 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)

**Add Virus/Tool to the model**

*This is done before the model has been initialized.*

*Parameters*

v	<i><a href="#">Virus</a> to be added</i>
t	<i><a href="#">Tool</a> to be added</i>
preval	<i>Initial prevalence (initial state.) It can be specified as a proportion (between zero and one,) or an integer indicating number of individuals.</i>

- void **add\_virus** ([Virus](#)< TSeq > v, epiworld\_double preval)
- void **add\_virus\_n** ([Virus](#)< TSeq > v, epiworld\_fast\_uint preval)
- void **add\_virus\_fun** ([Virus](#)< TSeq > v, VirusToAgentFun< TSeq > fun)
- void **add\_tool** ([Tool](#)< TSeq > t, epiworld\_double preval)
- void **add\_tool\_n** ([Tool](#)< TSeq > t, epiworld\_fast\_uint preval)
- void **add\_tool\_fun** ([Tool](#)< TSeq > t, ToolToAgentFun< TSeq > fun)
- void **add\_entity** ([Entity](#)< TSeq > e, epiworld\_double preval)
- void **add\_entity\_n** ([Entity](#)< TSeq > e, epiworld\_fast\_uint preval)
- void **add\_entity\_fun** ([Entity](#)< TSeq > e, EntityToAgentFun< TSeq > fun)

**Accessing population of the model***Parameters*

fn	<i>std::string Filename of the edgelist file.</i>
skip	<i>int Number of lines to skip in <i>fn</i>.</i>
directed	<i>bool Whether the graph is directed or not.</i>
size	<i>Size of the network.</i>
al	<i><a href="#">AdjList</a> to read into the model.</i>



- void **agents\_from\_adjlist** (std::string fn, int size, int skip=0, bool directed=false)
- void **agents\_from\_adjlist** (AdjList al)
- bool **is\_directed** () const
- std::vector< Agent< TSeq > > \* **get\_agents** ()
- void **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	<i>Seed to be used for Pseudo-RNG.</i>
ndays	<i>Number of days (steps) of the simulation.</i>
fun	<i>In the case of <code>run_multiple</code>, a function that is called after each experiment.</i>

- void **init** (epiworld\_fast\_uint ndays, epiworld\_fast\_uint seed)
  - void **update\_status** ()
  - void **mutate\_variant** ()
  - void **next** ()
  - void **run** ()
- Runs the simulation (after initialization)*
- void **run\_multiple** (epiworld\_fast\_uint nexperiments, 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  $\{(i,j), (k,l)\} \rightarrow \{(i,l), (k,j)\}$ , the reciprocal is also true, i.e.,  $\{(j,i), (l,k)\} \rightarrow \{(j,k), (l,i)\}$ .*

#### Parameters

proportion	<i>Proportion of ties to be rewired.</i>
------------	------------------------------------------

#### 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	<i>std::string. File name.</i>
source	<i>Integer vector</i>
target	<i>Integer vector</i>

*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< epiworld\_fast\_uint > &source, std::vector< epiworld\_fast\_uint > &target) const

### Manage status (states) in the model

The functions `get_status` return the current values for the statuses included in the model.

#### Parameters

lab	<i>std::string</i> Name of the status.
-----	----------------------------------------

#### Returns

`add_status*` returns nothing.  
`get_status*` returns a vector of pairs with the statuses and their labels.

- void **add\_status** (std::string lab, UpdateFun< TSeq > fun=nullptr)
- const std::vector< std::string > & **get\_status** () const
- const std::vector< UpdateFun< TSeq > > & **get\_status\_fun** () const
- void **print\_status\_codes** () const

### Set the user data object

#### Parameters

names	<i>string</i> 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 **queueing\_on** ()  
*Activates the queueing system (default.)*
- void **queueing\_off** ()  
*Deactivates the queueing system.*
- bool **is\_queueing\_on** () const  
*Query if the queueing 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)

### 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.

- std::vector< epiworld\_double > **array\_double\_tmp**
- std::vector< [Virus](#)< TSeq > \* > **array\_virus\_tmp**
- **Model** ()
- **Model** (const [Model](#)< TSeq > &m)
- **Model** ([Model](#)< TSeq > &&m)
- [Model](#)< TSeq > & **operator=** (const [Model](#)< TSeq > &m)
- void **clone\_population** (std::vector< [Agent](#)< TSeq > > &other\_population, std::vector< [Entity](#)< TSeq > > &other\_entities, [Model](#)< TSeq > \*other\_model, bool &other\_directed) const
- void **clone\_population** (const [Model](#)< TSeq > &other\_model)

### 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

<i>initial_val</i>	
<i>pname</i>	Name of the parameter to add or to fetch
<i>fn</i>	Path to the file containing parameters

## Returns

The current value of the parameter in the model.

- `epiworld_double * p0`
- `epiworld_double * p1`
- `epiworld_double * p2`
- `epiworld_double * p3`
- `epiworld_double * p4`
- `epiworld_double * p5`
- `epiworld_double * p6`
- `epiworld_double * p7`
- `epiworld_double * p8`
- `epiworld_double * p9`
- `epiworld_double * p10`
- `epiworld_double * p11`
- `epiworld_double * p12`
- `epiworld_double * p13`
- `epiworld_double * p14`
- `epiworld_double * p15`
- `epiworld_double * p16`
- `epiworld_double * p17`
- `epiworld_double * p18`
- `epiworld_double * p19`
- `epiworld_double * p20`
- `epiworld_double * p21`
- `epiworld_double * p22`
- `epiworld_double * p23`
- `epiworld_double * p24`
- `epiworld_double * p25`
- `epiworld_double * p26`
- `epiworld_double * p27`
- `epiworld_double * p28`
- `epiworld_double * p29`
- `epiworld_double * p30`
- `epiworld_double * p31`
- `epiworld_double * p32`
- `epiworld_double * p33`
- `epiworld_double * p34`
- `epiworld_double * p35`
- `epiworld_double * p36`
- `epiworld_double * p37`
- `epiworld_double * p38`
- `epiworld_double * p39`
- `epiworld_fast_uint npar_used = 0u`
- `epiworld_double add_param (epiworld_double initial_val, std::string pname)`
- `void read_params (std::string fn)`
- `epiworld_double get_param (epiworld_fast_uint k)`
- `epiworld_double get_param (std::string pname)`
- `epiworld_double par (epiworld_fast_uint k)`
- `epiworld_double par (std::string pname)`

### 13.19.1 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

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

### 13.19.2 Member Function Documentation

#### 13.19.2.1 add\_global\_action()

```
template<typename TSeq >
void Model< TSeq >::add_global_action (
    std::function< void(Model< TSeq > *)> fun,
    int date = -99 ) [inline]
```

Set a global action.

#### Parameters

<i>fun</i>	A function to be called on the prescribed dates
<i>date</i>	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.

#### 13.19.2.2 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

<i>fn</i>	Path to the file.
<i>skip</i>	How many rows to skip.

**13.19.2.3 reset()**

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

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

**13.19.2.4 run\_multiple()**

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

## Parameters

<i>n_experiments</i>	Multiple runs of the simulation
----------------------	---------------------------------

**13.19.2.5 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

<i>data</i> ↔ _	Pointer to the first element of an array of size <code>size() * ncols_</code> .
<i>ncols</i> ↔ _	Number of features included in the data.

#### 13.19.2.6 set\_name()

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

Set the name object.

#### Parameters

<i>name</i>	
-------------	--

#### 13.19.2.7 write\_data()

```
template<typename TSeq >
void Model< TSeq >::write_data (
    std::string fn_variant_info,
    std::string fn_variant_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 ) const [inline]
```

Wrapper of `DataBase::write_data`

#### Parameters

<i>fn_variant_info</i>	Filename. Information about the variant.
<i>fn_variant_hist</i>	Filename. History of the variant.
<i>fn_tool_info</i>	Filename. Information about the tool.
<i>fn_tool_hist</i>	Filename. History of the tool.
<i>fn_total_hist</i>	Filename. Aggregated history (status)
<i>fn_transmission</i>	Filename. Transmission history.
<i>fn_transition</i>	Filename. Markov transition history.
<i>fn_reproductive_number</i>	Filename. Case by case reproductive number

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

- epiworld.hpp

## 13.20 Model< TSeq > Class Template Reference

Core class of epiworld.

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

### Public Member Functions

- [DataBase](#)< TSeq > & **get\_db** ()
- 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.*
- size\_t **get\_n\_variants** () const
- size\_t **get\_n\_tools** () const
- epiworld\_fast\_uint **get\_ndays** () const
- epiworld\_fast\_uint **get\_n\_replicates** () const
- void **set\_ndays** (epiworld\_fast\_uint ndays)
- bool **get\_verbose** () const
- void **verbose\_off** ()
- void **verbose\_on** ()
- int [today](#) () const  
*The current time of the model.*
- void [write\\_data](#) (std::string fn\_variant\_info, std::string fn\_variant\_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) const  
*Wrapper of DataBase::write\_data*
- std::map< std::string, epiworld\_double > & **params** ()
- void [reset](#) ()  
*Reset the model.*
- void **print** () const
- [Model](#)< TSeq > && **clone** () 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\\_global\\_action](#) (std::function< void([Model](#)< TSeq > \*)> fun, int date=-99)  
*Set a global action.*
- void **run\_global\_actions** ()
- void **clear\_status\_set** ()
- const std::vector< VirusPtr< TSeq > > & **get\_viruses** () const
- const std::vector< ToolPtr< TSeq > > & **get\_tools** () const
- void [set\\_agents\\_data](#) (double \*data\_, size\_t ncols\_)  
*Set the agents data object.*
- void [set\\_name](#) (std::string name)  
*Set the name object.*
- std::string **get\_name** () const



### 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** ()
- void **restore\_backup** ()

### Random number generation

#### Parameters

eng	Random number generator
s	Seed

- void **set\_rand\_engine** (std::mt19937 &eng)
- std::mt19937 \* **get\_rand\_engine** ()
- void **seed** (epiworld\_fast\_uint 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)
- 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)

### Add Virus/Tool to the model

*This is done before the model has been initialized.*

#### Parameters

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

- void **add\_virus** (Virus< TSeq > v, epiworld\_double preval)
- void **add\_virus\_n** (Virus< TSeq > v, epiworld\_fast\_uint preval)
- void **add\_virus\_fun** (Virus< TSeq > v, VirusToAgentFun< TSeq > fun)
- void **add\_tool** (Tool< TSeq > t, epiworld\_double preval)
- void **add\_tool\_n** (Tool< TSeq > t, epiworld\_fast\_uint preval)
- void **add\_tool\_fun** (Tool< TSeq > t, ToolToAgentFun< TSeq > fun)
- void **add\_entity** (Entity< TSeq > e, epiworld\_double preval)
- void **add\_entity\_n** (Entity< TSeq > e, epiworld\_fast\_uint preval)
- void **add\_entity\_fun** (Entity< TSeq > e, EntityToAgentFun< TSeq > fun)

### Accessing population of the model

*Parameters*

fn	<i>std::string Filename of the edgelist file.</i>
skip	<i>int Number of lines to skip in <math>fn</math>.</i>
directed	<i>bool Whether the graph is directed or not.</i>
size	<i>Size of the network.</i>
al	<i><a href="#">AdjList</a> to read into the model.</i>

- void **agents\_from\_adjlist** (std::string fn, int size, int skip=0, bool directed=false)
- void **agents\_from\_adjlist** ([AdjList](#) al)
- bool **is\_directed** () const
- std::vector< [Agent](#)< TSeq > > \* **get\_agents** ()
- void **agents\_smallworld** (epiworld\_fast\_uint n=1000, epiworld\_fast\_uint k=5, bool d=false, epiworld\_fast\_uint p=.01)
- void **agents\_empty\_graph** (epiworld\_fast\_uint n=1000)

**Functions to run the model***Parameters*

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

- void **init** (epiworld\_fast\_uint ndays, epiworld\_fast\_uint seed)
- void **update\_status** ()
- void **mutate\_variant** ()
- void **next** ()
- void **run** ()  
*Runs the simulation (after initialization)*
- void **run\_multiple** (epiworld\_fast\_uint nexperiments, 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  $\{(i,j), (k,l)\} \rightarrow \{(i,l), (k,j)\}$ , the reciprocal is also true, i.e.,  $\{(j,i), (l,k)\} \rightarrow \{(j,k), (l,i)\}$ .*

*Parameters*

proportion	<i>Proportion of ties to be rewired.</i>
------------	------------------------------------------

*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	<i>std::string. File name.</i>
source	<i>Integer vector</i>
target	<i>Integer vector</i>

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< epiworld\_fast\_uint > &source, std::vector< epiworld\_fast\_uint > &target) const

**Manage status (states) in the model**

The functions *get\_status* return the current values for the statuses included in the model.

*Parameters*

lab	<i>std::string Name of the status.</i>
-----	----------------------------------------

*Returns*

*add\_status\** returns nothing.

*get\_status\_\** returns a vector of pairs with the statuses and their labels.

- void **add\_status** (std::string lab, UpdateFun< TSeq > fun=nullptr)
- const std::vector< std::string > & **get\_status** () const
- const std::vector< UpdateFun< TSeq > > & **get\_status\_fun** () const
- void **print\_status\_codes** () const

**Set the user data object***Parameters*

names	<i>string vector with the names of the variables.</i>
-------	-------------------------------------------------------

- 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 **queueing\_on** ()  
Activates the queueing system (default.)
- void **queueing\_off** ()  
Deactivates the queueing system.
- bool **is\_queueing\_on** () const  
Query if the queueing 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)

### 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.

- std::vector< epiworld\_double > **array\_double\_tmp**
- std::vector< [Virus](#)< TSeq > \* > **array\_virus\_tmp**
- **Model** ()
- **Model** (const [Model](#)< TSeq > &m)
- **Model** ([Model](#)< TSeq > &&m)
- [Model](#)< TSeq > & **operator=** (const [Model](#)< TSeq > &m)
- void **clone\_population** (std::vector< [Agent](#)< TSeq > > &other\_population, std::vector< [Entity](#)< TSeq > > &other\_entities, [Model](#)< TSeq > \*other\_model, bool &other\_directed) const
- void **clone\_population** (const [Model](#)< TSeq > &other\_model)

### 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

<i>initial_val</i>	
<i>pname</i>	Name of the parameter to add or to fetch
<i>fn</i>	Path to the file containing parameters

## Returns

The current value of the parameter in the model.

- `epiworld_double * p0`
- `epiworld_double * p1`
- `epiworld_double * p2`
- `epiworld_double * p3`
- `epiworld_double * p4`
- `epiworld_double * p5`
- `epiworld_double * p6`
- `epiworld_double * p7`
- `epiworld_double * p8`
- `epiworld_double * p9`
- `epiworld_double * p10`
- `epiworld_double * p11`
- `epiworld_double * p12`
- `epiworld_double * p13`
- `epiworld_double * p14`
- `epiworld_double * p15`
- `epiworld_double * p16`
- `epiworld_double * p17`
- `epiworld_double * p18`
- `epiworld_double * p19`
- `epiworld_double * p20`
- `epiworld_double * p21`
- `epiworld_double * p22`
- `epiworld_double * p23`
- `epiworld_double * p24`
- `epiworld_double * p25`
- `epiworld_double * p26`
- `epiworld_double * p27`
- `epiworld_double * p28`
- `epiworld_double * p29`
- `epiworld_double * p30`
- `epiworld_double * p31`
- `epiworld_double * p32`
- `epiworld_double * p33`
- `epiworld_double * p34`
- `epiworld_double * p35`
- `epiworld_double * p36`
- `epiworld_double * p37`
- `epiworld_double * p38`
- `epiworld_double * p39`
- `epiworld_fast_uint npar_used = 0u`
- `epiworld_double add_param (epiworld_double initial_val, std::string pname)`
- `void read_params (std::string fn)`
- `epiworld_double get_param (epiworld_fast_uint k)`
- `epiworld_double get_param (std::string pname)`
- `epiworld_double par (epiworld_fast_uint k)`
- `epiworld_double par (std::string pname)`

### 13.20.1 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

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

### 13.20.2 Member Function Documentation

#### 13.20.2.1 add\_global\_action()

```
template<typename TSeq >
void Model< TSeq >::add_global_action (
    std::function< void(Model< TSeq > *)> fun,
    int date = -99 ) [inline]
```

Set a global action.

#### Parameters

<i>fun</i>	A function to be called on the prescribed dates
<i>date</i>	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.

#### 13.20.2.2 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

<i>fn</i>	Path to the file.
<i>skip</i>	How many rows to skip.

**13.20.2.3 reset()**

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

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

**13.20.2.4 run\_multiple()**

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

## Parameters

<i>n_experiments</i>	Multiple runs of the simulation
----------------------	---------------------------------

**13.20.2.5 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

<i>data</i> ↔ _	Pointer to the first element of an array of size <code>size() * ncols_</code> .
<i>ncols</i> ↔ _	Number of features included in the data.

### 13.20.2.6 set\_name()

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

Set the name object.

#### Parameters

<i>name</i>	
-------------	--

### 13.20.2.7 write\_data()

```
template<typename TSeq >
void Model< TSeq >::write_data (
    std::string fn_variant_info,
    std::string fn_variant_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 ) const [inline]
```

Wrapper of `DataBase::write_data`

#### Parameters

<i>fn_variant_info</i>	Filename. Information about the variant.
<i>fn_variant_hist</i>	Filename. History of the variant.
<i>fn_tool_info</i>	Filename. Information about the tool.
<i>fn_tool_hist</i>	Filename. History of the tool.
<i>fn_total_hist</i>	Filename. Aggregated history (status)
<i>fn_transmission</i>	Filename. Transmission history.
<i>fn_transition</i>	Filename. Markov transition history.
<i>fn_reproductive_number</i>	Filename. Case by case reproductive number



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

## 13.21 epiworld::epimodels::ModelSEIR< TSeq > Class Template Reference

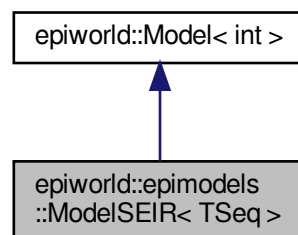
Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

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

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



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



### Public Member Functions

- **ModelSEIR** ([ModelSEIR](#)< TSeq > &model, std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double incubation\_days, epiworld\_double recovery)
- **ModelSEIR** (std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double incubation\_days, epiworld\_double recovery)

## Public Attributes

- `epiworld::UpdateFun< TSeq >` **update\_exposed\_seir**
- `epiworld::UpdateFun< TSeq >` **update\_infected\_seir**

### 13.21.1 Detailed Description

```
template<typename TSeq = int>
class epiworld::epimodels::ModelSEIR< TSeq >
```

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

#### Parameters

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

### 13.21.2 Member Data Documentation

#### 13.21.2.1 update\_exposed\_seir

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

##### Initial value:

```
= [] (
    epiworld::Agent<TSeq> * p,
    epiworld::Model<TSeq> * m
) -> void {
    if (m->runif() < 1.0/(*m->p1))
        p->change_status(m, ModelSEIR<TSeq>::INFECTED);
    return;
}
```

#### 13.21.2.2 update\_infected\_seir

```
template<typename TSeq = int>
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->p2))
        p->rm_virus(0, m);
    return;
}
```

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

- `epiworld.hpp`

## 13.22 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, std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double incubation\_days, epiworld\_double recovery)
- **ModelSEIR** (std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double incubation\_days, epiworld\_double recovery)

### Public Attributes

- epiworld::UpdateFun< TSeq > **update\_exposed\_seir**
- epiworld::UpdateFun< TSeq > **update\_infected\_seir**

#### 13.22.1 Detailed Description

```
template<typename TSeq = int>
class ModelSEIR< TSeq >
```

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

## Parameters

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

## 13.22.2 Member Data Documentation

### 13.22.2.1 update\_exposed\_seir

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

## Initial value:

```
= [] (
    epiworld::Agent<TSeq> * p,
    epiworld::Model<TSeq> * m
) -> void {
    if (m->runif() < 1.0/(*m->p1))
        p->change_status(m, ModelSEIR<TSeq>::INFECTED);
    return;
}
```

### 13.22.2.2 update\_infected\_seir

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

## Initial value:

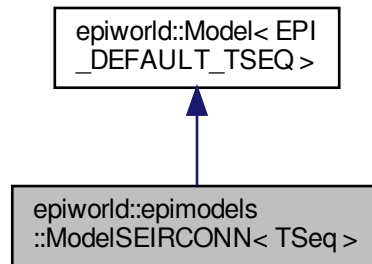
```
= [] (
    epiworld::Agent<TSeq> * p,
    epiworld::Model<TSeq> * m
) -> void {
    if (m->runif() < (*m->p2))
        p->rm_virus(0, m);
    return;
}
```

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

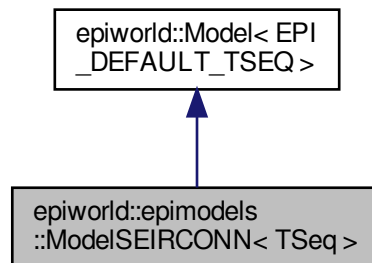
- include/epiworld/models/seir.hpp

## 13.23 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, std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double incubation\_days, epiworld\_double prob\_recovery)  
*Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.*
- **ModelSEIRCONN** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double incubation\_days, epiworld\_double prob\_recovery)

## Public Attributes

- `std::vector< epiworld::Agent<> * > tracked_agents_infected = {}`
- `std::vector< epiworld::Agent<> * > tracked_agents_infected_next = {}`
- `bool tracked_started = false`
- `int tracked_ninfected = 0`
- `int tracked_ninfected_next = 0`

## Static Public Attributes

- `static const int SUSCEPTIBLE = 0`
- `static const int EXPOSED = 1`
- `static const int INFECTED = 2`
- `static const int RECOVERED = 3`

## 13.23.1 Constructor & Destructor Documentation

### 13.23.1.1 ModelSEIRCONN()

```
template<typename TSeq >
ModelSEIRCONN< TSeq >::ModelSEIRCONN (
    ModelSEIRCONN< TSeq > & model,
    std::string vname,
    epiworld_uint n,
    epiworld_double prevalence,
    epiworld_double reproductive_number,
    epiworld_double prob_transmission,
    epiworld_double incubation_days,
    epiworld_double prob_recovery ) [inline]
```

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

#### Parameters

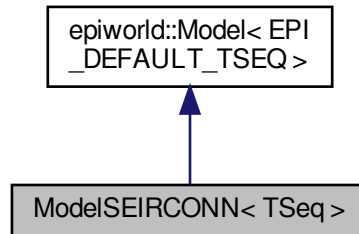
<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>prevalence</i>	Initial prevalence (proportion)
<i>reproductive_number</i>	Reproductive number (beta)
<i>prob_transmission</i>	Probability of transmission
<i>prob_recovery</i>	Probability of recovery

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

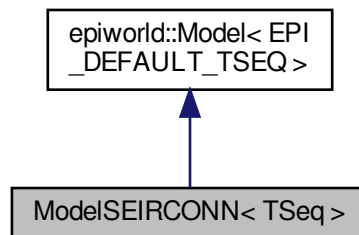
- `epiworld.hpp`

## 13.24 ModelSEIRCONN< TSeq > Class Template Reference

Inheritance diagram for ModelSEIRCONN< TSeq >:



Collaboration diagram for ModelSEIRCONN< TSeq >:



### Public Member Functions

- [ModelSEIRCONN](#) ([ModelSEIRCONN](#)< TSeq > &model, std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double incubation\_days, epiworld\_double prob\_recovery)  
*Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.*
- **ModelSEIRCONN** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double incubation\_days, epiworld\_double prob\_recovery)

### Public Attributes

- std::vector< [epiworld::Agent](#)<> \* > **tracked\_agents\_infected** = {}
- std::vector< [epiworld::Agent](#)<> \* > **tracked\_agents\_infected\_next** = {}
- bool **tracked\_started** = false
- int **tracked\_ninfected** = 0
- int **tracked\_ninfected\_next** = 0

## Static Public Attributes

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

## 13.24.1 Constructor & Destructor Documentation

### 13.24.1.1 ModelSEIRCONN()

```
template<typename TSeq >
ModelSEIRCONN< TSeq >::ModelSEIRCONN (
    ModelSEIRCONN< TSeq > & model,
    std::string vname,
    epiworld_fast_uint n,
    epiworld_double prevalence,
    epiworld_double reproductive_number,
    epiworld_double prob_transmission,
    epiworld_double incubation_days,
    epiworld_double prob_recovery ) [inline]
```

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

#### Parameters

<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>prevalence</i>	Initial prevalence (proportion)
<i>reproductive_number</i>	Reproductive number (beta)
<i>prob_transmission</i>	Probability of transmission
<i>prob_recovery</i>	Probability of recovery

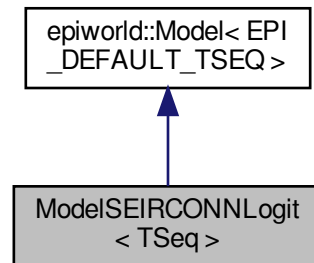
The documentation for this class was generated from the following file:

- include/epiworld/models/seirconnected.hpp

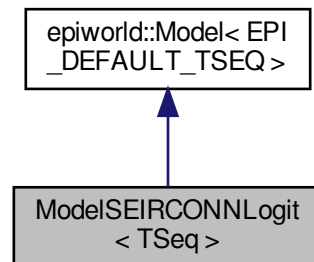


## 13.25 ModelSEIRCONNLogit< TSeq > Class Template Reference

Inheritance diagram for ModelSEIRCONNLogit< TSeq >:



Collaboration diagram for ModelSEIRCONNLogit< TSeq >:



### Public Member Functions

- [ModelSEIRCONNLogit](#) ([ModelSEIRCONNLogit](#)< TSeq > &model, std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double incubation\_days, epiworld\_double prob\_recovery, double \*covars, std::vector< double > logit\_params)

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

- **ModelSEIRCONNLogit** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double incubation\_days, epiworld\_double prob\_recovery double \*covars, std::vector< double > logit\_params)

### Public Attributes

- std::vector< [epiworld::Agent](#)<> \* > **tracked\_agents\_infected** = {}
- std::vector< [epiworld::Agent](#)<> \* > **tracked\_agents\_infected\_next** = {}
- bool **tracked\_started** = false
- int **tracked\_ninfected** = 0
- int **tracked\_ninfected\_next** = 0

## 13.25.1 Constructor & Destructor Documentation

### 13.25.1.1 ModelSEIRCONNLogit()

```
template<typename TSeq >
ModelSEIRCONNLogit< TSeq >::ModelSEIRCONNLogit (
    ModelSEIRCONNLogit< TSeq > & model,
    std::string vname,
    epiworld_fast_uint n,
    epiworld_double prevalence,
    epiworld_double reproductive_number,
    epiworld_double prob_transmission,
    epiworld_double incubation_days,
    epiworld_double prob_recovery,
    double * covars,
    std::vector< double > logit_params ) [inline]
```

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

#### Parameters

<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>prevalence</i>	Initial prevalence (proportion)
<i>reproductive_number</i>	Reproductive number (beta)
<i>prob_transmission</i>	Probability of transmission
<i>prob_recovery</i>	Probability of recovery

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

- include/epiworld/models/seirconnected\_logit.hpp

## 13.26 epiworld::epimodels::ModelSIR< TSeq > Class Template Reference

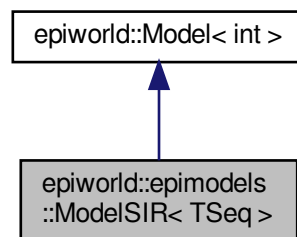
Template for a Susceptible-Infected-Removed (SIR) model.

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

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



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



## Public Member Functions

- **ModelSIR** ([ModelSIR](#)< TSeq > &model, std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double recovery)
- **ModelSIR** (std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double recovery)

## Additional Inherited Members

### 13.26.1 Detailed Description

```

template<typename TSeq = int>
class epiworld::epimodels::ModelSIR< TSeq >

```

Template for a Susceptible-Infected-Removed (SIR) model.

## Parameters

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

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

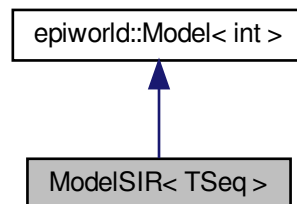
- epiworld.hpp

## 13.27 ModelSIR< TSeq > Class Template Reference

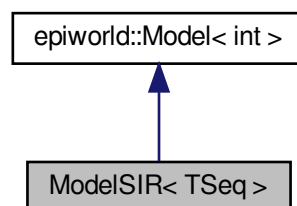
Template for a Susceptible-Infected-Removed (SIR) model.

```
#include <sir.hpp>
```

Inheritance diagram for ModelSIR< TSeq >:



Collaboration diagram for ModelSIR< TSeq >:



## Public Member Functions

- **ModelSIR** ([ModelSIR](#)< TSeq > &model, std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double recovery)
- **ModelSIR** (std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double recovery)

## Additional Inherited Members

### 13.27.1 Detailed Description

```
template<typename TSeq = int>
class ModelSIR< TSeq >
```

Template for a Susceptible-Infected-Removed (SIR) model.

#### Parameters

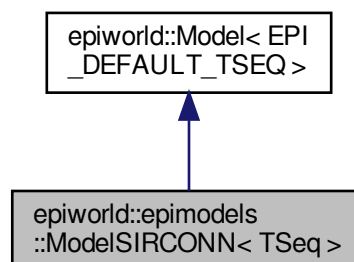
<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>initial_prevalence</i>	epiworld_double Initial prevalence
<i>initial_efficiency</i>	epiworld_double Initial susceptibility_reduction of the immune system
<i>initial_recovery</i>	epiworld_double Initial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

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

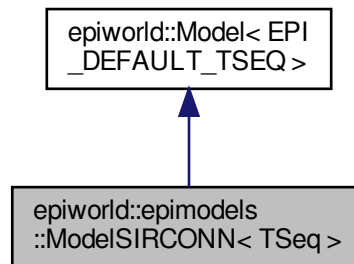
- include/epiworld/models/sir.hpp

## 13.28 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, std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double prob\_recovery)
- *Template for a Susceptible-Infected-Removed (SIR) model.*
- **ModelSIRCONN** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double prob\_recovery)

## Public Attributes

- std::vector< [epiworld::Agent](#)< TSeq > \* > **tracked\_agents\_infected** = {}
- std::vector< [epiworld::Agent](#)< TSeq > \* > **tracked\_agents\_infected\_next** = {}
- bool **tracked\_started** = false
- int **tracked\_ninfected** = 0
- int **tracked\_ninfected\_next** = 0
- epiworld\_double **tracked\_current\_infect\_prob** = 0.0

## 13.28.1 Constructor & Destructor Documentation

### 13.28.1.1 ModelSIRCONN()

```

template<typename TSeq >
ModelSIRCONN< TSeq >::ModelSIRCONN (
    ModelSIRCONN< TSeq > & model,
    std::string vname,
    epiworld_fast_uint n,
    epiworld_double prevalence,
    epiworld_double reproductive_number,
    epiworld_double prob_transmission,
    epiworld_double prob_recovery ) [inline]
  
```

Template for a Susceptible-Infected-Removed (SIR) model.

## Parameters

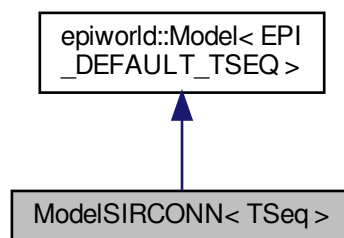
<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>prevalence</i>	Initial prevalence (proportion)
<i>reproductive_number</i>	Reproductive number (beta)
<i>prob_transmission</i>	Probability of transmission
<i>prob_recovery</i>	Probability of recovery

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

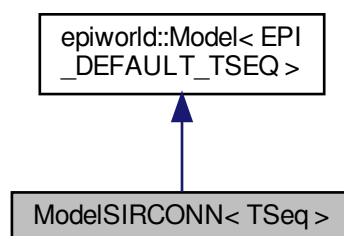
- epiworld.hpp

## 13.29 ModelSIRCONN< TSeq > Class Template Reference

Inheritance diagram for ModelSIRCONN< TSeq >:



Collaboration diagram for ModelSIRCONN< TSeq >:



## Public Member Functions

- [ModelSIRCONN](#) ([ModelSIRCONN](#)< TSeq > &model, std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double prob\_recovery)
- Template for a Susceptible-Infected-Removed (SIR) model.*
- **ModelSIRCONN** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double reproductive\_number, epiworld\_double prob\_transmission, epiworld\_double prob\_recovery)

## Public Attributes

- std::vector< [epiworld::Agent](#) < TSeq > \* > **tracked\_agents\_infected** = {}
- std::vector< [epiworld::Agent](#) < TSeq > \* > **tracked\_agents\_infected\_next** = {}
- bool **tracked\_started** = false
- int **tracked\_ninfected** = 0
- int **tracked\_ninfected\_next** = 0
- epiworld\_double **tracked\_current\_infect\_prob** = 0.0

## 13.29.1 Constructor & Destructor Documentation

### 13.29.1.1 ModelSIRCONN()

```
template<typename TSeq >
ModelSIRCONN< TSeq >::ModelSIRCONN (
    ModelSIRCONN< TSeq > & model,
    std::string vname,
    epiworld_fast_uint n,
    epiworld_double prevalence,
    epiworld_double reproductive_number,
    epiworld_double prob_transmission,
    epiworld_double prob_recovery ) [inline]
```

Template for a Susceptible-Infected-Removed (SIR) model.

#### Parameters

<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>prevalence</i>	Initial prevalence (proportion)
<i>reproductive_number</i>	Reproductive number (beta)
<i>prob_transmission</i>	Probability of transmission
<i>prob_recovery</i>	Probability of recovery

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

- include/epiworld/models/sirconnected.hpp

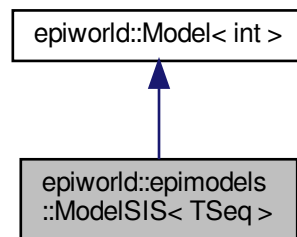


## 13.30 epiworld::epimodels::ModelSIS< TSeq > Class Template Reference

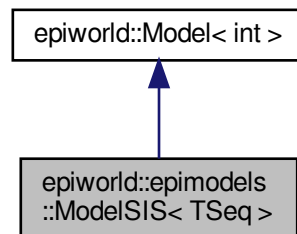
Template for a Susceptible-Infected-Susceptible (SIS) model.

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

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



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



### Public Member Functions

- **ModelSIS** ([ModelSIS](#)< TSeq > &model, std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double recovery)
- **ModelSIS** (std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double recovery)

## Additional Inherited Members

### 13.30.1 Detailed Description

```
template<typename TSeq = int>  
class epiworld::epimodels::ModelSIS< TSeq >
```

Template for a Susceptible-Infected-Susceptible (SIS) model.

## Parameters

<i>vname</i>	std::string Name of the virus
<i>initial_prevalence</i>	epiworld_double Initial prevalence
<i>initial_efficacy</i>	epiworld_double Initial susceptibility_reduction of the immune system
<i>initial_recovery</i>	epiworld_double Initial recovery rate of the immune system

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

- epiworld.hpp

## 13.31 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, std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double recovery)
- **ModelSIS** (std::string vname, epiworld\_double prevalence, epiworld\_double infectiousness, epiworld\_double recovery)

## Additional Inherited Members

### 13.31.1 Detailed Description

```
template<typename TSeq = int>
class ModelSIS< TSeq >
```

Template for a Susceptible-Infected-Susceptible (SIS) model.

#### Parameters

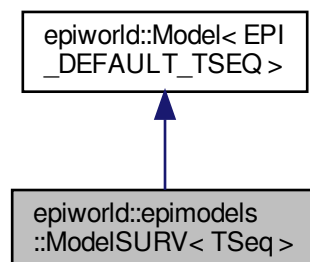
<i>vname</i>	std::string Name of the virus
<i>initial_prevalence</i>	epiworld_double Initial prevalence
<i>initial_effacy</i>	epiworld_double Initial susceptibility_reduction of the immune system
<i>initial_recovery</i>	epiworld_double Initial recovery rate of the immune system

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

- include/epiworld/models/sis.hpp

## 13.32 epiworld::epimodels::ModelSURV< TSeq > Class Template Reference

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



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



## Public Member Functions

### Construct a new ModelSURV object

The [\*ModelSURV\*](#) class simulates a surveillance model where agents can be isolated, even if asymptomatic.

#### Parameters

<code>vname</code>	<i>String. Name of the virus</i>
<code>prevalence</code>	<i>Integer. Number of initial cases of the virus.</i>
<code>efficacy_vax</code>	<i>Double. Efficacy of the vaccine (1 - P(acquire the disease)).</i>
<code>latent_period</code>	<i>Double. Shape parameter of a Gamma (latent_period, 1) distribution. This coincides with the expected number of latent days.</i>
<code>infect_period</code>	<i>Double. Shape parameter of a Gamma (infected_period, 1) distribution. This coincides with the expected number of infectious days.</i>
<code>prob_symptoms</code>	<i>Double. Probability of generating symptoms.</i>
<code>prop_vaccinated</code>	<i>Double. Probability of vaccination. Coincides with the initial prevalence of vaccinated individuals.</i>
<code>prop_vax_redux_transm</code>	<i>Double. Factor by which the vaccine reduces transmissibility.</i>
<code>prop_vax_redux_infect</code>	<i>Double. Factor by which the vaccine reduces the chances of becoming infected.</i>
<code>surveillance_prob</code>	<i>Double. Probability of testing an agent.</i>
<code>prob_transmission</code>	<i>Double. Raw transmission probability.</i>
<code>prob_death</code>	<i>Double. Raw probability of death for symptomatic individuals.</i>
<code>prob_noreinfect</code>	<i>Double. Probability of no re-infection.</i>

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, 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** (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)

### Additional Inherited Members

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

- `epiworld.hpp`

## 13.33 ModelSURV< TSeq > Class Template Reference

Inheritance diagram for ModelSURV< TSeq >:



Collaboration diagram for ModelSURV< TSeq >:



## Public Member Functions

### Construct a new ModelSURV object

The [ModelSURV](#) class simulates a surveillance model where agents can be isolated, even if asymptomatic.

#### Parameters

vname	String. Name of the virus
prevalence	Integer. Number of initial cases of the virus.
efficacy_vax	Double. Efficacy of the vaccine ( $1 - P(\text{acquire the disease})$ ).
latent_period	Double. Shape parameter of a <i>Gamma</i> (latent_period, 1) distribution. This coincides with the expected number of latent days.
infect_period	Double. Shape parameter of a <i>Gamma</i> (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, 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** (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)

### Additional Inherited Members

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

- include/epiworld/models/surveillance.hpp

## 13.34 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

## 13.35 epiworld::PersonTools< TSeq > Class Template Reference

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

- epiworld.hpp



## 13.36 PersonTools< TSeq > Class Template Reference

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

- include/epiworld/config.hpp

## 13.37 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** ()

#### 13.37.1 Detailed Description

A simple progress bar.

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

- epiworld.hpp

## 13.38 Progress Class Reference

A simple progress bar.

```
#include <progress.hpp>
```

### Public Member Functions

- **Progress** (int n\_, int width\_)
- void **start** ()
- void **next** ()
- void **end** ()

#### 13.38.1 Detailed Description

A simple progress bar.

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

- include/epiworld/progress.hpp

## 13.39 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 **set\_model** ([Model](#)< TSeq > \*m)

### 13.39.1 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

<i>TSeq</i>	
-------------	--

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

- epiworld.hpp

## 13.40 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 **set\_model** ([Model](#)< TSeq > \*m)

### 13.40.1 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

<i>TSeq</i>	
-------------	--

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

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

## 13.41 epiworld::QueueValues Class Reference

### Static Public Attributes

- static const int **NoOne** = 0
- static const int **OnlySelf** = 1
- static const int **Everyone** = 2

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

- epiworld.hpp

## 13.42 QueueValues Class Reference

### Static Public Attributes

- static const int **NoOne** = 0
- static const int **OnlySelf** = 1
- static const int **Everyone** = 2

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

- include/epiworld/epiworld-macros.hpp

## 13.43 RandGraph Class Reference

### Public Member Functions

- **RandGraph** (int N\_)
- void **init** (int s)
- void **set\_rand\_engine** (std::mt19937 &e)
- epiworld\_double **runif** ()

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

- include/epiworld/random\_graph.hpp

## 13.44 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

## 13.45 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

## 13.46 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")
- void **set\_sequence** (TSeq d)
- void **set\_sequence** (std::shared\_ptr< TSeq > d)
- std::shared\_ptr< TSeq > **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\_status** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **set\_queue** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **get\_status** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)
- void **get\_queue** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)

### Get and set the tool functions

#### Parameters

v	<i>The virus over which to operate</i>
fun	<i>the function to be used</i>

#### 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** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_tool** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)

### 13.46.1 Detailed Description

```
template<typename TSeq>  
class epiworld::Tool< TSeq >
```

[Tools](#) for defending the agent against the virus.

## Template Parameters

<i>TSeq</i>	Type of sequence
-------------	------------------

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

- epiworld.hpp

## 13.47 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")
- void **set\_sequence** (TSeq d)
- void **set\_sequence** (std::shared\_ptr< TSeq > d)
- std::shared\_ptr< TSeq > **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\_status** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **set\_queue** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **get\_status** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)
- void **get\_queue** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)

### Get and set the tool functions

## Parameters

v	<i>The virus over which to operate</i>
fun	<i>the function to be used</i>

## 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** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_tool** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)

### 13.47.1 Detailed Description

```
template<typename TSeq>
class Tool< TSeq >
```

[Tools](#) for defending the agent against the virus.

#### Template Parameters

<i>TSeq</i>	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

## 13.48 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



## Friends

- class **Tool**< TSeq >
- class **Agent**< TSeq >

### 13.48.1 Detailed Description

```
template<typename TSeq>
class epiworld::Tools< TSeq >
```

Set of tools (useful for building iterators)

#### Template Parameters

<i>TSeq</i>	
-------------	--

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

- epiworld.hpp

## 13.49 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

## Friends

- class **Tool**< TSeq >
- class **Agent**< TSeq >

### 13.49.1 Detailed Description

```
template<typename TSeq>
class Tools< TSeq >
```

Set of tools (useful for building iterators)

## Template Parameters

<i>TSeq</i>	
-------------	--

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

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

## 13.50 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

### Friends

- class **Tool**< TSeq >
- class **Agent**< TSeq >

### 13.50.1 Detailed Description

```
template<typename TSeq>
class epiworld::Tools_const< TSeq >
```

Set of [Tools](#) (const) (useful for iterators)

## Template Parameters

<i>TSeq</i>	
-------------	--

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

- epiworld.hpp

## 13.51 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

### Friends

- class **Tool**< TSeq >
- class **Agent**< TSeq >

#### 13.51.1 Detailed Description

```
template<typename TSeq>
class Tools_const< TSeq >
```

Set of [Tools](#) (const) (useful for iterators)

#### Template Parameters

<i>TSeq</i>	
-------------	--

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

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

## 13.52 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 <code>ncol()</code> (if vector), otherwise a <code>epiworld_double</code> .
j	Index of the data point, from 0 to <code>ncol()</code> - 1.

- void **add** (std::vector< epiworld\_double > x)
- void **add** (epiworld\_fast\_uint j, epiworld\_double x)

## Access data

### Parameters

i	Row (0 through <code>ndays</code> - 1.)
j	Column (0 through <code>ncols()</code> ).

### 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 >

## 13.52.1 Detailed Description

```
template<typename TSeq>
class epiworld::UserData< TSeq >
```

Personalized data by the user.

## Template Parameters

<i>TSeq</i>	
-------------	--

## 13.52.2 Constructor &amp; Destructor Documentation

## 13.52.2.1 UserData()

```
template<typename TSeq >
UserData< TSeq >::UserData (
    std::vector< std::string > names ) [inline]
```

Construct a new User Data object.

## Parameters

<i>names</i>	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

## 13.53 UserData&lt; TSeq &gt; 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 <code>ncol()</code> (if vector), otherwise a <code>epiworld_double</code> .
j	Index of the data point, from 0 to <code>ncol() - 1</code> .

- void **add** (std::vector< epiworld\_double > x)
- void **add** (epiworld\_fast\_uint j, epiworld\_double x)

**Access data***Parameters*

i	Row (0 through <code>ndays - 1</code> .)
j	Column (0 through <code>ncols()</code> ).

*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 >

**13.53.1 Detailed Description**

```
template<typename TSeq>
class UserData< TSeq >
```

Personalized data by the user.

**Template Parameters**

<i>TSeq</i>	
-------------	--

**13.53.2 Constructor & Destructor Documentation****13.53.2.1 UserData()**

```
template<typename TSeq >
UserData< TSeq >::UserData (
    std::vector< std::string > names ) [inline]
```

Construct a new User Data object.

## Parameters

<i>names</i>	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

## 13.54 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`

#### 13.54.1 Detailed Description

```
template<typename T>
struct epiworld::vecHasher< T >
```

Vector hasher.

#### Template Parameters

<i>T</i>	
----------	--

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

- epiworld.hpp

## 13.55 vecHasher< T > Struct Template Reference

Vector hasher.

```
#include <misc.hpp>
```

### Public Member Functions

- `std::size_t operator() (std::vector< T > const &dat) const noexcept`

### 13.55.1 Detailed Description

```
template<typename T>
struct vecHasher< T >
```

Vector hasher.

#### Template Parameters

<i>T</i>	
----------	--

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

- include/epiworld/misc.hpp

## 13.56 epiworld::Virus< TSeq > Class Template Reference

[Virus](#).

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

### Public Member Functions

- **Virus** (std::string name="unknown virus")
- void **mutate** ([Model](#)< TSeq > \*model)
- void **set\_mutation** (MutFun< TSeq > fun)
- const TSeq \* **get\_sequence** ()
- void **set\_sequence** (TSeq sequence)
- [Agent](#)< TSeq > \* **get\_agent** ()
- void **set\_agent** ([Agent](#)< TSeq > \*p, epiworld\_fast\_uint idx)
- 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
- std::vector< epiworld\_double > & **get\_data** ()

#### Get and set the tool functions

#### Parameters

v	<i>The virus over which to operate</i>
fun	<i>the function to be used</i>



### 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)
- 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\_prob\_infecting** (epiworld\_double \*prob)
- void **set\_prob\_recovery** (epiworld\_double \*prob)
- void **set\_prob\_death** (epiworld\_double \*prob)
- void **set\_prob\_infecting** (epiworld\_double prob)
- void **set\_prob\_recovery** (epiworld\_double prob)
- void **set\_prob\_death** (epiworld\_double prob)

### Get and set the status and queue

After applied, viruses can change the status 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 status 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 ( <a href="#">Agent</a> ) is removed.

- void **set\_status** (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\_status** (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)

### Friends

- class **Agent**< TSeq >
- class **Model**< TSeq >
- class **DataBase**< TSeq >
- void **default\_add\_virus** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_virus** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)

## 13.56.1 Detailed Description

```
template<typename TSeq>
class epiworld::Virus< TSeq >
```

[Virus](#).

### Template Parameters

<i>TSeq</i>	
-------------	--

Raw transmissibility of a virus should be a function of its genetic sequence. Nonetheless, transmissibility can be reduced as a result of having one or more tools to fight the virus. Because of this, transmissibility should be a function of the agent.

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

- epiworld.hpp

## 13.57 Virus< TSeq > Class Template Reference

[Virus.](#)

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

### Public Member Functions

- **Virus** (std::string name="unknown virus")
- void **mutate** ([Model](#)< TSeq > \*model)
- void **set\_mutation** (MutFun< TSeq > fun)
- const TSeq \* **get\_sequence** ()
- void **set\_sequence** (TSeq sequence)
- [Agent](#)< TSeq > \* **get\_agent** ()
- void **set\_agent** ([Agent](#)< TSeq > \*p, epiworld\_fast\_uint idx)
- 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
- std::vector< epiworld\_double > & **get\_data** ()

### Get and set the tool functions

#### Parameters

v	<i>The virus over which to operate</i>
fun	<i>the function to be used</i>

#### 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)
- 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\_prob\_infecting** (epiworld\_double \*prob)
- void **set\_prob\_recovery** (epiworld\_double \*prob)
- void **set\_prob\_death** (epiworld\_double \*prob)
- void **set\_prob\_infecting** (epiworld\_double prob)
- void **set\_prob\_recovery** (epiworld\_double prob)
- void **set\_prob\_death** (epiworld\_double prob)

### Get and set the status and queue

After applied, viruses can change the status 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 status 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 ( <a href="#">Agent</a> ) is removed.

- void **set\_status** (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\_status** (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)

### Friends

- class **Agent**< TSeq >
- class **Model**< TSeq >
- class **DataBase**< TSeq >
- void **default\_add\_virus** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)
- void **default\_rm\_virus** ([Action](#)< TSeq > &a, [Model](#)< TSeq > \*m)

## 13.57.1 Detailed Description

```
template<typename TSeq>
class Virus< TSeq >
```

[Virus](#).

#### Template Parameters

<i>TSeq</i>	
-------------	--

Raw transmissibility of a virus should be a function of its genetic sequence. Nonetheless, transmissibility can be reduced as a result of having one or more tools to fight the virus. Because of this, transmissibility 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

## 13.58 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 >::iterator **begin** ()
- std::vector< VIRUSPTR >::iterator **end** ()
- VIRUSPTR & **operator**() (size\_t i)
- VIRUSPTR & **operator**[] (size\_t i)
- size\_t **size** () const noexcept

### Friends

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

### 13.58.1 Detailed Description

```
template<typename TSeq>
class epiworld::Viruses< TSeq >
```

Set of viruses (useful for building iterators)

Template Parameters

<i>TSeq</i>	
-------------	--

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

- epiworld.hpp

## 13.59 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 >::iterator **begin** ()
- std::vector< VIRUSPTR >::iterator **end** ()
- VIRUSPTR & **operator**() (size\_t i)
- VIRUSPTR & **operator**[] (size\_t i)
- size\_t **size** () const noexcept

## Friends

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

### 13.59.1 Detailed Description

```
template<typename TSeq>
class Viruses< TSeq >
```

Set of viruses (useful for building iterators)

#### Template Parameters

<i>TSeq</i>	
-------------	--

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

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

## 13.60 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 >::const\_iterator **begin** () const
- std::vector< VIRUSPTR >::const\_iterator **end** () const
- const VIRUSPTR & **operator()** (size\_t i)
- const VIRUSPTR & **operator[]** (size\_t i)
- size\_t **size** () const noexcept

## Friends

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

### 13.60.1 Detailed Description

```
template<typename TSeq>
class epiworld::Viruses_const< TSeq >
```

Set of [Viruses](#) (const) (useful for iterators)

## Template Parameters

<i>TSeq</i>	
-------------	--

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

- epiworld.hpp

## 13.61 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 >::const\_iterator **begin** () const
- std::vector< VIRUSPTR >::const\_iterator **end** () const
- const VIRUSPTR & **operator()** (size\_t i)
- const VIRUSPTR & **operator[]** (size\_t i)
- size\_t **size** () const noexcept

### Friends

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

### 13.61.1 Detailed Description

```
template<typename TSeq>
class Viruses_const< TSeq >
```

Set of [Viruses](#) (const) (useful for iterators)

## Template Parameters

<i>TSeq</i>	
-------------	--

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

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

## Chapter 14

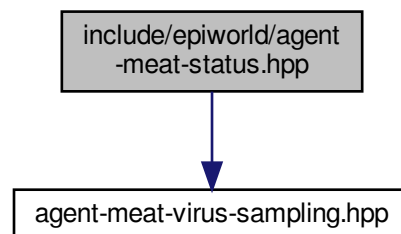
# File Documentation

### 14.1 include/epiworld/agent-meat-status.hpp File Reference

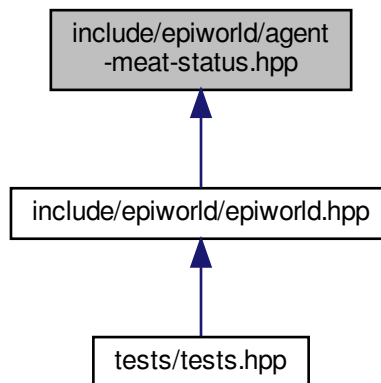
Sampling functions are getting big, so we keep them in a separate file.

```
#include "agent-meat-virus-sampling.hpp"
```

Include dependency graph for agent-meat-status.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)`

### 14.1.1 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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