

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 entities  : 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 states (arbitrary number of them).

Run

1. Distribute the tool(s) and virus(es)
2. For each t in 1 -> Duration:
 - Update state for susceptible/infected/removed(?)
 - Mutate virus(es) (each individual)
 - Run global 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 = state, 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="#">sampler</a>	Functions for sampling viruses . . . . .	<a href="#">25</a>
-------------------------	------------------------------------------	--------------------



## Chapter 9

# Hierarchical Index

### 9.1 Class Hierarchy

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

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ModelSIRCONN< TSeq > . . . . .	71
ModelSIRD< TSeq > . . . . .	72
ModelSIRDCONN< TSeq > . . . . .	74
ModelSIRLogit< TSeq > . . . . .	75
ModelSIS< TSeq > . . . . .	77
ModelSISD< TSeq > . . . . .	79
ModelSURV< TSeq > . . . . .	80
Model< TSeq > . . . . .	47
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## Chapter 10

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# Chapter 11

## File Index

### 11.1 File List

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include/epiworld/ <b>agent-actions-meat.hpp</b>	??
include/epiworld/ <b>agent-bones.hpp</b>	??
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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>	??
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include/epiworld/ <b>epiworld-macros.hpp</b>	??
include/epiworld/ <b>epiworld.hpp</b>	??
include/epiworld/ <b>globalactions-bones.hpp</b>	??
include/epiworld/ <b>globalactions-meat.hpp</b>	??
include/epiworld/ <b>misc.hpp</b>	??
include/epiworld/ <b>model-bones.hpp</b>	??
include/epiworld/ <b>model-meat-print.hpp</b>	??
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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>diffnet.hpp</b>	??
include/epiworld/models/ <b>globalactions.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>seird.hpp</b>	??
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include/epiworld/models/ <b>sirlogit.hpp</b>	??
include/epiworld/models/ <b>sis.hpp</b>	??
include/epiworld/models/ <b>sisd.hpp</b>	??
include/epiworld/models/ <b>surveillance.hpp</b>	??
tests/ <b>tests.hpp</b>	??



## Chapter 12

# Namespace Documentation

### 12.1 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>*)> 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>*)> 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>* 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\_state\_, 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\_state
- 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_state_,
 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_↔ state_</i>	Next state
<i>queue_</i>	Effect 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 AdjList Class Reference

### Public Member Functions

- [AdjList](#) (const std::vector< int > &source, const std::vector< int > &target, int size, bool directed)  
*Construct a new Adj List object.*
- **AdjList** ([AdjList](#) &&a)
- **AdjList** (const [AdjList](#) &a)
- [AdjList](#) & **operator=** (const [AdjList](#) &a)
- void [read\\_edgelist](#) (std::string fn, int size, int skip=0, bool directed=true)  
*Read an edgelist.*
- std::map< int, int > **operator()** (epiworld\_fast\_uint i) const
- void **print** (epiworld\_fast\_uint limit=20u) const
- size\_t [vcount](#) () const  
*Number of vertices/nodes in the network.*
- size\_t [ecount](#) () const  
*Number of edges/arcs/ties in the network.*
- std::vector< std::map< int, int > > & **get\_dat** ()
- bool [is\\_directed](#) () const  
*true if the network is directed.*

### 13.2.1 Constructor & Destructor Documentation

#### 13.2.1.1 AdjList()

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

Construct a new Adj List object.

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

#### Parameters

<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

### 13.2.2 Member Function Documentation

### 13.2.2.1 read\_edgelist()

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

Read an edgelist.

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

#### Parameters

<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 files:

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

## 13.3 Agent< TSeq > Class Template Reference

[Agent](#) (agents)

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

### Public Member Functions

- **Agent** ([Agent](#)< TSeq > &&p)
- **Agent** (const [Agent](#)< TSeq > &p)
- [Agent](#)< TSeq > & **operator=** (const [Agent](#)< TSeq > &other\_agent)
- int [get\\_id](#) () const  
*Id of the individual.*
- VirusPtr< TSeq > & **get\_virus** (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\_virus** ()
- void **add\_neighbor** ([Agent](#)< TSeq > &p, bool check\_source=true, bool check\_target=true)
- void **swap\_neighbors** ([Agent](#)< TSeq > &other, size\_t n\_this, size\_t n\_other)  
*Swaps neighbors between the current agent and agent *other**
- std::vector< [Agent](#)< TSeq > \* > **get\_neighbors** ()



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

#### Add/Remove Virus/Tool

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

##### Parameters

tool	<i>Tool to add</i>
virus	<i>Virus to add</i>
state_new	<i>state after the change</i>
queue	

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

- double & [operator\(\)](#) (size\_t j)  
*Access the j-th column of the agent.*
- double & **operator[]** (size\_t j)
- double **operator()** (size\_t j) const
- double **operator[]** (size\_t j) const

### Friends

- class **Model**< TSeq >
- class **Virus**< TSeq >
- class **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)

### 13.3.1 Detailed Description

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

[Agent](#) (agents)

## Template Parameters

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

## 13.3.2 Member Function Documentation

## 13.3.2.1 operator()

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

Access the j-th column of the agent.

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

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

## Parameters

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

## Returns

double&

## 13.3.2.2 swap\_neighbors()

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

Swaps neighbors between the current agent and agent `other`

## Parameters

<i>other</i>	
<i>n_this</i>	
<i>n_other</i>	

### 13.3.3 Friends And Related Function Documentation

#### 13.3.3.1 default\_rm\_entity

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

< Last entity of the agent

< Last agent of the entity

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

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

## 13.4 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

#### 13.4.1 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>	
-------------	--

## 13.4.2 Constructor &amp; Destructor Documentation

## 13.4.2.1 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

## 13.5 DataBase&lt; TSeq &gt; Class Template Reference

Statistical data about the process.

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

## Public Member Functions

- **DataBase** ([Model](#)< TSeq > &m)
- **DataBase** (const [DataBase](#)< TSeq > &db)
- void [record\\_virus](#) ([Virus](#)< TSeq > &v)
  - Registering a new variant.*
- void [record\\_tool](#) ([Tool](#)< TSeq > &t)
- void [set\\_seq\\_hasher](#) (std::function< std::vector< int >(TSeq)> fun)
- void [reset](#) ()
- [Model](#)< TSeq > \* [get\\_model](#) ()
- void [record](#) ()
- const std::vector< TSeq > & [get\\_sequence](#) () const
- const std::vector< int > & [get\\_nexposed](#) () const
- size\_t [size](#) () const
- void [write\\_data](#) (std::string fn\_virus\_info, std::string fn\_virus\_hist, std::string fn\_tool\_info, std::string fn\_↵  
\_tool\_hist, std::string fn\_total\_hist, std::string fn\_transmission, std::string fn\_transition, std::string fn\_↵  
reproductive\_number, std::string fn\_generation\_time) const
- void [record\\_transmission](#) (int i, int j, int virus, int i\_expo\_date)
- size\_t [get\\_n\\_viruses](#) () const
- size\_t [get\\_n\\_tools](#) () const
- 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.*
- bool [operator==](#) (const [DataBase](#)< TSeq > &other) const
- bool [operator!=](#) (const [DataBase](#)< TSeq > &other) const
- bool [operator==](#) (const [DataBase](#)< std::vector< int >> &other) const

### Get recorded information from the model

#### Parameters

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

#### Returns

*In [get\\_today\\_total](#), the current counts of what.*

*In [get\\_today\\_virus](#), the current counts of what for each virus.*

*In [get\\_hist\\_total](#), the time series of what*

*In [get\\_hist\\_virus](#), the time series of what for each virus.*

*In [get\\_hist\\_total\\_date](#) and [get\\_hist\\_virus\\_date](#) the corresponding date*

- int [get\\_today\\_total](#) (std::string what) const
- int [get\\_today\\_total](#) (epiworld\_fast\_uint what) const
- void [get\\_today\\_total](#) (std::vector< std::string > \*state=nullptr, std::vector< int > \*counts=nullptr) const
- void [get\\_today\\_virus](#) (std::vector< std::string > &state, std::vector< int > &id, std::vector< int > &counts) const
- void [get\\_hist\\_total](#) (std::vector< int > \*date, std::vector< std::string > \*state, std::vector< int > \*counts) const
- void [get\\_hist\\_virus](#) (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &state, std::vector< int > &counts) const
- void [get\\_hist\\_tool](#) (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &state, std::vector< int > &counts) const

- void **get\_hist\_transition\_matrix** (std::vector< std::string > &state\_from, std::vector< std::string > &state\_to, std::vector< int > &date, std::vector< int > &counts, bool skip\_zeros) const
- void **get\_transmissions** (std::vector< int > &date, std::vector< int > &source, std::vector< int > &target, std::vector< int > &virus, std::vector< int > &source\_exposure\_date) const  
*Get the transmissions object.*
- void **get\_transmissions** (int \*date, int \*source, int \*target, int \*virus, int \*source\_exposure\_date) const
- MapVec\_type< int, int > **reproductive\_number** () const  
*Computes the reproductive number of each case.*
- void **reproductive\_number** (std::string fn) const
- void **generation\_time** (std::vector< int > &agent\_id, std::vector< int > &virus\_id, std::vector< int > &time, std::vector< int > &gentime) const
- void **generation\_time** (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)

### 13.5.1 Detailed Description

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

Statistical data about the process.

#### Template Parameters

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

### 13.5.2 Member Function Documentation

### 13.5.2.1 generation\_time()

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

Calculates the generating time

#### Parameters

<i>agent_id, virus_id, time, gentime</i>	vectors where to save the values agent_id
------------------------------------------	-------------------------------------------

### 13.5.2.2 get\_transmissions()

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

Get the transmissions object.

#### Parameters

<i>date</i>	
<i>source</i>	
<i>target</i>	
<i>virus</i>	
<i>source_exposure_date</i>	

### 13.5.2.3 operator==( ) [1/2]

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

< Date of the transmission eve,

< Id of the sour,

< Id of the targ,

< Id of the varia,

< Date when the source acquired the varia,



**13.5.2.4 operator==( ) [2/2]**

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

< Date of the transmission eve

< Id of the sour

< Id of the targ

< Id of the varia

< Date when the source acquired the varia

**13.5.2.5 record\_virus()**

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

Registering a new variant.

**Parameters**

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

**13.5.2.6 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.
-----------	--------------------------------------------------

**13.5.2.7 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

## 13.6 Entities< TSeq > Class Template Reference

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

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

### Public Member Functions

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

### Friends

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

#### 13.6.1 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

## 13.7 Entities\_const< TSeq > Class Template Reference

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

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

### Public Member Functions

- **Entities\_const** (const [Agent](#)< TSeq > &p)
- std::vector< [Entity](#)< TSeq > \* >::const\_iterator **begin** ()
- std::vector< [Entity](#)< TSeq > \* >::const\_iterator **end** ()
- const [Entity](#)< TSeq > & **operator()** (size\_t i)
- const [Entity](#)< TSeq > & **operator[]** (size\_t i)
- size\_t **size** () const noexcept
- bool **operator==** (const [Entities\\_const](#)< TSeq > &other) const

### Friends

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

#### 13.7.1 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

## 13.8 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\_state** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **set\_queue** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **get\_state** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)
- void **get\_queue** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)
- void **reset** ()
- bool **operator==** (const [Entity](#)< TSeq > &other) const
- bool **operator!=** (const [Entity](#)< TSeq > &other) const

## 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)

## 13.8.1 Friends And Related Function Documentation

### 13.8.1.1 default\_rm\_entity

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

< Last entity of the agent

< Last agent of the entity

< Last entity of the agent

< Last agent of the entity

< Last entity of the agent

< Last agent of the entity

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

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

## 13.9 GlobalAction< TSeq > Class Template Reference

Template for a Global [Action](#).

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

### Public Member Functions

- [GlobalAction](#) (GlobalFun< TSeq > fun, std::string name, int day=-99)  
*Construct a new Global [Action](#) object.*
- void **operator()** ([Model](#)< TSeq > \*m, int day)
- void **set\_name** (std::string name)
- std::string **get\_name** () const
- void **set\_day** (int day)
- int **get\_day** () const
- void **print** () const
- bool **operator==** (const [GlobalAction](#)< TSeq > &other) const
- bool **operator!=** (const [GlobalAction](#)< TSeq > &other) const

### 13.9.1 Detailed Description

```
template<typename TSeq>
class GlobalAction< TSeq >
```

Template for a Global [Action](#).

Global actions are functions that [Model](#)<TSeq> executes at the end of a day.

### 13.9.2 Constructor & Destructor Documentation

#### 13.9.2.1 GlobalAction()

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

Construct a new Global [Action](#) object.

#### Parameters

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

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

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

## 13.10 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)`

### 13.10.1 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:

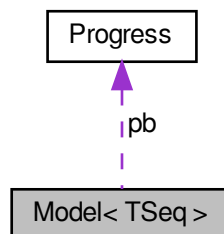
- `include/epiworld/math/lfmcmc/lfmcmc-bones.hpp`
- `include/epiworld/math/lfmcmc/lfmcmc-meat-print.hpp`
- `include/epiworld/math/lfmcmc/lfmcmc-meat.hpp`

## 13.11 Model< TSeq > Class Template Reference

Core class of epiworld.

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

Collaboration diagram for Model< TSeq >:



## 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\_viruses** () 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\_virus\_info, std::string fn\_virus\_hist, std::string fn\_tool\_info, std::string fn\_↵  
\_↵\_tool\_hist, std::string fn\_total\_hist, std::string fn\_transmission, std::string fn\_transition, std::string fn\_↵  
reproductive\_number, std::string fn\_generation\_time) const  
*Wrapper of DataBase::write\_data*
- std::map< std::string, epiworld\_double > & **params** ()
- virtual void **reset** ()  
*Reset the model.*
- void **print** (bool lite=false) 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, std::string **name**="A global action", int  
date=-99)  
*Set a global action.*
- void **add\_global\_action** ([GlobalAction](#)< TSeq > action)
- [GlobalAction](#)< TSeq > & **get\_global\_action** (std::string **name**)  
*Retrieve a global action by name.*
- [GlobalAction](#)< TSeq > & **get\_global\_action** (size\_t i)  
*Retrieve a global action by index.*
- void **rm\_global\_action** (std::string **name**)  
*Remove a global action by name.*
- void **rm\_global\_action** (size\_t i)  
*Remove a global action by index.*
- void **run\_global\_actions** ()
- void **clear\_state\_set** ()
- const std::vector< VirusPtr< TSeq > > & **get\_viruses** () const
- const std::vector< ToolPtr< TSeq > > & **get\_tools** () const
- [Virus](#)< TSeq > & **get\_virus** (size\_t id)
- [Tool](#)< TSeq > & **get\_tool** (size\_t id)
- void **set\_agents\_data** (double \*data\_, size\_t ncols\_)  
*Set the agents data object.*
- double \* **get\_agents\_data** ()
- size\_t **get\_agents\_data\_ncols** () const
- void **set\_name** (std::string **name**)  
*Set the name object.*
- std::string **get\_name** () const



- bool **operator==** (const [Model](#)< TSeq > &other) const
- bool **operator!=** (const [Model](#)< TSeq > &other) const

### Set the backup object

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

- void **set\_backup** ()

### Random number generation

#### Parameters

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

- void **set\_rand\_engine** (std::mt19937 &eng)
- std::mt19937 & **get\_rand\_engine** ()
- void **seed** (size\_t s)
- void **set\_rand\_norm** (epiworld\_double mean, epiworld\_double sd)
- void **set\_rand\_unif** (epiworld\_double a, epiworld\_double b)
- void **set\_rand\_exp** (epiworld\_double lambda)
- void **set\_rand\_gamma** (epiworld\_double alpha, epiworld\_double beta)
- void **set\_rand\_lognormal** (epiworld\_double mean, epiworld\_double shape)
- void **set\_rand\_binom** (int n, epiworld\_double p)
- epiworld\_double **runif** ()
- epiworld\_double **runif** (epiworld\_double a, epiworld\_double b)
- epiworld\_double **rnorm** ()
- epiworld\_double **rnorm** (epiworld\_double mean, epiworld\_double sd)
- epiworld\_double **rgamma** ()
- epiworld\_double **rgamma** (epiworld\_double alpha, epiworld\_double beta)
- epiworld\_double **rexp** ()
- epiworld\_double **rexp** (epiworld\_double lambda)
- epiworld\_double **rlognormal** ()
- epiworld\_double **rlognormal** (epiworld\_double mean, epiworld\_double shape)
- int **rbinom** ()
- int **rbinom** (int n, epiworld\_double p)

### 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)

- void **rm\_virus** (size\_t virus\_pos)
- void **rm\_tool** (size\_t tool\_pos)
- void **rm\_entity** (size\_t entity\_pos)

### 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 fn.</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\_edgelist** (const std::vector< int > &source, const std::vector< int > &target, int size, bool directed)
- void **agents\_from\_adjlist** ([AdjList](#) al)
- bool **is\_directed** () const
- std::vector< [Agent](#)< TSeq > > & **get\_agents** ()  
*Returns a reference to the vector of agents.*
- std::vector< [epiworld\\_fast\\_uint](#) > **get\_agents\_states** () const  
*Returns a vector with the states of the agents.*
- std::vector< [Viruses\\_const](#)< TSeq > > **get\_agents\_viruses** () const  
*Returns a const vector with the viruses of the agents.*
- std::vector< [Viruses](#)< TSeq > > **get\_agents\_viruses** ()  
*Returns a vector with the viruses of the agents.*
- std::vector< [Entity](#)< TSeq > > & **get\_entities** ()
- 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 **update\_state** ()
- void **mutate\_virus** ()
- void **next** ()
- virtual void **run** ([epiworld\\_fast\\_uint](#) ndays, int seed=-1)  
*Runs the simulation (after initialization)*
- void **run\_multiple** ([epiworld\\_fast\\_uint](#) ndays, [epiworld\\_fast\\_uint](#) nexperiments, int seed\_=-1, std::function< void(size\_t, [Model](#)< TSeq > \*)> fun=make\_save\_run< TSeq >(), bool **reset**=true, bool verbose=true, int nthreads=1)

### Rewire the network preserving the degree sequence.

*This implementation assumes an undirected network, thus if  $\{(i,j), (k,l)\} \rightarrow \{(i,l), (k,j)\}$ , 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< int > &source, std::vector< int > &target) const

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

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

*Parameters*

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

*Returns*

*add\_state\* returns nothing.*

*get\_state\_\* returns a vector of pairs with the states and their labels.*

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

**Setting and accessing parameters from the model**

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

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

*In the case of the function `read_params`, users can pass a file listing parameters to be included in the model.*

*Each line in the file should have the following structure:*

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

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

**Parameters**

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

**Returns**

*The current value of the parameter in the model.*

- epiworld\_double **add\_param** (epiworld\_double initial\_val, std::string pname)
- void **read\_params** (std::string fn)
- epiworld\_double **get\_param** (epiworld\_double k)
- epiworld\_double **get\_param** (std::string pname)
- void **set\_param** (std::string pname, epiworld\_double val)
- epiworld\_double **par** (std::string pname)

**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\_double 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)

## Protected Member Functions

- void **dist\_tools** ()
- void **dist\_virus** ()
- void **chrono\_start** ()
- void **chrono\_end** ()
- void **actions\_add** (Agent< TSeq > \*agent\_, VirusPtr< TSeq > virus\_, ToolPtr< TSeq > tool\_, Entity< TSeq > \*entity\_, epiworld\_fast\_uint new\_state\_, epiworld\_fast\_int queue\_, ActionFun< TSeq > call\_, int idx\_agent\_, int idx\_object\_)  
*Construct a new Action object.*
- void **actions\_run** ()  
*Executes the stored action.*

## Protected Attributes

- std::string **name** = ""  
*Name of the model.*
- DataBase< TSeq > **db** = DataBase<TSeq>(\*this)
- std::vector< Agent< TSeq > > **population** = {}
- bool **using\_backup** = true
- std::vector< Agent< TSeq > > **population\_backup** = {}
- bool **directed** = false
- std::vector< VirusPtr< TSeq > > **viruses** = {}
- std::vector< epiworld\_double > **prevalence\_virus** = {}  
*Initial prevalence\_virus of each virus.*
- std::vector< bool > **prevalence\_virus\_as\_proportion** = {}
- std::vector< VirusToAgentFun< TSeq > > **viruses\_dist\_funs** = {}
- std::vector< ToolPtr< TSeq > > **tools** = {}
- std::vector< epiworld\_double > **prevalence\_tool** = {}
- std::vector< bool > **prevalence\_tool\_as\_proportion** = {}
- std::vector< ToolToAgentFun< TSeq > > **tools\_dist\_funs** = {}
- std::vector< Entity< TSeq > > **entities** = {}
- std::vector< Entity< TSeq > > **entities\_backup** = {}
- std::mt19937 **engine**
- std::uniform\_real\_distribution **runifd**
- std::normal\_distribution **rnormd**
- std::gamma\_distribution **rgammad**
- std::lognormal\_distribution **rlognormald**
- std::exponential\_distribution **rexp**
- std::binomial\_distribution **rbinomd**
- std::function< void(std::vector< Agent< TSeq > > \*, Model< TSeq > \*, epiworld\_double)> **rewire\_fun**
- epiworld\_double **rewire\_prop** = 0.0
- std::map< std::string, epiworld\_double > **parameters**
- epiworld\_fast\_uint **ndays** = 0
- **Progress pb**
- std::vector< UpdateFun< TSeq > > **state\_fun** = {}
- std::vector< std::string > **states\_labels** = {}
- epiworld\_fast\_uint **nstates** = 0
- bool **verbose** = true
- int **current\_date** = 0
- std::chrono::time\_point< std::chrono::steady\_clock > **time\_start**
- std::chrono::time\_point< std::chrono::steady\_clock > **time\_end**
- std::chrono::duration< epiworld\_double, std::micro > **time\_elapsed**

- `epiworld_fast_uint n_replicates = 0u`
- `std::vector< GlobalAction< TSeq > > global_actions`
- `Queue< TSeq > queue`
- `bool use_queueing = true`
- `std::vector< Action< TSeq > > actions = {}`

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

- `epiworld_fast_uint nactions = 0u`

#### Auxiliary variables for AgentsSample<TSeq> iterators

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

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

#### Agents features

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

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

#### Friends

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

#### Tool Mixers

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

- `MixerFun< TSeq > susceptibility_reduction_mixer = susceptibility_reduction_mixer_default<TSeq>`
- `MixerFun< TSeq > transmission_reduction_mixer = transmission_reduction_mixer_default<TSeq>`
- `MixerFun< TSeq > recovery_enhancer_mixer = recovery_enhancer_mixer_default<TSeq>`
- `MixerFun< TSeq > death_reduction_mixer = death_reduction_mixer_default<TSeq>`
- `std::vector< epiworld_double > array_double_tmp`
- `std::vector< Virus< TSeq > * > array_virus_tmp`
- `virtual Model< TSeq > * clone_ptr ()`  
*Advanced usage: Makes a copy of data and returns it as undeleted pointer.*
- `Model ()`
- `Model (const Model< TSeq > &m)`
- `Model (Model< TSeq > &m)=delete`
- `Model (Model< TSeq > &&m)`
- `Model< TSeq > & operator= (const Model< TSeq > &m)`
- `virtual ~Model ()`
- `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)`

### 13.11.1 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.)
-------------	-----------------------------------------------------------------------------------------------------------------------------------------

### 13.11.2 Member Function Documentation

#### 13.11.2.1 actions\_add()

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

Construct a new [Action](#) object.

#### Parameters

<i>agent_</i>	<a href="#">Agent</a> over which the action will be called
<i>virus_</i>	<a href="#">Virus</a> pointer included in the action
<i>tool_</i>	<a href="#">Tool</a> pointer included in the action
<i>entity_</i>	<a href="#">Entity</a> pointer included in the action
<i>new_state_</i>	New state of the agent
<i>call_</i>	Function the action will call
<i>queue_</i>	Change in the queue
<i>idx_agent_</i>	Location of agent in object.
<i>idx_object_</i>	Location of object in agent.

### 13.11.2.2 actions\_run()

```
template<typename TSeq >
void Model< TSeq >::actions_run [inline], [protected]
```

Executes the stored action.

#### Parameters

<i>model</i> ↔	Model over which it will be executed.
—	

### 13.11.2.3 add\_global\_action()

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

Set a global action.

#### Parameters

<i>fun</i>	A function to be called on the prescribed date
<i>name</i>	Name of the action.
<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.

### 13.11.2.4 clone\_ptr()

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

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

#### Parameters

<i>copy</i>	
-------------	--



### 13.11.2.5 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.

### 13.11.2.6 reset()

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

Reset the model.

Resetting the model will:

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

### 13.11.2.7 run\_multiple()

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

## Parameters

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

**13.11.2.8 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.

**13.11.2.9 set\_name()**

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

Set the name object.

## Parameters

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

**13.11.2.10 write\_data()**

```
template<typename TSeq >
void Model< TSeq >::write_data (
 std::string fn_virus_info,
 std::string fn_virus_hist,
 std::string fn_tool_info,
 std::string fn_tool_hist,
```

```

std::string fn_total_hist,
std::string fn_transmission,
std::string fn_transition,
std::string fn_reproductive_number,
std::string fn_generation_time) const [inline]

```

Wrapper of DataBase::write\_data

#### Parameters

<i>fn_virus_info</i>	Filename. Information about the virus.
<i>fn_virus_hist</i>	Filename. History of the virus.
<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 (state)
<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

### 13.11.3 Member Data Documentation

#### 13.11.3.1 rbinomd

```

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

```

##### Initial value:

```

=
 std::binomial_distribution<>()

```

#### 13.11.3.2 rexp

```

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

```

##### Initial value:

```

=
 std::exponential_distribution<>()

```

#### 13.11.3.3 rgammad

```

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

```

##### Initial value:

```

=
 std::gamma_distribution<>()

```

#### 13.11.3.4 rlognormald

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

**Initial value:**

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

#### 13.11.3.5 rnormd

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

**Initial value:**

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

#### 13.11.3.6 runifd

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

**Initial value:**

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

#### 13.11.3.7 time\_elapsed

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

**Initial value:**

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

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

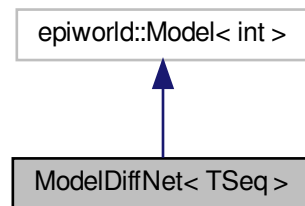
- include/epiworld/agent-bones.hpp
- include/epiworld/model-bones.hpp
- include/epiworld/model-meat-print.hpp
- include/epiworld/model-meat.hpp

## 13.12 ModelDiffNet< TSeq > Class Template Reference

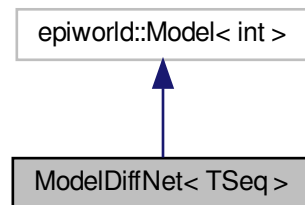
Template for a [Network](#) Diffusion [Model](#).

```
#include <diffnet.hpp>
```

Inheritance diagram for ModelDiffNet< TSeq >:



Collaboration diagram for ModelDiffNet< TSeq >:



### Public Member Functions

- **ModelDiffNet** ([ModelDiffNet](#)< TSeq > &model, std::string innovation\_name, epiworld\_double prevalence, epiworld\_double prob\_adopt, bool normalize\_exposure=true, double \*agents\_data=nullptr, size\_t data\_ncols=0u, std::vector< size\_t > data\_cols={}, std::vector< double > params={})
- **ModelDiffNet** (std::string innovation\_name, epiworld\_double prevalence, epiworld\_double prob\_adopt, bool normalize\_exposure=true, double \*agents\_data=nullptr, size\_t data\_ncols=0u, std::vector< size\_t > data\_cols={}, std::vector< double > params={})

### Public Attributes

- bool **normalize\_exposure** = true
- std::vector< size\_t > **data\_cols**
- std::vector< double > **params**

## Static Public Attributes

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

### 13.12.1 Detailed Description

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

Template for a [Network](#) Diffusion [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:

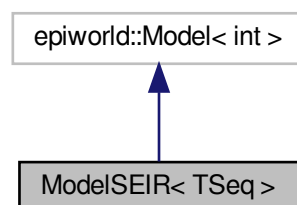
- include/epiworld/models/diffnet.hpp

## 13.13 ModelSEIR< TSeq > Class Template Reference

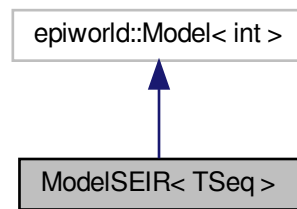
Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.

```
#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 transmission\_rate, epiworld\_double avg\_incubation\_days, epiworld\_double recovery\_rate)
- **ModelSEIR** (std::string vname, epiworld\_double prevalence, epiworld\_double transmission\_rate, epiworld\_double avg\_incubation\_days, epiworld\_double recovery\_rate)

## Public Attributes

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

### 13.13.1 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>prevalence</i>	epiworld_double Initial prevalence the immune system
<i>transmission_rate</i>	epiworld_double Transmission rate of the virus
<i>avg_incubation_days</i>	epiworld_double Average incubation days of the virus.
<i>recovery_rate</i>	epiworld_double Recovery rate of the virus.

### 13.13.2 Member Data Documentation

### 13.13.2.1 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 {
 auto v = p->get_virus(0);
 if (m->runif() < 1.0/(v->get_incubation(m)))
 p->change_state(m, ModelSEIR<TSeq>::INFECTED);
 return;
}
```

### 13.13.2.2 update\_infected\_seir

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

#### Initial value:

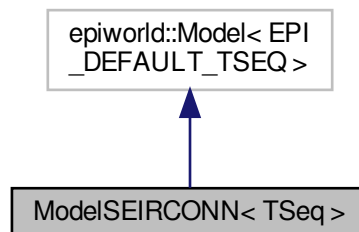
```
= [] (
 epiworld::Agent<TSeq> * p,
 epiworld::Model<TSeq> * m
) -> void {
 if (m->runif() < (m->par("Recovery rate")))
 p->rm_virus(0, m);
 return;
}
```

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

- include/epiworld/models/seir.hpp

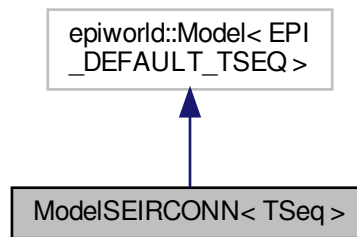
## 13.14 ModelSEIRCONN< TSeq > Class Template Reference

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 contact\_rate, epiworld\_double transmission\_rate, epiworld\_double avg\_incubation\_days, epiworld\_double recovery\_rate)  
*Template for a Susceptible-Exposed-Infected-Removed (SEIR) model.*
- **ModelSEIRCONN** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double contact\_rate, epiworld\_double transmission\_rate, epiworld\_double avg\_incubation\_days, epiworld\_double recovery\_rate)
- void **run** (epiworld\_fast\_uint ndays, int seed=-1)
- void **reset** ()
- [Model](#)< TSeq > \* **clone\_ptr** ()

## Static Public Attributes

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

## 13.14.1 Constructor & Destructor Documentation

### 13.14.1.1 ModelSEIRCONN()

```

template<typename TSeq >
ModelSEIRCONN< TSeq >::ModelSEIRCONN (
 ModelSEIRCONN< TSeq > & model,
 std::string vname,
 epiworld_fast_uint n,
 epiworld_double prevalence,
 epiworld_double contact_rate,
 epiworld_double transmission_rate,
 epiworld_double avg_incubation_days,
 epiworld_double recovery_rate) [inline]

```

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

## Parameters

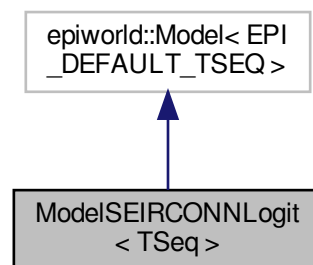
<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>prevalence</i>	Initial prevalence (proportion)
<i>contact_rate</i>	Average number of contacts (interactions) per step.
<i>transmission_rate</i>	Probability of transmission
<i>recovery_rate</i>	Probability of recovery

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

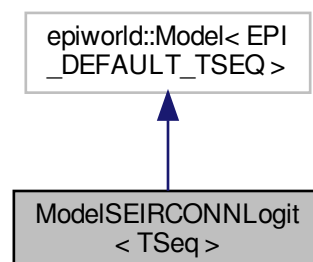
- include/epiworld/models/seirconnected.hpp

### 13.15 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 contact\_rate, epiworld\_double transmission\_rate, epiworld\_double avg\_incubation\_days, epiworld\_double recovery\_rate, 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 contact\_rate, epiworld\_double transmission\_rate, epiworld\_double avg\_incubation\_days, epiworld\_double recovery\_rate 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

## 13.15.1 Constructor & Destructor Documentation

### 13.15.1.1 ModelSEIRCONNLogit()

```
template<typename TSeq >
ModelSEIRCONNLogit< TSeq >::ModelSEIRCONNLogit (
 ModelSEIRCONNLogit< TSeq > & model,
 std::string vname,
 epiworld_fast_uint n,
 epiworld_double prevalence,
 epiworld_double contact_rate,
 epiworld_double transmission_rate,
 epiworld_double avg_incubation_days,
 epiworld_double recovery_rate,
 double * covars,
 std::vector< double > logit_params) [inline]
```

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

#### Parameters

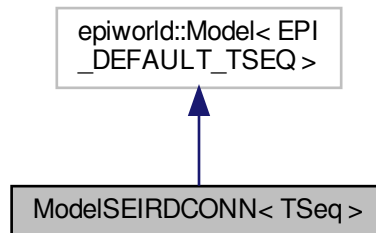
<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>prevalence</i>	Initial prevalence (proportion)
<i>contact_rate</i>	Reproductive number (beta)
<i>transmission_rate</i>	Probability of transmission
<i>recovery_rate</i>	Probability of recovery

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

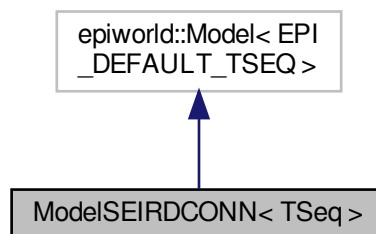
- `include/epiworld/models/seirconnected_logit.hpp`

## 13.16 ModelSEIRDCONN< TSeq > Class Template Reference

Inheritance diagram for ModelSEIRDCONN< TSeq >:



Collaboration diagram for ModelSEIRDCONN< TSeq >:



### Public Member Functions

- [ModelSEIRDCONN](#) ([ModelSEIRDCONN](#)< TSeq > &model, std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double contact\_rate, epiworld\_double transmission\_rate, epiworld\_double avg\_incubation\_days, epiworld\_double recovery\_rate, epiworld\_double death\_rate)

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

- **ModelSEIRDCONN** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double contact\_rate, epiworld\_double transmission\_rate, epiworld\_double avg\_incubation\_days, epiworld\_double recovery\_rate, epiworld\_double death\_rate)
- void **run** (epiworld\_fast\_uint ndays, int seed=-1)
- void **reset** ()
- [Model](#)< TSeq > \* **clone\_ptr** ()

## Static Public Attributes

- static const int **SUSCEPTIBLE** = 0
- static const int **EXPOSED** = 1
- static const int **INFECTED** = 2
- static const int **REMOVED** = 3
- static const int **DECEASED** = 4

## 13.16.1 Constructor & Destructor Documentation

### 13.16.1.1 ModelSEIRDCONN()

```
template<typename TSeq >
ModelSEIRDCONN< TSeq >::ModelSEIRDCONN (
 ModelSEIRDCONN< TSeq > & model,
 std::string vname,
 epiworld_uint n,
 epiworld_double prevalence,
 epiworld_double contact_rate,
 epiworld_double transmission_rate,
 epiworld_double avg_incubation_days,
 epiworld_double recovery_rate,
 epiworld_double death_rate) [inline]
```

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

#### Parameters

<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>contact_rate</i>	Average number of contacts (interactions) per step.
<i>transmission_rate</i>	Probability of transmission
<i>recovery_rate</i>	Probability of recovery
<i>death_rate</i>	Probability of death

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

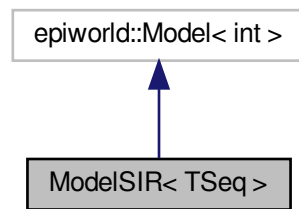
- include/epiworld/models/seirdconnected.hpp

## 13.17 ModelSIR< TSeq > Class Template Reference

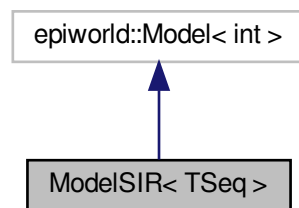
Template for a Susceptible-Infected-Removed (SIR) model.

```
#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 transmission\_rate, epiworld\_double recovery\_rate)
- **ModelSIR** (std::string vname, epiworld\_double prevalence, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate)

### 13.17.1 Detailed Description

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

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

#### Parameters

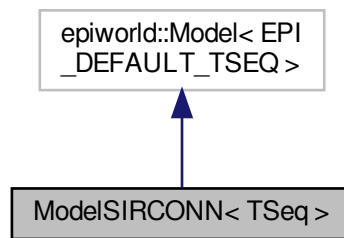
<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>initial_prevalence</i>	epiworld_double Initial prevalence
<i>initial_efficacy</i>	epiworld_double Initial susceptibility_reduction of the immune system
<i>initial_recovery</i>	epiworld_double Initial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

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

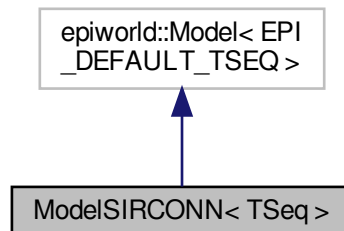
- include/epiworld/models/sir.hpp

## 13.18 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 contact\_rate, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate)  
*Template for a Susceptible-Infected-Removed (SIR) model.*
- **ModelSIRCONN** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double contact\_rate, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate)
- void **run** (epiworld\_fast\_uint ndays, int seed=-1)
- void **reset** ()
- [Model](#)< TSeq > \* **clone\_ptr** ()

## 13.18.1 Constructor & Destructor Documentation

### 13.18.1.1 ModelSIRCONN()

```
template<typename TSeq >
ModelSIRCONN< TSeq >::ModelSIRCONN (
 ModelSIRCONN< TSeq > & model,
 std::string vname,
 epiworld_fast_uint n,
 epiworld_double prevalence,
 epiworld_double contact_rate,
 epiworld_double transmission_rate,
 epiworld_double recovery_rate) [inline]
```

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

#### Parameters

<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>contact_rate</i>	Average number of contacts (interactions) per step.
<i>transmission_rate</i>	Probability of transmission
<i>recovery_rate</i>	Probability of recovery

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

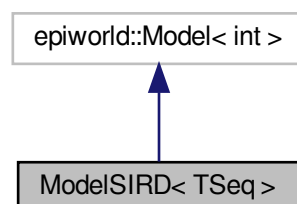
- include/epiworld/models/sirconnected.hpp

## 13.19 ModelSIRD< TSeq > Class Template Reference

Template for a Susceptible-Infected-Removed-Deceased (SIRD) model.

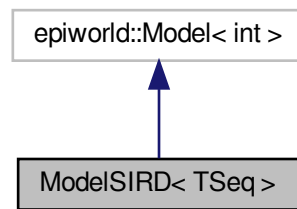
```
#include <sird.hpp>
```

Inheritance diagram for ModelSIRD< TSeq >:





Collaboration diagram for ModelSIRD< TSeq >:



## Public Member Functions

- **ModelSIRD** ([ModelSIRD](#)< TSeq > &model, std::string vname, epiworld\_double prevalence, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate, epiworld\_double death\_rate)
- **ModelSIRD** (std::string vname, epiworld\_double prevalence, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate, epiworld\_double death\_rate)

### 13.19.1 Detailed Description

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

Template for a Susceptible-Infected-Removed-Deceased (SIRD) model.

#### Parameters

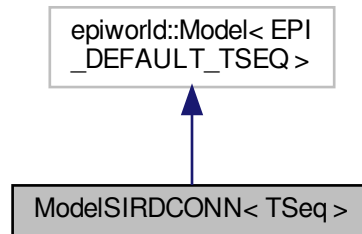
<i>model</i>	A Model<TSeq> object where to set up the SIRD.
<i>vname</i>	std::string Name of the virus
<i>initial_prevalence</i>	epiworld_double Initial prevalence
<i>initial_efficacy</i>	epiworld_double Initial susceptibility_reduction of the immune system
<i>initial_recovery</i>	epiworld_double Initial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

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

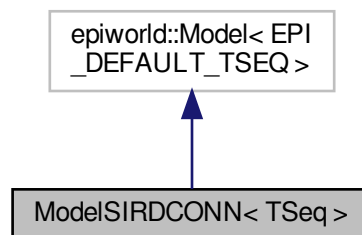
- include/epiworld/models/sird.hpp

## 13.20 ModelSIRDCONN< TSeq > Class Template Reference

Inheritance diagram for ModelSIRDCONN< TSeq >:



Collaboration diagram for ModelSIRDCONN< TSeq >:



### Public Member Functions

- [ModelSIRDCONN](#) ([ModelSIRDCONN](#)< TSeq > &model, std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double contact\_rate, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate, epiworld\_double death\_rate)  
*Template for a Susceptible-Infected-Removed (SIR) model.*
- **ModelSIRDCONN** (std::string vname, epiworld\_fast\_uint n, epiworld\_double prevalence, epiworld\_double contact\_rate, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate, epiworld\_double death\_rate)
- void **run** (epiworld\_fast\_uint ndays, int seed=-1)
- void **reset** ()
- [Model](#)< TSeq > \* **clone\_ptr** ()

### 13.20.1 Constructor & Destructor Documentation

## 13.20.1.1 ModelSIRDCONN()

```
template<typename TSeq >
ModelSIRDCONN< TSeq >::ModelSIRDCONN (
 ModelSIRDCONN< TSeq > & model,
 std::string vname,
 epiworld_fast_uint n,
 epiworld_double prevalence,
 epiworld_double contact_rate,
 epiworld_double transmission_rate,
 epiworld_double recovery_rate,
 epiworld_double death_rate) [inline]
```

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

## Parameters

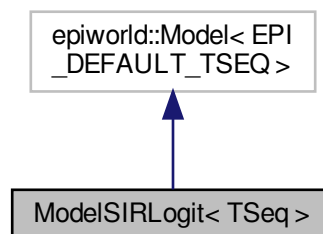
<i>model</i>	A Model<TSeq> object where to set up the SIR.
<i>vname</i>	std::string Name of the virus
<i>prevalence</i>	Initial prevalence (proportion)
<i>contact_rate</i>	Average number of contacts (interactions) per step.
<i>transmission_rate</i>	Probability of transmission
<i>recovery_rate</i>	Probability of recovery
<i>death_rate</i>	Probability of death

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

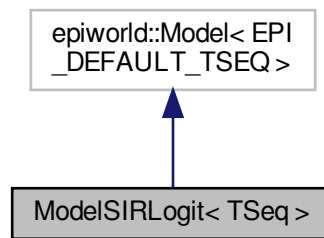
- include/epiworld/models/sirdconnected.hpp

## 13.21 ModelSIRLogit&lt; TSeq &gt; Class Template Reference

Inheritance diagram for ModelSIRLogit< TSeq >:



Collaboration diagram for `ModelSIRLogit< TSeq >`:



## Public Member Functions

- [ModelSIRLogit](#) ([ModelSIRLogit](#)< TSeq > &model, std::string vname, double \*data, size\_t ncols, std::vector< double > coefs\_infect, std::vector< double > coefs\_recover, std::vector< size\_t > coef\_infect\_cols, std::vector< size\_t > coef\_recover\_cols, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate, epiworld\_double prevalence)  
*Template for a Susceptible-Infected-Removed (SIR) model.*
- **ModelSIRLogit** (std::string vname, double \*data, size\_t ncols, std::vector< double > coefs\_infect, std::vector< double > coefs\_recover, std::vector< size\_t > coef\_infect\_cols, std::vector< size\_t > coef\_recover\_cols, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate, epiworld\_double prevalence)
- void **run** (epiworld\_fast\_uint ndays, int seed=-1)
- [Model](#)< TSeq > \* **clone\_ptr** ()
- void **reset** ()

## Public Attributes

- std::vector< double > **coefs\_infect**
- std::vector< double > **coefs\_recover**
- std::vector< size\_t > **coef\_infect\_cols**
- std::vector< size\_t > **coef\_recover\_cols**

### 13.21.1 Constructor & Destructor Documentation

### 13.21.1.1 ModelSIRLogit()

```
template<typename TSeq >
ModelSIRLogit< TSeq >::ModelSIRLogit (
 ModelSIRLogit< TSeq > & model,
 std::string vname,
 double * data,
 size_t ncols,
 std::vector< double > coefs_infect,
 std::vector< double > coefs_recover,
 std::vector< size_t > coef_infect_cols,
 std::vector< size_t > coef_recover_cols,
 epiworld_double transmission_rate,
 epiworld_double recovery_rate,
 epiworld_double prevalence) [inline]
```

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

#### Parameters

<i>vname</i>	Name of the virus.
<i>coefs_infect</i>	Double ptr. Infection coefficients.
<i>coefs_recover</i>	Double ptr. Recovery coefficients.
<i>ncoenf_infect</i>	Unsigned int. Number of infection coefficients.
<i>ncoenf_recover</i>	Unsigned int. Number of recovery coefficients.
<i>coef_infect_cols</i>	Vector<unsigned int>. Ids of infection vars.
<i>coef_recover_cols</i>	Vector<unsigned int>. Ids of recover vars.
<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>contact_rate</i>	Average number of contacts (interactions) per step.
<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:

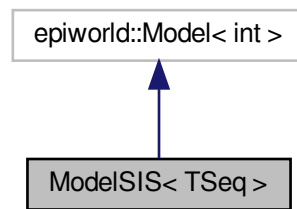
- include/epiworld/models/sirlogit.hpp

## 13.22 ModelSIS< TSeq > Class Template Reference

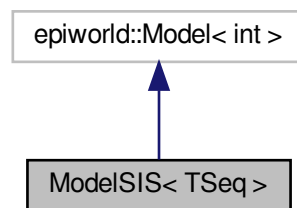
Template for a Susceptible-Infected-Susceptible (SIS) model.

```
#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 transmission\_rate, epiworld\_double recovery\_rate)
- **ModelSIS** (std::string vname, epiworld\_double prevalence, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate)

### 13.22.1 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_efficacy</i>	epiworld_double Initial susceptibility_reduction of the immune system
<i>initial_recovery</i>	epiworld_double Initial recovery_rate rate of the immune system

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

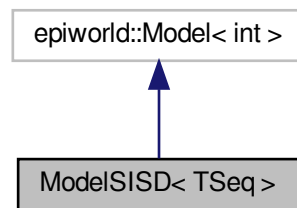
- include/epiworld/models/sis.hpp

## 13.23 ModelSISD< TSeq > Class Template Reference

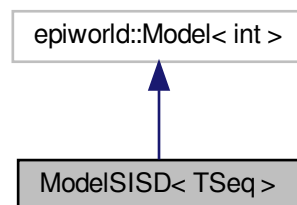
Template for a Susceptible-Infected-Susceptible-Deceased (SISD) model.

```
#include <sisd.hpp>
```

Inheritance diagram for ModelSISD< TSeq >:



Collaboration diagram for ModelSISD< TSeq >:



### Public Member Functions

- **ModelSISD** ([ModelSISD](#)< TSeq > &model, std::string vname, epiworld\_double prevalence, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate, epiworld\_double death\_rate)
- **ModelSISD** (std::string vname, epiworld\_double prevalence, epiworld\_double transmission\_rate, epiworld\_double recovery\_rate, epiworld\_double death\_rate)

#### 13.23.1 Detailed Description

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

Template for a Susceptible-Infected-Susceptible-Deceased (SISD) model.

## Parameters

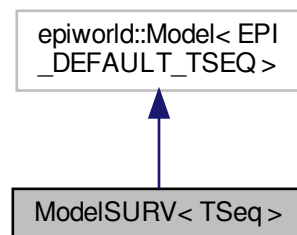
<i>vname</i>	std::string Name of the virus
<i>initial_prevalence</i>	epiworld_double Initial prevalence
<i>initial_efficacy</i>	epiworld_double Initial susceptibility_reduction of the immune system
<i>initial_recovery</i>	epiworld_double Initial recovery_rate rate of the immune system
<i>inital_death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

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

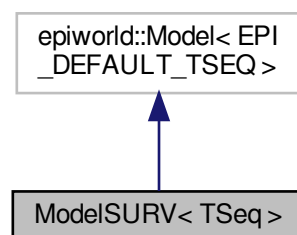
- include/epiworld/models/sisd.hpp

## 13.24 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 asyptomatic.



*Parameters*

vname	<i>String. Name of the virus</i>
prevalence	<i>Integer. Number of initial cases of the virus.</i>
efficacy_vax	<i>Double. Efficacy of the vaccine (1 - P(acquire the disease)).</i>
latent_period	<i>Double. Shape parameter of a Gamma(latent_period, 1) distribution. This coincides with the expected number of latent days.</i>
infect_period	<i>Double. Shape parameter of a Gamma(infected_period, 1) distribution. This coincides with the expected number of infectious days.</i>
prob_symptoms	<i>Double. Probability of generating symptoms.</i>
prop_vaccinated	<i>Double. Probability of vaccination. Coincides with the initial prevalence of vaccinated individuals.</i>
prop_vax_redux_transm	<i>Double. Factor by which the vaccine reduces transmissibility.</i>
prop_vax_redux_infect	<i>Double. Factor by which the vaccine reduces the chances of becoming infected.</i>
surveillance_prob	<i>Double. Probability of testing an agent.</i>
prob_transmission	<i>Double. Raw transmission probability.</i>
prob_death	<i>Double. Raw probability of death for symptomatic individuals.</i>
prob_noreinfect	<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)

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

- include/epiworld/models/surveillance.hpp

## 13.25 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

## 13.26 PersonTools< TSeq > Class Template Reference

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

- include/epiworld/config.hpp

## 13.27 Progress Class Reference

A simple progress bar.

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

### Public Member Functions

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

### 13.27.1 Detailed Description

A simple progress bar.

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

- include/epiworld/progress.hpp

## 13.28 Queue< TSeq > Class Template Reference

Controls which agents are verified at each step.

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

### Public Member Functions

- void **operator+=** ([Agent](#)< TSeq > \*p)
- void **operator-=** ([Agent](#)< TSeq > \*p)
- epiworld\_fast\_int & **operator[]** (epiworld\_fast\_uint i)
- void **reset** ()
- bool **operator==** (const [Queue](#)< TSeq > &other) const
- bool **operator!=** (const [Queue](#)< TSeq > &other) const

### Static Public Attributes

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

### Friends

- class **Model**< TSeq >

### 13.28.1 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

## 13.29 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

## 13.30 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

## 13.31 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\_state** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **set\_queue** (epiworld\_fast\_int init, epiworld\_fast\_int post)
- void **get\_state** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)
- void **get\_queue** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*post)
- bool **operator==** (const [Tool](#)< TSeq > &other) const
- bool **operator!=** (const [Tool](#)< TSeq > &other) const
- void **print** () const
- bool **operator==** (const [Tool](#)< std::vector< int >> &other) const

**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)

**13.31.1 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

**13.32 Tools< TSeq > Class Template Reference**

Set of tools (useful for building iterators)

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

## Public Member Functions

- **Tools** ([Agent](#)< TSeq > &p)
- std::vector< ToolPtr< TSeq > >::iterator **begin** ()
- std::vector< ToolPtr< TSeq > >::iterator **end** ()
- ToolPtr< TSeq > & **operator**() (size\_t i)
- ToolPtr< TSeq > & **operator**[] (size\_t i)
- size\_t **size** () const noexcept
- void **print** () const noexcept

## Friends

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

### 13.32.1 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

## 13.33 Tools\_const< TSeq > Class Template Reference

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

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

## Public Member Functions

- **Tools\_const** (const [Agent](#)< TSeq > &p)
- std::vector< ToolPtr< TSeq > >::const\_iterator **begin** () const
- std::vector< ToolPtr< TSeq > >::const\_iterator **end** () const
- const ToolPtr< TSeq > & **operator**() (size\_t i)
- const ToolPtr< TSeq > & **operator**[] (size\_t i)
- size\_t **size** () const noexcept
- void **print** () const noexcept

## Friends

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

### 13.33.1 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

## 13.34 UserData< TSeq > Class Template Reference

Personalized data by the user.

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

### Public Member Functions

- **UserData** ([Model](#)< TSeq > &m)
- **UserData** ([Model](#)< TSeq > \*m)
- **UserData** (std::vector< std::string > names)  
*Construct a new User Data object.*
- std::vector< std::string > & **get\_names** ()
- std::vector< int > & **get\_dates** ()
- std::vector< epiworld\_double > & **get\_data** ()
- void **get\_all** (std::vector< std::string > \*names=nullptr, std::vector< int > \*date=nullptr, std::vector< epiworld\_double > \*data=nullptr)
- epiworld\_fast\_uint **nrow** () const
- epiworld\_fast\_uint **ncol** () const
- void **write** (std::string fn)
- void **print** () const

#### Append data

*Parameters*

x	A vector of length <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 >

**13.34.1 Detailed Description**

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

Personalized data by the user.

**Template Parameters**

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

**13.34.2 Constructor & Destructor Documentation****13.34.2.1 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

## 13.35 vecHasher< T > Struct Template Reference

Vector hasher.

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

### Public Member Functions

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

### 13.35.1 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

## 13.36 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)
- std::shared\_ptr< 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** ()
- bool **operator==** (const [Virus](#)< TSeq > &other) const
- bool **operator!=** (const [Virus](#)< TSeq > &other) const
- void **print** () const
- bool **operator==** (const [Virus](#)< std::vector< int >> &other) const

### 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)
- epiworld\_double **get\_incubation** ([Model](#)< TSeq > \*model)
- void **post\_recovery** ([Model](#)< TSeq > \*model)
- void **set\_post\_recovery** (PostRecoveryFun< TSeq > fun)
- void **set\_post\_immunity** (epiworld\_double prob)
- void **set\_post\_immunity** (epiworld\_double \*prob)
- void **set\_prob\_infecting\_fun** (VirusFun< TSeq > fun)
- void **set\_prob\_recovery\_fun** (VirusFun< TSeq > fun)
- void **set\_prob\_death\_fun** (VirusFun< TSeq > fun)
- void **set\_incubation\_fun** (VirusFun< TSeq > fun)
- void **set\_prob\_infecting** (const epiworld\_double \*prob)
- void **set\_prob\_recovery** (const epiworld\_double \*prob)
- void **set\_prob\_death** (const epiworld\_double \*prob)
- void **set\_incubation** (const epiworld\_double \*prob)
- void **set\_prob\_infecting** (epiworld\_double prob)
- void **set\_prob\_recovery** (epiworld\_double prob)
- void **set\_prob\_death** (epiworld\_double prob)
- void **set\_incubation** (epiworld\_double prob)

### Get and set the state and queue

After applied, viruses can change the state and affect the queue of agents. These function sets the default values, which are retrieved when adding or removing a virus does not specify a change in state or in queue.

*Parameters*

init	After the virus/tool is added to the agent.
end	After the virus/tool is removed.
removed	After the agent ( <a href="#">Agent</a> ) is removed.

- void **set\_state** (epiworld\_fast\_int init, epiworld\_fast\_int end, epiworld\_fast\_int removed=-99)
- void **set\_queue** (epiworld\_fast\_int init, epiworld\_fast\_int end, epiworld\_fast\_int removed=-99)
- void **get\_state** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*end, epiworld\_fast\_int \*removed=nullptr)
- void **get\_queue** (epiworld\_fast\_int \*init, epiworld\_fast\_int \*end, epiworld\_fast\_int \*removed=nullptr)

**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)

**13.36.1 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

**13.37 Viruses< TSeq > Class Template Reference**

Set of viruses (useful for building iterators)

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

## Public Member Functions

- **Viruses** ([Agent](#)< TSeq > &p)
- std::vector< VirusPtr< TSeq > >::iterator **begin** ()
- std::vector< VirusPtr< TSeq > >::iterator **end** ()
- VirusPtr< TSeq > & **operator**() (size\_t i)
- VirusPtr< TSeq > & **operator**[] (size\_t i)
- size\_t **size** () const noexcept
- void **print** () const noexcept

## Friends

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

### 13.37.1 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

## 13.38 Viruses\_const< TSeq > Class Template Reference

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

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

## Public Member Functions

- **Viruses\_const** (const [Agent](#)< TSeq > &p)
- std::vector< VirusPtr< TSeq > >::const\_iterator **begin** () const
- std::vector< VirusPtr< TSeq > >::const\_iterator **end** () const
- const VirusPtr< TSeq > & **operator**() (size\_t i)
- const VirusPtr< TSeq > & **operator**[] (size\_t i)
- size\_t **size** () const noexcept
- void **print** () const noexcept

## Friends

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

### 13.38.1 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-state.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-state.hpp:



This graph shows which files directly or indirectly include this file:



## Functions

- `template<typename TSeq = EPI_DEFAULT_TSEQ>`  
`void default_update_susceptible (Agent< TSeq > *p, Model< TSeq > *m)`
- `template<typename TSeq = EPI_DEFAULT_TSEQ>`  
`void default_update_exposed (Agent< TSeq > *p, Model< TSeq > *m)`

### 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

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#### Copyright

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