

epiworld

0.0-1

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# Chapter 1

## Main Page

### 1.1 epiworld

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.

### 1.2 Hello world

Here is a simple SIRS model implemented with

```
#include "../include/epiworld/epiworld.hpp"
using namespace epiworld;
int main()
{
    // Creating a model
    Model<> model;
    // Adding the tool and virus
    Virus<> virus("covid 19");
    virus.set_post_immunity(1.0);
    model.add_virus_n(virus, 5);

    Tool<> tool("vaccine");
    model.add_tool(tool, .5);
    // Generating a random pop
    model.pop_from_random(100000);
    // Initializing setting days and seed
    model.init(100, 123);
}
```

```
// Running the model
model.run();
model.print();

}
```

And you should get something like the following:

Running the model...

```
||||| done.

SIMULATION STUDY
Population size      : 100000
Days (duration)     : 100 (of 100)
Number of variants  : 1
Last run elapsed t  : 280.00ms
Rewiring             : off
Virus(es):
- covid 19 (baseline prevalence: 5 seeds)
Tool(s):
- vaccine (baseline prevalence: 50.00%)
Model parameters:
Distribution of the population at time 100:
- Total healthy (S)   : 99995 -> 97390
- Total recovered (S) : 0 -> 2554
- Total infected (I)  : 5 -> 56
- Total removed (R)   : 0 -> 0
(S): Susceptible, (I): Infected, (R): Recovered
```

Which took about 0.280 seconds.

## 1.2.1 Tools

## 1.2.2 Contagion

Susceptible individuals can acquire a virus from any of their infected connections. The probability that susceptible individual  $i$  gets the virus  $v$  from individual  $j$  depends on how three things:

1. The transmissibility of the virus,  $P_v$  in  $[0,1]$ ,
2. The contagion reduction factor of  $i$ ,  $Cr$  in  $[0,1]$ , and
3. The host's transmission reduction factor,  $Tr$   $[0,1]$ .

The last two are computed from  $i$  and  $j$ 's tools. Ultimately, the probability of  $i$  getting virus  $v$  from  $j$  equals:

$$P(\text{Virus } v) = P_v * (1 - Cr) * (1 - Tr)$$

Nonetheless, the default behavior of the simulation model is to assume that individuals can acquire only one disease at a time, if any. This way, the actual probability is:

$$P(\text{Virus } v | \text{ at most one virus}) = \text{Prcond}(i, v, j)$$

The latter is calculated using Bayes' rule

$$\begin{aligned} \text{Prcond}(i, v, j) &= P(\text{at most one virus} | \text{Virus } v) * P(\text{Variant } v) / P(\text{at most one virus}) \\ &= P(\text{Only Virus } v) / P(\text{Virus } v) * P(\text{Virus } v) / P(\text{at most one virus}) \\ &= P(\text{Only Virus } v) / P(\text{at most one virus}) \end{aligned}$$

Where

$$\begin{aligned} P(\text{Only Virus } V) &= P(\text{Virus } V) * \text{Prod}(m \neq V) (1 - P(\text{Virus } m)) \\ P(\text{at most one virus}) &= P(\text{None}) + \text{Sum}(k \text{ in viruses}) P(\text{Virus } k) * \text{Prod}(m \neq k) (1 - P(\text{Virus } m)) \\ P(\text{None}) &= \text{Prod}(k \text{ in Viruses}) (1 - P(\text{Virus } k)) \end{aligned}$$

This way, viruses with higher transmissibility will be more likely to be acquired when competing with other variants.

## Chapter 2

# Class Index

### 2.1 Class List

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

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## Chapter 3

# Class Documentation

### 3.1 AdjList Class Reference

#### Public Member Functions

- [AdjList](#) (const std::vector< unsigned int > &source, const std::vector< unsigned int > &target, bool directed, int min\_id=-1, int max\_id=-1)  
*Construct a new Adj List object.*
- void **read\_edgelist** (std::string fn, int skip=0, bool directed=true, int min\_id=-1, int max\_id=-1)
- std::map< unsigned int, unsigned int > **operator()** (unsigned int i) const
- void **print** (unsigned int limit=20u) const
- unsigned int **get\_id\_max** () const
- unsigned int **get\_id\_min** () const
- size\_t **vcount** () const
- size\_t **ecount** () const
- std::map< unsigned int, std::map< unsigned int, unsigned int > > & **get\_dat** ()
- bool **is\_directed** () const

#### 3.1.1 Constructor & Destructor Documentation

##### 3.1.1.1 AdjList()

```
AdjList::AdjList (
    const std::vector< unsigned int > & source,
    const std::vector< unsigned int > & target,
    bool directed,
    int min_id = -1,
    int max_id = -1 ) [inline]
```

Construct a new Adj List object.

It will create an adjacency list object with  $\text{maxid} - \text{minid} + 1$  nodes. If min\_id and max\_id are not specified (both < 0), then the program will try to figure them out automatically by looking at the range of the observed ids.

## Parameters

<i>source</i>	Unsigned int vector with the source
<i>target</i>	Unsigned int vector with the target
<i>directed</i>	Bool true if the network is directed
<i>min_id</i>	int min id.
<i>max_id</i>	int max id.

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

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

## 3.2 DataBase< TSeq > Class Template Reference

Statistical data about the process.

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

### Public Member Functions

- **DataBase** (int freq=1)
- void **record\_variant** ([Virus](#)< TSeq > \*v)  
*Registering a new variant.*
- void **set\_seq\_hasher** (std::function< std::vector< int >(TSeq)> fun)
- void **set\_model** ([Model](#)< TSeq > &m)
- [Model](#)< TSeq > \* **get\_model** ()
- void **record** ()
- const std::vector< TSeq > & **get\_sequence** () const
- const std::vector< int > & **get\_nexposed** () const
- size\_t **size** () const
- void **up\_exposed** ([Virus](#)< TSeq > \*v, epiworld\_fast\_uint new\_status)
- void **down\_exposed** ([Virus](#)< TSeq > \*v, epiworld\_fast\_uint prev\_status)
- void **state\_change** (epiworld\_fast\_uint prev\_status, epiworld\_fast\_uint new\_status)
- void **record\_transition** (epiworld\_fast\_uint from, epiworld\_fast\_uint to)
- void **write\_data** (std::string fn\_variant\_info, std::string fn\_variant\_hist, std::string fn\_total\_hist, std::string fn←\_transmission, std::string fn\_transition) const
- void **record\_transmission** (int i, int j, int variant)
- size\_t **get\_nvariants** () const
- void **reset** ()
- void **set\_user\_data** (std::vector< std::string > names)
- void **add\_user\_data** (std::vector< epiworld\_double > x)
- void **add\_user\_data** (unsigned int j, epiworld\_double x)
- [UserData](#)< TSeq > & **get\_user\_data** ()

**Get recorded information from the model**

#### Parameters

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

#### Returns

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

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

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

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

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

- int **get\_today\_total** (std::string what) const
- int **get\_today\_total** (epiworld\_fast\_uint what) const
- void **get\_today\_total** (std::vector< std::string > \*status=nullptr, std::vector< int > \*counts=nullptr) const
- void **get\_today\_variant** (std::vector< std::string > &status, std::vector< int > &id, std::vector< int > &counts) const
- void **get\_hist\_total** (std::vector< int > \*date, std::vector< std::string > \*status, std::vector< int > \*counts) const
- void **get\_hist\_variant** (std::vector< int > &date, std::vector< int > &id, std::vector< std::string > &status, std::vector< int > &counts) const

#### Friends

- class **Model**< TSeq >

### 3.2.1 Detailed Description

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

Statistical data about the process.

#### Template Parameters

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

### 3.2.2 Member Function Documentation

#### 3.2.2.1 record\_variant()

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

Registering a new variant.

**Parameters**

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

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

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

### 3.3 LFMCMC< TData > Class Template Reference

Likelihood-Free Markov Chain Monte Carlo.

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

**Public Member Functions**

- void **run** (VEC(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** (FUN< void(VEC(epiworld\_double)&, LFMCMC< TData > \*)> fun)
- void **set\_simulation\_fun** (FUN< TData(VEC(epiworld\_double)&, LFMCMC< TData > \*)> fun)
- void **set\_summary\_fun** (FUN< VEC(epiworld\_double)(TData &, LFMCMC< TData > \*)> fun)
- void **set\_kernel\_fun** (FUN< epiworld\_double(VEC(epiworld\_double)&, epiworld\_double, LFMCMC< TData > \*)> fun)
- const size\_t **get\_n\_samples** ()
- const size\_t **get\_n\_statistics** ()
- const size\_t **get\_n\_parameters** ()
- const epiworld\_double **get\_epsilon** ()
- const **VEC** (epiworld\_double) &get\_params\_now()
- const **VEC** (epiworld\_double) &get\_params\_prev()
- const **VEC** (epiworld\_double) &get\_params\_init()
- const **VEC** (epiworld\_double) &get\_statistics\_obs()
- const **VEC** (epiworld\_double) &get\_statistics\_hist()
- const **VEC** (bool) &get\_statistics\_accepted()
- const **VEC** (epiworld\_double) &get\_posterior\_lf\_prob()
- const **VEC** (epiworld\_double) &get\_acceptance\_prob()
- const **VEC** (epiworld\_double) &get\_drawn\_prob()
- **VEC** (TData) \*get\_sampled\_data()

**Random number generation****Parameters**

eng	
-----	--

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

- `std::mt19937 * get_rand_engine ()`
- `void seed (unsigned int s)`
- `void set_rand_gamma (epiworld_double alpha, epiworld_double beta)`
- `epiworld_double runif ()`
- `epiworld_double rnorm ()`
- `epiworld_double rnorm (epiworld_double mean, epiworld_double sd)`
- `epiworld_double rgamma ()`
- `epiworld_double rgamma (epiworld_double alpha, epiworld_double beta)`

### 3.3.1 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 file:

- `include/epiworld/math/lfcmc.cpp`

## 3.4 Location< TSeq > Class Template Reference

### Public Member Functions

- `add_person (Person< TSeq > &p)`
- `add_person (Person< TSeq > *p)`
- `size_t count () const`
- `void reset ()`

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

- `include/epiworld/location-bones.cpp`

## 3.5 Model< TSeq > Class Template Reference

Core class of epiworld.

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

## Public Member Functions

- **Model** (const [Model](#)< TSeq > &m)
  - **Model** ([Model](#)< TSeq > &&m)
  - [Model](#)< TSeq > & **operator=** (const [Model](#)< TSeq > &m)
  - void **clone\_population** (std::vector< [Person](#)< TSeq > > &p, std::map< int, int > &p\_ids, bool &d, [Model](#)< TSeq > \*m=nullptr) const
  - void **clone\_population** (const [Model](#)< TSeq > &m)
  - [DataBase](#)< TSeq > & **get\_db** ()
  - epiworld\_double & **operator()** (std::string pname)
  - size\_t **size** () const
  - void **add\_virus** ([Virus](#)< TSeq > v, epiworld\_double preval)
  - void **add\_virus\_n** ([Virus](#)< TSeq > v, unsigned int preval)
  - void **add\_tool** ([Tool](#)< TSeq > t, epiworld\_double preval)
  - void **add\_tool\_n** ([Tool](#)< TSeq > t, unsigned int preval)
  - void **record\_variant** ([Virus](#)< TSeq > \*v)
  - int **get\_nvariants** () const
  - unsigned int **get\_ndays** () const
  - unsigned int **get\_n\_replicates** () const
  - void **set\_ndays** (unsigned int ndays)
  - bool **get\_verbose** () const
  - void **verbose\_off** ()
  - void **verbose\_on** ()
  - int **today** () const
- The current time of the model.*
- void **set\_update\_susceptible** (UpdateFun< TSeq > fun)
  - void **set\_update\_exposed** (UpdateFun< TSeq > fun)
  - void **set\_update\_removed** (UpdateFun< TSeq > fun)
  - void **write\_data** (std::string fn\_variant\_info, std::string fn\_variant\_hist, std::string fn\_total\_hist, std::string fn\_transmission, std::string fn\_transition) const
- Wrapper of `DataBase::write_data`*
- std::map< std::string, epiworld\_double > & **params** ()
  - void **reset** ()
- Reset the model.*
- void **print** () const
  - [Model](#)< TSeq > && **clone** () const
  - void **reset\_status\_codes** (std::vector< epiworld\_fast\_uint > codes, std::vector< std::string > names, bool verbose=true)
- Reset all the status codes of the model.*
- void **get\_elapsed** (std::string unit="auto", epiworld\_double \*last\_elapsed=nullptr, epiworld\_double \*total\_elapsed=nullptr, std::string \*unit\_abbrev=nullptr, bool print=true) const
  - void **add\_global\_action** (std::function< void([Model](#)< TSeq > \*)> fun, int date)
- Set a global action.*
- void **run\_global\_actions** ()
  - void **clear\_status\_set** ()

### Set the backup object

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

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

### Random number generation

*Parameters*

eng	
-----	--

- void **set\_rand\_engine** (std::mt19937 &eng)
- std::mt19937 \* **get\_rand\_engine** ()
- void **seed** (unsigned int s)
- void **set\_rand\_gamma** (epiworld\_double alpha, epiworld\_double beta)
- epiworld\_double **runif** ()
- epiworld\_double **rnorm** ()
- epiworld\_double **rnorm** (epiworld\_double mean, epiworld\_double sd)
- epiworld\_double **rgamma** ()
- epiworld\_double **rgamma** (epiworld\_double alpha, epiworld\_double beta)

**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>
min_id	<i>int Minimum id number (if negative, the program will try to guess from the data.)</i>
max_id	<i>int Maximum id number (if negative, the program will try to guess from the data.)</i>
al	<i><a href="#">AdjList</a> to read into the model.</i>

- void **pop\_from\_adjlist** (std::string fn, int skip=0, bool directed=false, int min\_id=-1, int max\_id=-1)
- void **pop\_from\_adjlist** ([AdjList](#) al)
- bool **is\_directed** () const
- std::vector< [Person](#)< TSeq > > \* **get\_population** ()
- void **pop\_from\_random** (unsigned int n=1000, unsigned int k=5, bool d=false, epiworld\_double p=.01)

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

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

- void **init** (unsigned int ndays, unsigned int seed)
- void **update\_status** ()
- void **mutate\_variant** ()
- void **next** ()
- void **run** ()
- *Runs the simulation (after initialization)*
- void **run\_multiple** (unsigned int nexperiments, std::function< void([Model](#)< TSeq > \*)> fun, bool [reset](#), bool verbose)

**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< [Person](#)< 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< unsigned int > &source, std::vector< unsigned int > &target) const

### Manage status (states) in the model

*Adding values of s that are already present in the model will result in an error.*

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

### Parameters

s	<i>unsigned int Code of the status</i>
lab	<i>std::string Name of the status.</i>

### Returns

*add\_status\* returns nothing.*

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

- void **add\_status\_susceptible** (epiworld\_fast\_uint s, std::string lab)
- void **add\_status\_exposed** (epiworld\_fast\_uint s, std::string lab)
- void **add\_status\_removed** (epiworld\_fast\_uint s, std::string lab)
- void **add\_status\_susceptible** (std::string lab)
- void **add\_status\_exposed** (std::string lab)
- void **add\_status\_removed** (std::string lab)
- const std::vector< epiworld\_fast\_uint > & **get\_status\_susceptible** () const
- const std::vector< epiworld\_fast\_uint > & **get\_status\_exposed** () const
- const std::vector< epiworld\_fast\_uint > & **get\_status\_removed** () const
- const std::vector< std::string > & **get\_status\_susceptible\_labels** () const
- const std::vector< std::string > & **get\_status\_exposed\_labels** () const
- const std::vector< std::string > & **get\_status\_removed\_labels** () const
- void **print\_status\_codes** () const
- epiworld\_fast\_uint **get\_default\_susceptible** () const
- epiworld\_fast\_uint **get\_default\_exposed** () const



- `epiworld_fast_uint` **get\_default\_removed** () const

### Set the user data object

#### Parameters

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

- void **set\_user\_data** (std::vector< std::string > names)  
[@
- void **add\_user\_data** (unsigned int j, epiworld\_double x)
- void **add\_user\_data** (std::vector< epiworld\_double > x)
- **UserData**< TSeq > & **get\_user\_data** ()

### Queuing system

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

- void **queuing\_on** ()  
*Activates the queuing system (default.)*
- void **queuing\_off** ()  
*Deactivates the queuing system.*
- bool **is\_queuing\_on** () const  
*Query if the queuing system is on.*
- **Queue**< TSeq > & **get\_queue** ()  
*Retrieve the **Queue** object.*

### Public Attributes

- std::vector< epiworld\_double > **array\_double\_tmp**
- std::vector< **Virus**< TSeq > \* > **array\_virus\_tmp**

### Friends

- class **Person**< TSeq >
- class **DataBase**< TSeq >
- class **Queue**< TSeq >

### 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 `unsigned int` 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 function `set_param()` can be used when the parameter already exists in the model.

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

## Parameters

<i>initial_val</i>	
<i>pname</i>	Name of the parameter to add or to fetch

## Returns

The current value of the parameter in the model.

- `epiworld_double * p0`
- `epiworld_double * p1`
- `epiworld_double * p2`
- `epiworld_double * p3`
- `epiworld_double * p4`
- `epiworld_double * p5`
- `epiworld_double * p6`
- `epiworld_double * p7`
- `epiworld_double * p8`
- `epiworld_double * p9`
- `epiworld_double * p10`
- `epiworld_double * p11`
- `epiworld_double * p12`
- `epiworld_double * p13`
- `epiworld_double * p14`
- `epiworld_double * p15`
- `epiworld_double * p16`
- `epiworld_double * p17`
- `epiworld_double * p18`
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- `epiworld_double * p27`
- `epiworld_double * p28`
- `epiworld_double * p29`
- `epiworld_double * p30`
- `epiworld_double * p31`
- `epiworld_double * p32`
- `epiworld_double * p33`
- `epiworld_double * p34`
- `epiworld_double * p35`
- `epiworld_double * p36`
- `epiworld_double * p37`
- `epiworld_double * p38`
- `epiworld_double * p39`
- `unsigned int npar_used = 0u`
- `epiworld_double add_param (epiworld_double initial_val, std::string pname)`
- `epiworld_double set_param (std::string pname)`
- `epiworld_double get_param (unsigned int k)`
- `epiworld_double get_param (std::string pname)`
- `epiworld_double par (unsigned int k)`
- `epiworld_double par (std::string pname)`

### 3.5.1 Detailed Description

```
template<typename TSeq = bool>
class Model< TSeq >
```

Core class of epiworld.

The model class provides the wrapper that puts together [Person](#), [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.)
-------------	---

### 3.5.2 Member Function Documentation

#### 3.5.2.1 add\_global\_action()

```
template<typename TSeq = bool>
void Model< TSeq >::add_global_action (
    std::function< void (Model< TSeq > *)> fun,
    int date )
```

Set a global action.

#### Parameters

<i>fun</i>	A function to be called on the prescribed dates
<i>date</i>	Integer indicating when the function is called (see details)

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

#### 3.5.2.2 reset()

```
template<typename TSeq = bool>
void Model< TSeq >::reset ( )
```

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

### 3.5.2.3 reset\_status\_codes()

```
template<typename TSeq = bool>
void Model< TSeq >::reset_status_codes (
    std::vector< epiworld_fast_uint > codes,
    std::vector< std::string > names,
    bool verbose = true )
```

Reset all the status codes of the model.

The default values are those specified in the enum STATUS.

#### Parameters

<i>codes</i>	In the following order: Susceptible, Infected, Removed
<i>names</i>	Names matching the codes
<i>verbose</i>	When <code>true</code> , it will print the new mappings.

### 3.5.2.4 run\_multiple()

```
template<typename TSeq = bool>
void Model< TSeq >::run_multiple (
    unsigned int n_experiments,
    std::function< void(Model< TSeq > *)> fun,
    bool reset,
    bool verbose )
```

#### Parameters

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

### 3.5.2.5 write\_data()

```
template<typename TSeq = bool>
void Model< TSeq >::write_data (
    std::string fn_variant_info,
    std::string fn_variant_hist,
```

```
std::string fn_total_hist,
std::string fn_transmission,
std::string fn_transition ) const
```

Wrapper of DataBase::write\_data

#### Parameters

<i>fn_variant_info</i>	Filename. Information about the variant.
<i>fn_variant_hist</i>	Filename. History of the variant.
<i>fn_total_hist</i>	Filename. Aggregated history (status)
<i>fn_transmission</i>	Filename. Transmission history.
<i>fn_transition</i>	Filename. Markov transition history.

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

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

## 3.6 Person< TSeq > Class Template Reference

Person (agents)

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

### Public Member Functions

- void **init** (epiworld\_fast\_uint baseline\_status)
- void **add\_tool** (int d, Tool< TSeq > tool)
- void **add\_virus** (Virus< TSeq > \*virus)
- void **rm\_virus** (Virus< TSeq > \*virus)
- int **get\_id** () const  
*Id of the individual.*
- unsigned int **get\_index** () const  
*Location (0, ..., n-1).*
- std::mt19937 \* **get\_rand\_engine** ()
- Model< TSeq > \* **get\_model** ()
- Virus< TSeq > & **get\_virus** (int i)
- PersonViruses< TSeq > & **get\_viruses** ()
- Tool< TSeq > & **get\_tool** (int i)
- PersonTools< TSeq > & **get\_tools** ()
- void **mutate\_variant** ()
- void **add\_neighbor** (Person< TSeq > \*p, bool check\_source=true, bool check\_target=true)
- std::vector< Person< TSeq > \* > & **get\_neighbors** ()
- void **update\_status** ()
- void **update\_status** (epiworld\_fast\_uint new\_status)
- const epiworld\_fast\_uint & **get\_status** () const
- const epiworld\_fast\_uint & **get\_status\_next** () const
- void **reset** ()
- bool **has\_tool** (unsigned int t) const
- bool **has\_tool** (std::string name) const
- bool **has\_virus** (unsigned int t) const
- bool **has\_virus** (std::string name) const

**Get the rates (multipliers) for the agent**

### Parameters

v	A pointer to a virus.
---	-----------------------

### Returns

*epiworld\_double*

- epiworld\_double **get\_susceptibility\_reduction** ([Virus](#)< TSeq > \*v)
  - epiworld\_double **get\_transmission\_reduction** ([Virus](#)< TSeq > \*v)
  - epiworld\_double **get\_recovery\_enhancer** ([Virus](#)< TSeq > \*v)
  - epiworld\_double **get\_death\_reduction** ([Virus](#)< TSeq > \*v)
- 
- void **set\_update\_susceptible** (UpdateFun< TSeq > fun)  
*Set the update functions.*
  - void **set\_update\_exposed** (UpdateFun< TSeq > fun)
  - void **set\_update\_removed** (UpdateFun< TSeq > fun)

### Friends

- class **Model**< TSeq >
- class **Tool**< TSeq >
- class **Queue**< TSeq >

## 3.6.1 Detailed Description

```
template<typename TSeq = bool>
class Person< TSeq >
```

[Person](#) (agents)

#### Template Parameters

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

## 3.6.2 Member Function Documentation

### 3.6.2.1 set\_update\_susceptible()

```
template<typename TSeq >
void Person< TSeq >::set_update_susceptible (
    UpdateFun< TSeq > fun ) [inline]
```

Set the update functions.

## Parameters

<i>fun</i>	
------------	--

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

- include/epiworld/config.hpp
- include/epiworld/person-bones.hpp
- include/epiworld/person-meat.hpp

## 3.7 PersonTools< TSeq > Class Template Reference

List of tools available for the individual to.

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

### Public Member Functions

- void **add\_tool** (int date, [Tool](#)< TSeq > tool)
- epiworld\_double **get\_susceptibility\_reduction** ([Virus](#)< TSeq > \*v)
- epiworld\_double **get\_transmission\_reduction** ([Virus](#)< TSeq > \*v)
- epiworld\_double **get\_recovery\_enhancer** ([Virus](#)< TSeq > \*v)
- epiworld\_double **get\_death\_reduction** ([Virus](#)< TSeq > \*v)
- 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)
- size\_t **size** () const
- [Tool](#)< TSeq > & **operator()** (int i)
- [Person](#)< TSeq > \* **get\_person** ()
- [Model](#)< TSeq > \* **get\_model** ()
- void **reset** ()
- bool **has\_tool** (unsigned int t) const
- bool **has\_tool** (std::string name) const

### Friends

- class **Person**< TSeq >
- class **Model**< TSeq >

### 3.7.1 Detailed Description

```
template<typename TSeq = bool>
class PersonTools< TSeq >
```

List of tools available for the individual to.

## Template Parameters

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

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

- include/epiworld/config.hpp
- include/epiworld/persontools-bones.hpp
- include/epiworld/persontools-meat.hpp

### 3.8 PersonViruses< TSeq > Class Template Reference

Set of viruses in host.

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

#### Public Member Functions

- void **add\_virus** (epiworld\_fast\_uint new\_status, [Virus](#)< TSeq > v)
- size\_t **size** () const
- int **size\_active** () const
- [Virus](#)< TSeq > & **operator()** (int i)
- void **mutate** ()
- void **reset** ()
- void **deactivate** ([Virus](#)< TSeq > &v)
- [Person](#)< TSeq > \* **get\_host** ()
- bool **has\_virus** (unsigned int v) const
- bool **has\_virus** (std::string vname) const

#### Friends

- class **Person**< TSeq >
- class **Model**< TSeq >

#### 3.8.1 Detailed Description

```
template<typename TSeq = bool>
class PersonViruses< TSeq >
```

Set of viruses in host.

## Template Parameters

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

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



- `include/epiworld/person-bones.hpp`
- `include/epiworld/personviruses-bones.hpp`
- `include/epiworld/personviruses-meat.hpp`

## 3.9 Progress Class Reference

A simple progress bar.

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

### Public Member Functions

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

#### 3.9.1 Detailed Description

A simple progress bar.

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

- `include/epiworld/progress.hpp`

## 3.10 Queue< TSeq > Class Template Reference

Controls which agents are verified at each step.

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

### Public Member Functions

- void **operator+=** ([Person](#)< TSeq > \*p)
- void **operator-=** ([Person](#)< TSeq > \*p)
- `epiworld_fast_int` **operator[]** (unsigned int i) const
- void **set\_model** ([Model](#)< TSeq > \*m)
- void **update** ()

#### 3.10.1 Detailed Description

```
template<typename TSeq = bool>
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/model-bones.hpp
- include/epiworld/queue-bones.hpp

### 3.11 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

### 3.12 Tool< TSeq > Class Template Reference

Tools for defending the host against the virus.

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

#### Public Member Functions

- **Tool** (std::string name="unknown tool")
- void **set\_sequence** (TSeq d)
- void **set\_sequence\_unique** (TSeq d)
- void **set\_sequence** (std::shared\_ptr< TSeq > d)
- std::shared\_ptr< TSeq > **get\_sequence** ()
- TSeq & **get\_sequence\_unique** ()
- void **set\_name** (std::string name)
- std::string **get\_name** () const
- [Person](#)< TSeq > \* **get\_person** ()
- unsigned int **get\_id** () 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** ([Virus](#)< TSeq > \*v)
- *epiworld\_double* **get\_transmission\_reduction** ([Virus](#)< TSeq > \*v)
- *epiworld\_double* **get\_recovery\_enhancer** ([Virus](#)< TSeq > \*v)
- *epiworld\_double* **get\_death\_reduction** ([Virus](#)< TSeq > \*v)
- 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 **PersonTools**< TSeq >
- class **Person**< TSeq >
- class **Model**< TSeq >

**3.12.1 Detailed Description**

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

Tools for defending the host against the virus.

**Template Parameters**

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

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

- include/epiworld/config.hpp
- include/epiworld/tools-bones.hpp
- include/epiworld/tools-meat.hpp

**3.13 UserData< TSeq > Class Template Reference**

Personalized data by the user.

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

## Public Member Functions

- [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)
- unsigned int **nrow** () const
- unsigned int **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** (unsigned int 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()` (unsigned int i, unsigned int j)
- `epiworld_double & operator()` (unsigned int i, std::string name)

## Friends

- class **Model**< TSeq >
- class **DataBase**< TSeq >

### 3.13.1 Detailed Description

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

Personalized data by the user.

## Template Parameters

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

## 3.13.2 Constructor &amp; Destructor Documentation

## 3.13.2.1 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

## 3.14 vecHasher&lt; T &gt; Struct Template Reference

Vector hasher.

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

## Public Member Functions

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

## 3.14.1 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

### 3.15 Virus< TSeq > Class Template Reference

[Virus.](#)

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

#### Public Member Functions

- **Virus** (std::string name="unknown virus")
- void **mutate** ()
- void **set\_mutation** (MutFun< TSeq > fun)
- const TSeq \* **get\_sequence** ()
- void **set\_sequence** (TSeq sequence)
- [Person](#)< TSeq > \* **get\_host** ()
- [Model](#)< TSeq > \* **get\_model** ()
- void **set\_date** (int d)
- int **get\_date** () const
- void **set\_id** (int idx)
- int **get\_id** () const
- bool **is\_active** () const
- void **deactivate** ()
- void **set\_name** (std::string name)
- std::string **get\_name** () const
- std::vector< epiworld\_double > & **get\_data** ()

#### Get and set the tool functions

##### Parameters

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

##### Returns

*epiworld\_double*

- epiworld\_double **get\_prob\_infecting** ()
- epiworld\_double **get\_prob\_recovery** ()
- epiworld\_double **get\_prob\_death** ()
- void **post\_recovery** ()
- void **set\_post\_recovery** (PostRecoveryFun< TSeq > fun)
- void **set\_post\_immunity** (epiworld\_double prob)

- void **set\_post\_immunity** (epiworld\_double \*prob)
- void **set\_prob\_infecting\_fun** (VirusFun< TSeq > fun)
- void **set\_prob\_recovery\_fun** (VirusFun< TSeq > fun)
- void **set\_prob\_death\_fun** (VirusFun< TSeq > fun)
- void **set\_prob\_infecting** (epiworld\_double \*prob)
- void **set\_prob\_recovery** (epiworld\_double \*prob)
- void **set\_prob\_death** (epiworld\_double \*prob)
- void **set\_prob\_infecting** (epiworld\_double prob)
- void **set\_prob\_recovery** (epiworld\_double prob)
- void **set\_prob\_death** (epiworld\_double prob)

## Friends

- class **Person**< TSeq >
- class **Model**< TSeq >
- class **PersonViruses**< TSeq >
- class **DataBase**< TSeq >

### 3.15.1 Detailed Description

```
template<typename TSeq = bool>
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 host.

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

- include/epiworld/config.hpp
- include/epiworld/virus-bones.hpp
- include/epiworld/virus-meat.hpp





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