



Stockholm R useR Group: Microsimulation

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Who am I?

- Lektor in Biostatistics at Karolinska Institutet (colleagues with Alex Ploner)
- I did my undergraduate in statistics at the Department of Auckland in New Zealand (where  was developed)
-  user since 1998

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-  user since 1998
- Currently using microsimulation to model prostate cancer screening for a large randomised controlled trial planned for Stockholm

Disclaimers

- 1 This is work in progress!
- 2 This is a health-centric (chronic diseases) view of microsimulation

I welcome comments during the presentation.

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- 1 Background
- 2 R implementation of microsimulation
- 3 Random number streams
- 4 C++ implementation of microsimulation
- 5 Additional material

Simulation: model taxonomy

Cross-classification by the following factors

- Group-level (G) versus individual-level (I)
- Markov (M) versus non-Markov (nM)
- Discrete time (DT) versus continuous time (CT)

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- (I,nM,CT) =

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- (I,nM,DT) = Agent-based simulation
- (I,nM,CT) = Discrete event simulation

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- The International Microsimulation Association defines microsimulation as a **modelling technique** that operates at the level of **individual units** such as persons, households, vehicles or firms.
- In health sciences, microsimulation refers to a type of simulation modeling that generates **individual life histories**.
 - The technique is used when 'stock-and-flow' type modeling of proportions (macrosimulation) of the population cannot sufficiently describe the system of interest.
 - This type of modeling does not necessarily involve interaction between individuals and in that case can generate individuals independently of each other, and can easily work with continuous time instead of discrete time steps.

Microsimulation in health:

Two common approaches

① Discrete time, Markov

- Popular with health economists, who like their Markov models (e.g. TreeAge software)
- Alex Ploner is working on such a framework for modelling cervical cancer, with model specification and post-processing in



- and the simulation engine in C
- The [TraMineR](#) package is very useful for visualising discrete time life histories

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2 Continuous time, non-Markov

- Most generally implemented as a [discrete event simulation](#)
- We are working on an  and  implementation for prostate cancer

What is discrete event simulation?

Conceptually, we have an event queue which is ordered by event times, where events are defined by their type and time¹.

¹Law AM. (2007) *Simulation Modeling and Analysis*. Fourth edition. New York: McGraw-Hill.

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- ① Initialise an empty event queue; insert initial events into the queue
- ② Repeat until the queue is empty:
 - (i) Retrieve the event at the head of the queue
 - (ii) Process the event, possibly updating any variables, or insert/delete events from the queue

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The algorithm is:

- ❶ Initialise an empty event queue; insert initial events into the queue
- ❷ Repeat until the queue is empty:
 - (i) Retrieve the event at the head of the queue
 - (ii) Process the event, possibly updating any variables, or insert/delete events from the queue
- ❸ Finalise the simulation (e.g. return statistics).

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Discrete event simulation: Software


- Proprietary: Arena, Extend, GPSS, SIMSCRIPT, etc.
- Open source: NS-2, Omnet++, Simpy, SSJ, etc.
- : Only one simple example by Norm Matlof (<http://www.esg.montana.edu/R/revent.pdf>)

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Event queue (example)

R

```
> eq <- EventQueue$new() # R5 class (to be defined)
> eq$insert(3, "Clear drains")
> eq$insert(1, "Solve RC tasks")
> eq$insert(2, "Tax return")
> while(!eq$empty()) {
+   print(eq$pop())
+ }
```

```
[1] "Solve RC tasks"
attr("time")
[1] 1
[1] "Tax return"
attr("time")
[1] 2
[1] "Clear drains"
attr("time")
[1] 3
```



Event queue (using a closure)

In computer science, this is a **priority queue** or a **heap**.

```
1 EventQueue <- function() {  
2   times <- events <- NULL  
3   insert <- function(time, event) {  
4     ord <- order(newtimes <- c(times, time))  
5     times <-< newtimes[ord]  
6     events <-< c(events, list(event))[ord]  
7   }  
8   pop <- function() {  
9     head <- structure(events[[1]], time=times[1])  
10    events <-< events[-1]  
11    times <-< times[-1]  
12    return(head)  
13  }  
14  empty <- function() length(events) == 0  
15  list(insert = insert, pop = pop, empty = empty)  
16 }
```




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3   insert <- function(time, event) {  
4     ord <- order(newtimes <- c(times, time))  
5     times <-- newtimes[ord]  
6     events <-- c(events, list(event))[ord]  
7   }  
8   pop <- function() {  
9     head <- structure(events[[1]], time=times[1])  
10    events <-- events[-1]  
11    times <-- times[-1]  
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16 }
```



Event queue (using an R5 class)

```
1 EventQueue <-  
2   setRefClass("EventQueue",  
3     fields = list(times = "numeric", events = "list"),  
4     methods = list(  
5       insert = function(time, event) {  
6         ord <- order(newtimes <- c(times, time))  
7         times <-< newtimes[ord]  
8         events <-< c(events, list(event))[ord]  
9       },  
10      pop = function() {  
11        head <- structure(events[[1]], time=times[1])  
12        times <-< times[-1]  
13        events <-< events[-1]  
14        return(head)  
15      },  
16      empty = function() length(times) == 0  
17    ))
```

- R5 classes and closures look very similar!
- Closures provide a simple approach to working with fields and methods
- R5 classes allow for inheritance (see next), but they are [slow](#).



Running the simulation

R

```
> set.seed(123)
> sim <- Simulation$new()
> sim$run()

[1] "Cancer diagnosis"
attr(,"time")
[1] 55.76424
[1] "Cancer death"
attr(,"time")
[1] 59.29142

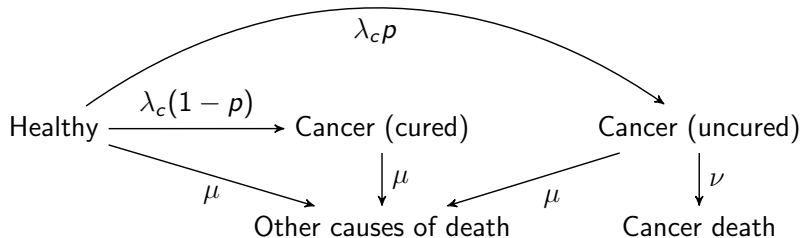
> sim$run()

[1] "Death due to other causes"
attr(,"time")
[1] 59.96818
```

Outline of the BaseDiscreteEventSimulation class

- Inherit from the `EventQueue` class (with methods: `insert`, `pop` and `empty`)
- Define `init()` to set up the initial events
- Schedule events using `scheduleAt(time, event)`, where `event` can be any object (e.g. a list or a character string)
- Define `handleMessage(event)` to respond to different events, possibly scheduling other events or `clear()`ing the queue
- Define `final()` to finish the simulation (if required)
- After the model is defined, `run()` the simulation

Simulation: Concrete example



where $p = 0.5$, and μ , λ_c and μ are rates for Weibull distributions. In practise for competing risks, we sample from the event time distributions and take the first event.



Concrete class example

```
1 Simulation <-
2   setRefClass("Simulation",
3     contains = "BaseDiscreteEventSimulation")
4 Simulation$methods(init = function() {
5   clear()
6   scheduleAt(rweibull(1,8,85), "Death due to other causes")
7   scheduleAt(rweibull(1,3,90), "Cancer diagnosis")
8 })
9 Simulation$methods(handleMessage = function(event) {
10  now <- attr(event, "time")
11  if (event %in% c("Death due to other causes", "Cancer death")) {
12    clear()
13    print(event)
14  }
15  else if (event == "Cancer diagnosis") {
16    if (runif(1) < 0.5)
17      scheduleAt(now + rweibull(1,2,10), "Cancer death")
18    print(event)
19  }
20 })
```



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17      scheduleAt(now + rweibull(1,2,10), "Cancer death")
18    print(event)
19  }
20 })
```



Discrete event simulation (R5)

```
1 BaseDiscreteEventSimulation <-  
2   setRefClass("BaseDiscreteEventSimulation",  
3     contains = "EventQueue",  
4     methods = list(  
5       clear = function() {  
6         times <-< numeric()  
7         events <-< list()  
8       },  
9       scheduleAt = function(time, event) insert(time,  
10        event),  
11       init = function() stop("VIRTUAL!"),  
12       handleMessage = function(event) stop("VIRTUAL!"),  
13       final = function() {},  
14       run = function() {  
15         init()  
16         while(!empty()) {  
17           event <- pop()  
18           handleMessage(event)  
19         }  
20         final()  
21       })
```

Some class extensions

- Define fields for `currentTime` and `previousEventTime`
- Define a utility function `now()` for the current time
- Include a `report` field for returning statistics



Running the simulation

R

```
> set.seed(123)
> sim <- Simulation$new()
> system.time(for (i in 1:5000) sim$run())
```

```
   user  system elapsed
14.96    0.02   15.03
```

```
> subset(sim$report,id<=4)
```

	id	state	begin	end	event
1	1	Healthy	0.00000	55.76424	Cancer diagnosis
2	1	Cancer	55.76424	59.29142	Cancer death
3	2	Healthy	0.00000	59.96818	Death due to other causes
4	3	Healthy	0.00000	43.61622	Cancer diagnosis
5	3	Cancer	43.61622	80.36382	Death due to other causes
6	4	Healthy	0.00000	31.80345	Cancer diagnosis
7	4	Cancer	31.80345	38.04237	Cancer death



Concrete class example 2

```
1 Simulation <-  
2   setRefClass("Simulation",  
3     contains = "BaseDiscreteEventSimulation2", # See  
4       Additional material  
5     fields = list(id = "numeric", state = "character",  
6       report = "data.frame"),  
7     methods = list(initialize = function(id = 0)  
8       callSuper(id = id)))  
9 Simulation$methods(init = function() {  
10   clear()  
11   id <- id + 1  
12   state <- "Healthy"  
13   scheduleAt(rweibull(1,8,85), "Death due to other causes")  
14   scheduleAt(rweibull(1,3,90), "Cancer diagnosis")  
15 })
```




Concrete class example 2

```
1 Simulation$methods(handleMessage = function(event) {  
2   report <- rbind(report, data.frame(id = id,  
3                                     state = state,  
4                                     begin = previousEventTime,  
5                                     end = currentTime,  
6                                     event=event,  
7                                     stringsAsFactors = FALSE))  
8   if (event %in% c("Death due to other causes", "Cancer death")) {  
9     clear()  
10  }  
11  else if (event == "Cancer diagnosis") {  
12    state <- "Cancer"  
13    if (runif(1) < 0.5)  
14      scheduleAt(now() + rweibull(1,2,10), "Cancer death")  
15  }  
16 })
```

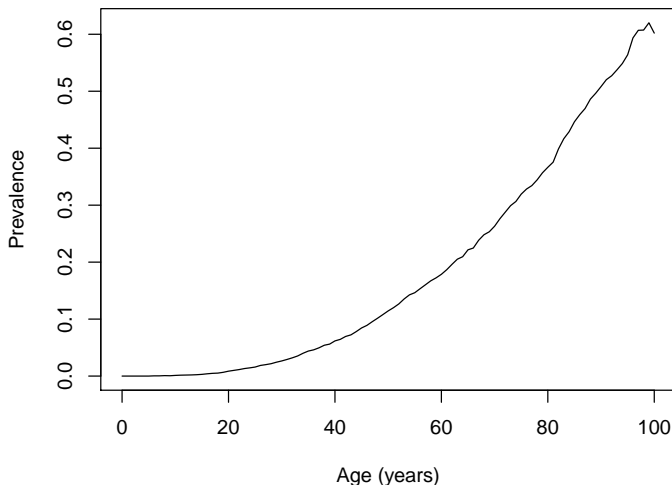
Life histories: calculating prevalence using SQL

R

```
> require(sqldf)
> report <- sim$report
> ages <- transform(data.frame(lhs = seq(0,100,1)),
+                     rhs = lhs + 1)
> prev <- sqldf("select t.*, a.lhs as age
+               from report as t
+               inner join ages as a on t.begin<=a.lhs and a.lhs<t.end")
> xtabs(~state+age, prev, subset = age %% 10 == 0)
```

	age										
state	0	10	20	30	40	50	60	70	80	90	100
Cancer	0	6	43	132	302	539	769	909	788	374	59
Healthy	5000	4991	4947	4836	4589	4173	3536	2546	1362	362	39

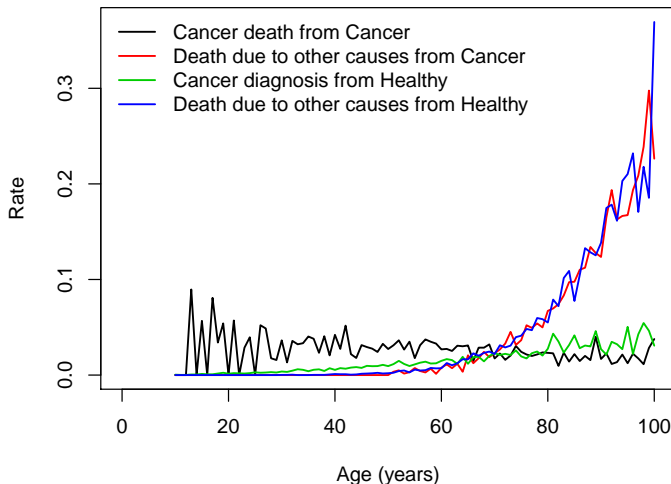
Life histories: Prevalence of cancer



Life histories: calculating rates using SQL

```
1 pt <- sqldf("select t.*, a.lhs as age, min(a.rhs,t.end)
  - max(a.lhs,t.begin) as pt, (a.lhs<=t.end and t.end<=
    a.rhs) as eventp from ages as a outer left join
    report as t on a.lhs<=t.end and a.rhs>t.begin")
2 rates <- sqldf("select event, state, age, events/
  persontime as rate from (select state, age, sum(pt)
    as persontime from pt group by state, age) natural
  join (select state, age, event, sum(eventp) as events
    from pt group by state, age, event) order by event,
    state, age")
```

Life histories: Rates



Microsimulation: Outline of tasks

- Define the microsimulation model
- For different **scenarios**:
 - Define the input parameters
 - Possibly **initial histories** based on observed individuals (e.g. a survey or **registers**)
 - Transition probabilities or time to event distributions
 - Run the microsimulation (in cancer, for 10^5 to 10^7 individuals)
 - Summarise the results

Microsimulation: Calibration/estimation

- Define
 - Microsimulation model
 - Fixed input parameters
 - Prior distributions for the uncertain input parameters
 - Calibration targets (i.e. data to fit)
- Sample from the posterior distribution
 - 1 Run the microsimulation (in cancer, for 10^5 to 10^7 individuals)
 - 2 Calculate the likelihood for the calibration targets
- Summarise the posterior distribution

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Common random numbers and variance reduction

- For calibration/estimation and comparing scenarios in microsimulation, we want to reduce the **Monte Carlo variation**. Best practice advises the use of **common random numbers**
- The simplest approach for common random numbers is to have a different random seed for each individual
- A better approach is to have a different random seed for each individual for each “random process”

Random streams and sub-streams

Imagine that we have a random number generator that produces a long, independent series of random numbers:



Random streams and sub-streams

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Now, we split this series into a set of **streams**:

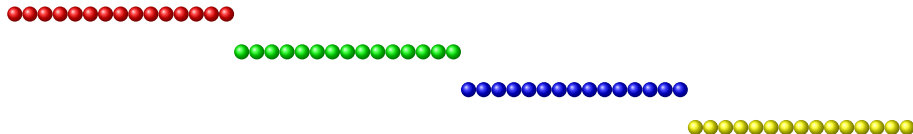


Random streams and sub-streams

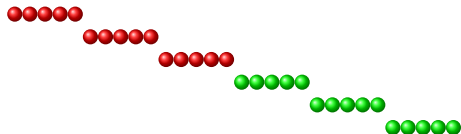
Imagine that we have a random number generator that produces a long, independent series of random numbers:



Now, we split this series into a set of **streams**:



And we can split the streams into a set of **sub-streams**:



Random streams and sub-streams: microsimulation

- Streams \rightarrow random processes

Random streams and sub-streams: microsimulation

- Streams \rightarrow random processes
- Sub-streams for a given stream \rightarrow individuals



Random number streams

- Random number streams are implemented in the [parallel](#) core package (see also the [rlecuyer](#), [rstream](#) and [rsprng](#) packages)
- [parallel](#) uses the "L'Ecuyer-CMRG" random number generator, which has a period of around 2^{191}
(=3138550867693340381917894711603833208051177722232017256448;
the default "Mersenne-Twister" RNG has a period of $2^{19937} - 1$)
- Each stream is a subsequence of the period of length 2^{127} which is in turn divided into substreams of length 2^{76}
- The parallel package adapts and simplifies the [RngStreams](#) C package, losing some useful functionality

RNGStream object

- `open`, `close` and `with` methods for using an RNGStream object
- `resetSubStream`, `resetStream`, `nextSubStream` and `nextStream` methods for changing the object seed



Example of random number streams

R

```
> set.seed(101)
> s1 <- RNGStream(nextStream=FALSE)
> s2 <- RNGStream()
> with(s1,rnorm(1))
```

```
[1] 2.189189
```

```
> with(s2,rnorm(1))
```

```
[1] 0.5205894
```

```
> s1$nextSubStream()
> with(s1,rnorm(1))
```

```
[1] -1.461113
```

R

```
>
> s1$resetStream()
> s2$resetStream()
> with(s1,rnorm(2))
```

```
[1] 2.1891887 -0.6045821
```

```
> with(s2,rnorm(2))
```

```
[1] 0.5205894 0.8820710
```

```
> s1$nextSubStream()
> with(s1,rnorm(2))
```

```
[1] -1.4611126 -0.8230108
```



RNGStream object

```
1 require(parallel)
2 RNGkind("L'Ecuyer-CMRG")
3 RNGStream <- function(nextStream = TRUE) {
4   current <- if (nextStream) nextRNGStream(.Random.seed) else .
      Random.seed
5   .Random.seed <<- startOfStream <- startOfSubStream <- current
6   structure(list(open = function() .Random.seed <<- current,
7     close = function() current <<- .Random.seed,
8     resetSubStream = function() .Random.seed <<-
        current <<- startOfSubStream,
9     resetStream = function() .Random.seed <<- current
        <<- startOfSubStream <<- startOfStream,
10    nextSubStream = function() .Random.seed <<-
        current <<- startOfSubStream <<-
        nextRNGSubStream(startOfSubStream),
11    nextStream = function() .Random.seed <<- current
        <<- startOfSubStream <<- startOfStream <<-
        nextRNGStream(startOfStream)),
12     class="RNGStream")
13 }
```



with method for RNGStream object

```
1 with.RNGStream <- function(stream, expr, ...) {  
2   stream$open()  
3   out <- eval(substitute(expr), enclos = parent.frame(), ...)  
4   stream$close()  
5   out  
6 }
```


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Why C++?



-  is too slow!

Why C++?

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 - We like 
 - We may miss 's dynamic typing, closures, extensive packages, etc.
 - We may not really want to program in C++

- An elegant C++ framework for passing data and structures between R and C++
- Increasingly popular solution for dealing with large and slow computational tasks in 
- We can now do all of our pre- and post-processing with , and use C++ as the engine

Do everything for **two** reasons



Running the simulation

R

```
> require(microsimulation)
```

```
Loading required package: microsimulation
```

```
Loading required package: Rcpp
```

```
> set.seed(123)
```

```
> system.time(df <- callSimplePerson(100000))
```

```
   user  system elapsed  
0.688   0.016   0.705
```

```
> head(df)
```

	endtime	event	id	startTime	state
1	55.76424	toCancer	0	0.00000	Healthy
2	59.29142	toCancerDeath	0	55.76424	Cancer
3	59.96818	toOtherDeath	1	0.00000	Healthy
4	43.61622	toCancer	2	0.00000	Healthy
5	80.36382	toOtherDeath	2	43.61622	Cancer
6	31.80345	toCancer	3	0.00000	Healthy

- Ongoing work
 - Methods for calibration (with Alexandra Jauhiainen)
 - Application to prostate cancer (with Hatef Darabi)
 - Statistics collection in C++
 - Visualisation; the Biograph package looks very interesting
- Issues and challenges
 - User-defined random number generators use one C function (`double *user_unif_rand ()`) → name conflict??
 - How to encourage R programmers to learn C++?
- The microsimulation package is available at <https://github.com/mclements/microsimulation>

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“Process-oriented” discrete event simulation

- The concept on the previous slide describes **event-oriented** simulation
- At a higher level, we can consider a **process-oriented** simulation, where we have a process that includes a series of events. The processes run as “continuations”.



Discrete event simulation 2

```
1 BaseDiscreteEventSimulation2 <-  
2   setRefClass("BaseDiscreteEventSimulation2",  
3             contains = "BaseDiscreteEventSimulation",  
4             fields = list(currentTime = "numeric",  
5                           previousEventTime = "numeric"),  
6             methods = list(  
7               now = function() currentTime,  
8               run = function() {  
9                 previousEventTime <- 0.0  
10                init()  
11                while(!empty()) {  
12                  event <- pop()  
13                  currentTime <- attr(event, "time")  
14                  handleMessage(event)  
15                  previousEventTime <- currentTime  
16                }  
17                final()  
18              })  
19            ))
```



Common random numbers in a microsimulation

```
1 setOldClass("RNGStream")
2 Simulation <-
3   setRefClass("Simulation",
4     contains = "BaseDiscreteEventSimulation2",
5     fields = list(id = "numeric", state = "character",
6       report = "data.frame", rng = "RNGStream"),
7     methods= list(initialize = function(id = 0) {
8       callSuper(id = id)
9       rng <-< RNGStream(nextStream = FALSE)
10     })))
11 Simulation$methods(init = function() {
12   clear()
13   id <-< id + 1
14   state <-< "Healthy"
15   scheduleAt(with(rng, rweibull(1,8,85)), "Death due to other
16     causes")
17   scheduleAt(with(rng, rweibull(1,3,90)), "Cancer diagnosis")
18 })
19 Simulation$methods(final = function() rng$nextSubStream())
```



Common random numbers in a microsimulation II

```
1 Simulation$methods(handleMessage = function(event) {  
2   report <- rbind(report, data.frame(id = id,  
3                                     state = state,  
4                                     begin = previousEventTime,  
5                                     end = currentTime,  
6                                     event=event,  
7                                     stringsAsFactors = FALSE))  
8   if (event %in% c("Death due to other causes", "Cancer death")) {  
9     clear()  
10  }  
11  else if (event == "Cancer diagnosis") {  
12    state <- "Cancer"  
13    if (with(rng, runif(1)) < 0.5)  
14      scheduleAt(now() + with(rng, rweibull(1,2,10)), "Cancer death  
15      ")  
16  }  
17 })
```


C++: A simple microsimulation example (R code)

```
1 enum <- function(obj, labels)
2   factor(obj, levels=0:(length(labels)-1), labels=labels)
3
4 callSimplePerson <- function(n=100) {
5   stateT <- c("Healthy", "Cancer", "Death")
6   eventT <- c("toOtherDeath", "toCancer", "toCancerDeath")
7   out <- .Call("callSimplePerson",
8               parms=list(n=as.integer(n)),
9               PACKAGE="microsimulation")
10  out <- transform(as.data.frame(out),
11                  state=enum(state, stateT),
12                  event=enum(event, eventT))
13  out
14 }
```

C++: A simple microsimulation example

```
1 // include headers for microsimulation and Rcpp
2 #include "microsimulation.h"
3 #include <Rcpp.h>
4
5 using namespace std;
6
7 enum state_t { Healthy, Cancer, Death };
8
9 enum event_t { toOtherDeath, toCancer, toCancerDeath };
10
11 // for returning life histories
12 map<string, vector<double> > report;
13
14 #define Reporting(name,value) report[name].push_back(value);
```

C++: A simple microsimulation example

```
1 class SimplePerson : public cProcess
2 {
3 public:
4     state_t state;
5     int id;
6     SimplePerson(const int i = 0) : id(i) {};
7     void init();
8     virtual void handleMessage(const cMessage* msg);
9 };
10
11 void SimplePerson::init() {
12     state = Healthy;
13     scheduleAt(R::rweibull(8.0,85.0),toOtherDeath);
14     scheduleAt(R::rweibull(3.0,90.0),toCancer);
15 }
```

C++: A simple microsimulation example

```
1 void SimplePerson::handleMessage(const cMessage* msg) {
2     double dwellTime, pDx;
3     Reporting("id",id);
4     Reporting("startTime",previousEventTime);
5     Reporting("endtime",now());
6     Reporting("state",state);
7     Reporting("event",msg->kind);
8
9     switch(msg->kind) {
10    case toOtherDeath:
11    case toCancerDeath:
12        Sim::stop_simulation();
13        break;
14    case toCancer:
15        state = Cancer;
16        if (R::runif(0.0,1.0) < 0.5)
17            scheduleAt(now() + R::rweibull(2.0,10.0), toCancerDeath);
18        break;
19    default:
20        REprintf("No valid kind of event\n");
21        break;
22    }
23 }
```

C++: A simple microsimulation example

```
1 RcppExport SEXP callSimplePerson(SEXP parms) {  
2     SimplePerson person;  
3     Rcpp::RNGScope scope;  
4     Rcpp::List parmsl(parms);  
5     int n = Rcpp::as<int>(parmsl["n"]);  
6     for (int i = 0; i < n; i++) {  
7         person = SimplePerson(i);  
8         Sim::create_process(&person);  
9         Sim::run_simulation();  
10        Sim::clear();  
11    }  
12    return Rcpp::wrap(report);  
13 }
```