

SimpactCyan: a simulation engine for individual-based models in HIV epidemiology



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Introduction

Individual-based models (IBMs) are used to simulate transmission of diseases that are subject to high individual heterogeneity [1]. Common limitations of available simulation engines for IBMs include propriety software, being overly complicated and/or poorly documented, being available for a single operating system and being implemented in discrete time. SimpactCyan (<http://www.simpact.org/>), is a freely available simulator for IBMs, written in C++ with R and Python interfaces. Simpact is implemented in continuous time: models are updated each time an event happens, and not at fixed time intervals.

Data and Methods

Modeling approach

- event-driven individual-based model
- discrete event simulation in continuous time
- uses a hazard function for each event, describing the instantaneous rate of that event
- modified Next Reaction Method (mNRM)[2]: events occur relative to their hazard (see Figure 1)

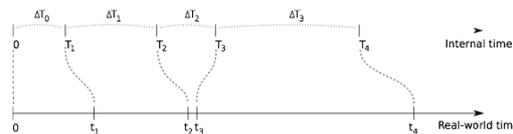


Figure 1: Main idea of the mNRM: internal time intervals ΔT_i are chosen from a certain distribution, and they get mapped onto real-world time intervals Δt_i through hazards.

Initialization and overview of events

To create the initial population: (1) a number of people is added to the population; (2) age is drawn from an age distribution file; (3) when the age is larger or equal to the debut age, a person is marked as sexually active. The following initial events are scheduled: (1) mortality event for each person; (2) debut event if needed; (3) an HIV seeding event to get the epidemic started; (4) formation events for pairs of sexually active persons. Figure 2 gives an overview of the events currently implemented in Simpact.

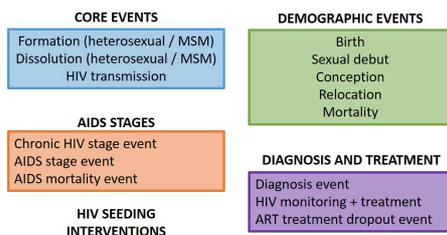


Figure 2: Events implemented in the current version of Simpact

Hazard functions

The following types of hazard functions are used in Simpact:

- constant hazard: $h(t) = a \rightarrow$ exponentially distributed event time
- $h(t) = at \rightarrow$ Weibull distributed event time
- $h(t) = \exp(a + bt)$

Research questions

Various questions in HIV epidemiology have already been addressed using Simpact, e.g.

- How do heritability of HIV set point viral load (SPVL) and sexual network connectivity jointly influence the evolution of HIV infectivity?
- What is the role of age-mixing patterns in the spread of HIV?

References

- [1] Railsback SF, Grimm V (2011). Agent-based and individual-based modeling: a practical introduction. Princeton university press.
- [2] Anderson DF (2007). A modified next reaction method for simulating chemical systems with time dependent propensities and delays." The Journal of Chemical Physics, 127(21),214107.

Results

Set point viral load heritability

Figure 3 illustrates how heritability of HIV SPVL (correlation between SPVL of infector and newly infected) and sexual network connectivity jointly influence the evolution of HIV infectivity, by calculating the difference of HIV SPVL at the time of seeding and 15 years later. The figure shows synergistic facilitating effects of higher sexual network connectivity and heritability of set point viral load on HIV infectivity levels over time.

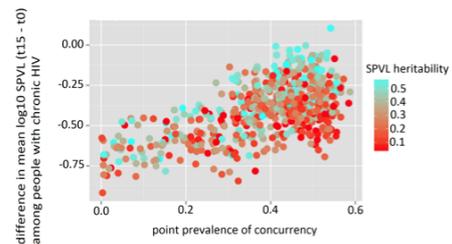


Figure 3: Difference in mean log₁₀ SPVL $t_{15} - t_0$ among chronically infected people, against the point prevalence of being engaged in concurrent relationships, and colour-coded by SPVL heritability.

Age mixing patterns

Figure 4 shows HIV incidence over time for two age-mixing patterns: one with low variance in age-differences between partners (upper panel), and one with high variance in age-differences. The figure illustrates that high variance in age-differences between individuals and their partners facilitates long-term HIV transmission.

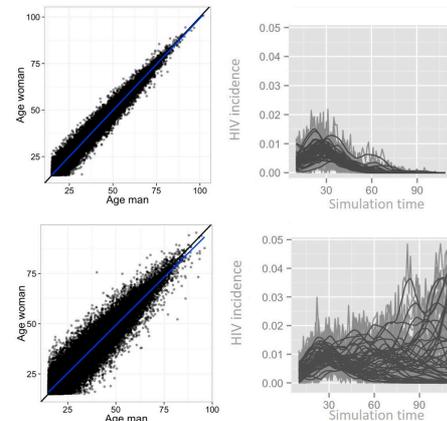


Figure 4: Influence of age mixing patterns on the spread of HIV. Left: age woman against age man; right: HIV incidence against simulation time in years. Upper panel: Everybody has the same preferred age gap (0 years) and the standard deviation in age gaps is 2 years; lower panel: preferred age gap of 0 years, standard deviation of 4 years

Summary

SimpactCyan is a freely available simulator for individual-based models in HIV epidemiology. It combines the computational efficiency of C++ with the accessibility of R and Python. The continuous time implementation of SimpactCyan has the advantage that it elegantly handles competing risks to multiple events. Furthermore, events happening on short and long time periods can be included in a single simulation. The examples above show that SimpactCyan is a useful simulator to answer epidemiological questions.

Acknowledgments

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