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Simpact White User Guide

User guide

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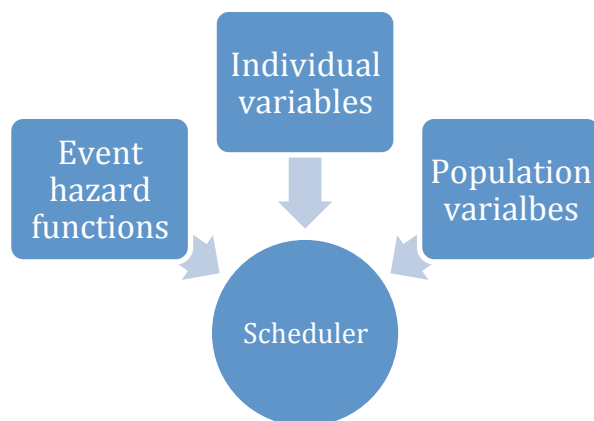
1. Overview

Simpact is a simulation tool to develop, run and analyse event-driven, individual-based models in a continuous time framework. Individuals in the model population are socially and biologically connected to each other through sexual relationships and parent-child relationships. HIV can be transmitted in this network either by heterosexual intercourse or perinatally from mother to child. Possible events include pregnancy, birth, AIDS-related and non-AIDS-related death, relationship formation and relationship dissolution, HIV testing, medical male circumcision, attending antenatal care (ANC), initiating and discontinuing antiretroviral therapy (ART), and behavioural intervention that increases condom use or reduces HIV-related risky behaviours across the population. [1]

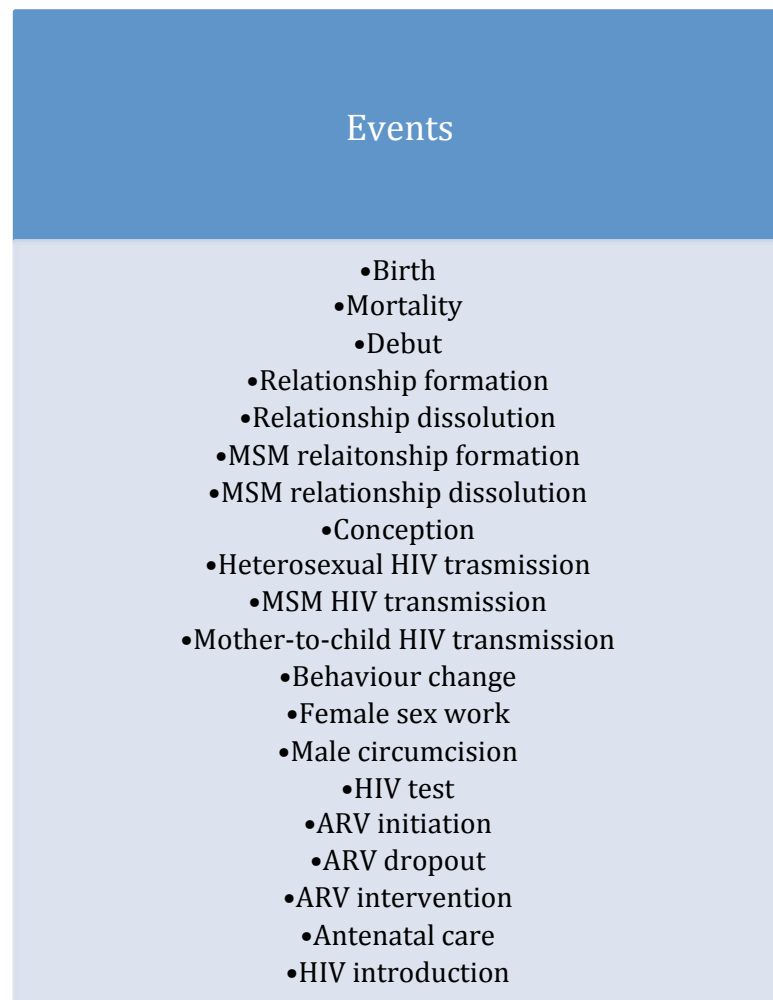
Simpact White is the foundational member of Simpack software family. It is developed with MatLab 2012b [2] by an inter-institutional team. Information about Simpack software tools and relevant research projects can be found in [1] and our website (<http://www.simpact.org>). Source code of Simpack White is regularly updated on GitHub (<https://github.com/yfmeng/SimpactWhite>).

2. Software Architecture

Simpact White consists of two types of elements, individuals and events. A hazard function is defined for each event and the time until events happening to an individual is calculated using the hazard functions. A scheduler function (`/lib/modelHIV.m`) decides the sequence and time intervals of possible events. The statuses of individuals are updated after an event is fired, then the expected times of remained events are recalculated accordingly.



Simpect White provides 20 events up to date (Section 5). New events can be added using a template code file (`/lib/events/eventTemplate.m`). Individuals in simulated population are heterogenized by 21 personal variables (Section 4.3).



3. Working with Simpact White

3.1. Software prerequisite and default simulation

The current version of Simpact White is developed with MatLab 2012b. Minor adaptations might be required for running with older versions ([contact me for help](#)). Installation downloads and system requirements of MatLab can be found on the official website <http://www.mathworks.nl/>.

When MatLab is installed, save the entire Simpact White folder under your MatLab paths or add the folder of Simpact White to your MatLab paths. Then simulations can be run with the MatLab console. The output of simulation is a MatLab data structure.

Example 1. Run Simpact White with default configuration.

% Method I.

% Directly run with default configuration

SDS = spRun;

% Method II.

% Create an initial data structure

SDS = modelHIV('new');

% Run with default configuration using the data structure

SDS = spRun('start', SDS);

3.2. Configuration

The Simpact Data Structure (SDS) contains substructures of global variables, individual variables, and event configurations. Once an initial data structure is created by using Method II in Example 1, configurations and parameters can be directly assigned as following:

Example 2. Configuration

% Create an initial data structure

SDS = modelHIV('new');

% Configuration.

% Global variables: SDS.{variable name} = value;

SDS.number_of_males = 1000;

% Individual variables: SDS.{gender}.{variable name} = value;

SDS.males.born = zeros(1, 1000);

SDS.males.born(20) = -1;

% Event configuration: SDS.{event name}.{variable name} = value;

SDS.formation.baseline = log(0.1);

% Run the simulation

SDS = spRun('start', SDS);

3.3. Exporting outputs

The output SDS can be either saved as data structure in .mat format or exported to .csv files by using exportCSV.m function. In the latter case, 4 .csv files will be created, containing information on individuals, sexual relationships, HIV tests and ARV treatment respectively.

```
Example 3. Save Simpact Data Structure
% Method I. Save MatLab data structure
    file_name = 'SDS_0001_baseline_scenario.mat';
    save file_name SDS;
% Method II. Export data structure into comma separated files
    path = '/SimpactWhite/output/'
    index = 1;
    file_identifier = 'baseline_scenario';
    exportCSV(SDS, path, index, file_identifier);
```

4. Population and Individuals

4.1. Population variables

Name	Comment	Type
number_of_communities		Integer
number_of_males	limitation of number of males	Integer
number_of_females	limitation of number of females	Integer
initial_number_of_males		Integer
initial_number_of_females		Integer
percentage_of_MSM		Float

4.2. Simulation variables

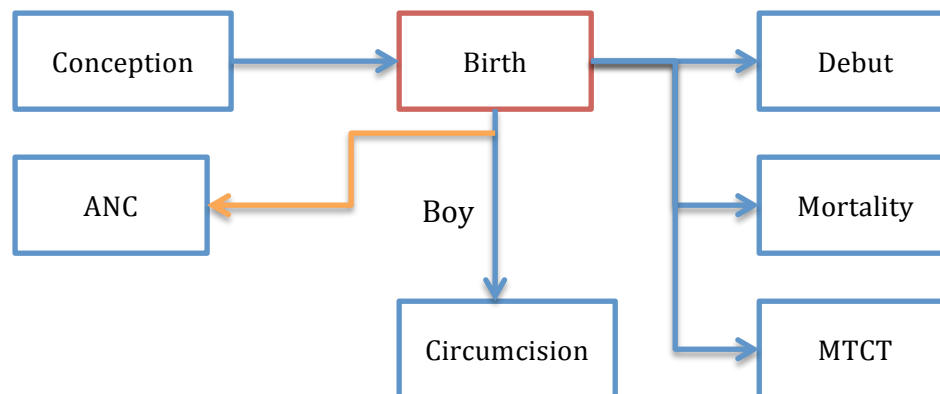
Name	Comment	Default	Type
age_file	a .csv file containing initial age distribution	'none'	String
start_date			Date
end_date			Date
iteration_limit			Integer
model_function		'modelHIV'	String

4.3. Individual variables

Name	Comment	Default	Type
(gender).father	ID of father	0	Integer
(gender).mother	ID of mother	0	Integer
(gender).born	Time of birth	NaN	Float
(gender).deceased	Time of death	NaN	Float
(gender).HIV_source	ID of HIV source	0	Integer
(gender).HIV_positive	Time of HIV infection	NaN	Float
(gender).AIDS_death	Death due to AIDS	0	Logical
(gender).HIV_test	Time of HIV test	NaN	Float
(gender).ARV_start	Time of ARV initiation	NaN	Float
(gender).ARV_stop	Time of ARV dropout	NaN	Float
(gender).community	Community	0	Integer
(gender).partnering	Sexuality level, 0~1	Random	Float
(gender).ARV_eligible	Time at becoming ARV eligible	NaN	Float
(gender).CD4Infection	CD4 count at infection	NaN	Float
(gender).CD4ARV	CD4 count at ARV initiation	NaN	Float
(gender).CD4Death	CD4 count at death	NaN	Float
(gender).CD4_500	Time of CD4 count reaching 500	NaN	Float
(gender).CD4_350	Time of CD4 count reaching 350	NaN	Float
(gender).CD4_200	Time of CD4 count reaching 200	NaN	Float
males.MSM	Having sex with men	Random	Logical
males.circumcision	Time of circumcision	NaN	Float
females.sex_worker	Being a female sex worker	Random	Logical

5. Events

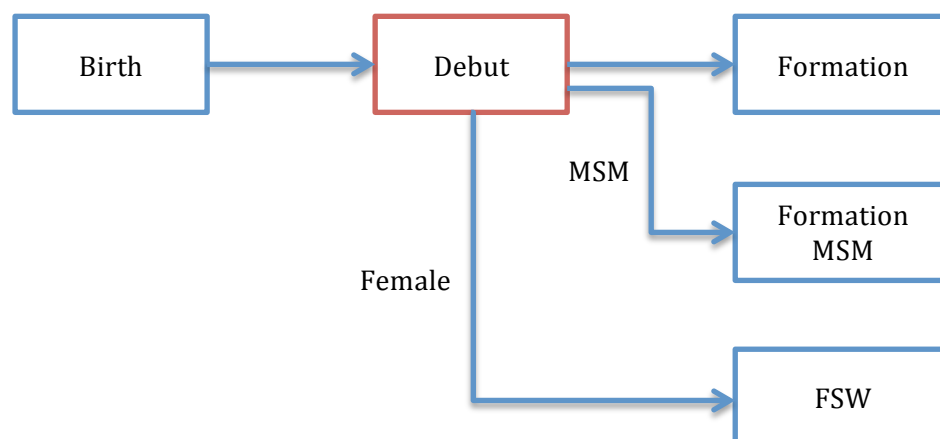
5.1. eventBirth



Hazard function

$$h \equiv h_0$$

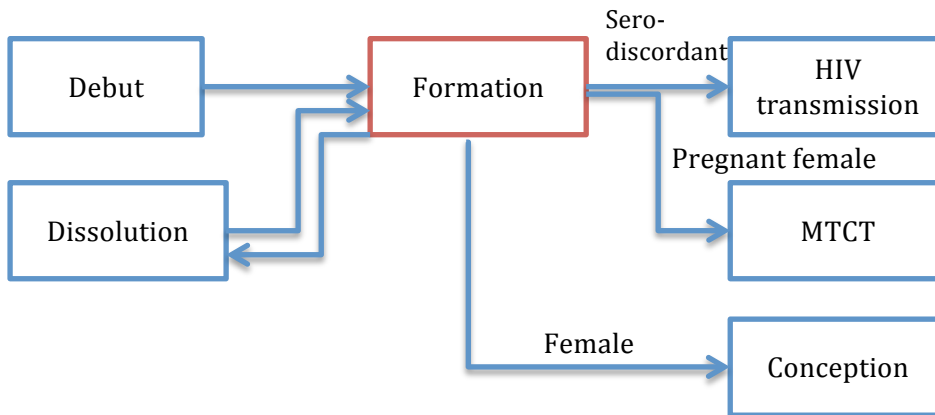
5.2. eventDebut



Hazard function

$$h \equiv h_0$$

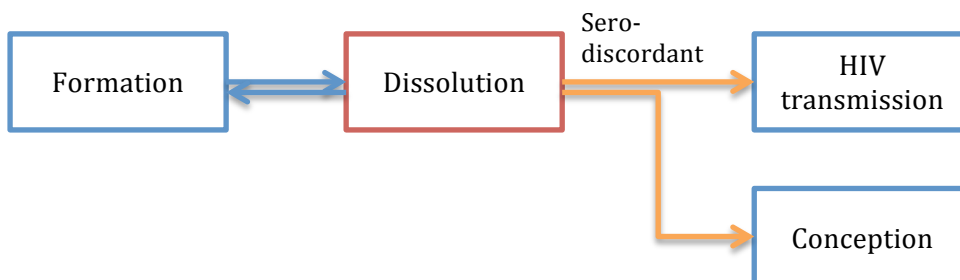
5.3. eventFormation



Hazard function

$$\begin{aligned}
 h(x,t) = & \exp(\alpha_0 + \alpha_1 partners_i + \alpha_2 partners_j + \alpha_3 |partners_i - partners_j| \\
 & + \alpha_4 (\frac{age_i + age_j}{2}) + \alpha_5 |age_i - age_j - age_{preferred}| \\
 & + \alpha_6 proximity_{i,j} + \alpha_7 fsw_j \\
 & + \beta t)
 \end{aligned}$$

5.4. eventDissolution



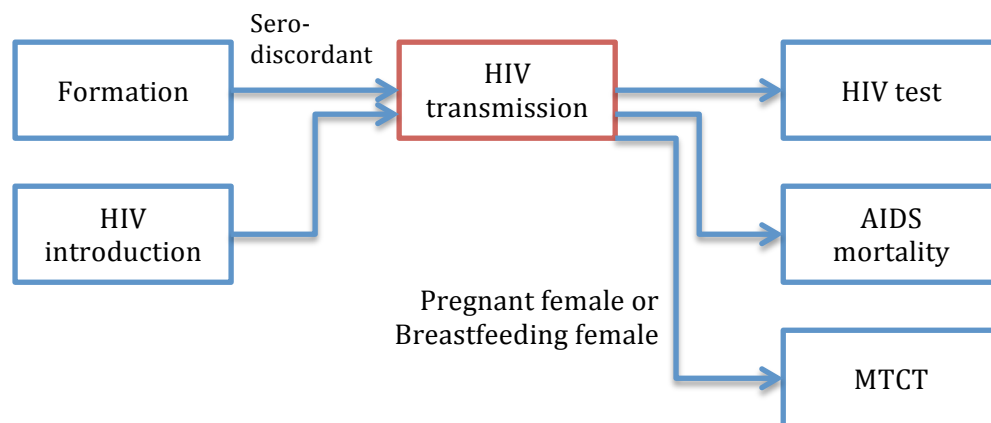
Hazard function

$$\begin{aligned}
 h(x,t) = & \exp(\alpha_0 + \alpha_1 partners_i + \alpha_2 partners_j + \alpha_3 |partners_i - partners_j| \\
 & + \alpha_4 (\frac{age_i + age_j}{2}) + \alpha_5 |age_i - age_j - age_{preferred}| \\
 & + \alpha_6 proximity_{i,j} + \alpha_7 fsw_j \\
 & + \beta t)
 \end{aligned}$$

5.5. eventFormationMSM

5.6. eventDissolutionMSM

5.7. eventTransmission



Hazard function

$$h(x,t) = \alpha_p c f_i (1 - ART_i)(1 - circumcised_i)$$

5.8. eventTransmissionMSM

5.9. eventConception

5.10. eventANC

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5.21. eventIntroduction

6. Supplementary functions

6.1. Calibration functions

6.2. Facilitating functions

6.3. Output analysis functions

7. Output

8. Appendix