ever, mlele j is 16 years oldnction.or its turn to take place.

**November 2013**

V.16

**All right reserved to Simpact**

08

**Fall**



Simpact White

User guide

Simpact White

An individual-based simulation software for HIV modelling

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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 Simpact software family. It is developed with MatLab 2012b [2] by an inter-institutional team. Information about Simpact software tools and relevant research projects can be found in [1] and our website (<http://www.simpact.org>). Source code of Simpact 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 updat ever, mlele j is 16 years oldnction.or its turn to take place. ed after an event is fired, then the expected times of remained events are recalculated accordingly.

Simpact 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 prerequisition and default simulation

The current version of Simpact White is developed with MatLab 2012b. Minor adaptions might be required for running with older versions ([contact me for help](mailto:fei.d.meng@gmail.com?subject=Simpact%20White%20consultation)). 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 package under your MatLab paths or add the folder of Simpact White to your MatLab paths. Then simulations can be run in 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 Strucure (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. Saving and 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

filen\_ame = ‘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: SDS.{name}

|  |  |  |
| --- | --- | --- |
| Name | Comment | Type |
| number\_of\_communities |  | Integer |
| number\_of\_males | Limitation of male population | Integer |
| number\_of\_females | Limitation of female population | Integer |
| initial\_number\_of\_males | Initial male population | Integer |
| initial\_number\_of\_females | Initial female population | Integer |
| percentage\_of\_MSM | Percentage of men who have sex with men | Float |

## 4.2. Simulation variables: SDS.{name}

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| age\_file | A .csv file containing initial age distribution | ‘none’ | String |
| start\_date | “dd-Mmm-yyyy” format date |  | Date |
| end\_date | “dd-Mmm-yyyy” format date |  | Date |
| iteration\_limit | Limitation of fired events |  | Integer |
| model\_function | Name of the main model function | ‘modelHIV’ | String |

## 4.3. Individual variables: SDS.{gender}.{name}

|  |  |  |  |
| --- | --- | --- | --- |
| 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

Event substructures are stored in SDS as SDS.{event name}. Each event substructure consists of three essential fields and a set of pre-defined parameters. Users can configure event features before starting a simulation.

|  |  |  |  |
| --- | --- | --- | --- |
| Field | Comment | Default | Type |
| enable | Event is turned off if false | True | Logical |
| event\_file | Name of the MatLab file that supports this event | ‘event{Name}’ | Date |
| object\_type | Not to be changed | ‘event’ | Date |
| {parameter} | Optional |  |  |

This section gives details of currently available events. The event descriptions consist of name of the event as appears in SDS, a flowchart that represent interdependency between relevant events, a hazard function (if applicable) and a table of optional parameters. In the flowcharts, red rectangles are the referred events while blue rectangles are relevant events. Arrows in blue, orange and dashed purple means to trigger, to block and to influence respectively.

**ATTENTION: Most of the influencing interactions are omitted for clarity purpose.**

When a possible event is triggered on an individual by a preceding event, time since present until the happening of this triggered event is either calculated using a hazard function or determined by a predefined formula. Then this event would join the event queue and wait for its turn to take place. Event times in the queue are frequently updated as the simulation proceeds.

Example 4. Calculate event times with hazard functions.

## 5.1. eventBirth

**Name:** birth

**Interdependency**

ANC

Circumcision

MTCT

Mortality

Conception

Birth

Debut

Boy

**Hazard function**



**Parameters**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Symbol | Name | Comment | Default | Type |
| 1/h | **boy\_girl\_ratio** | Proportion of boys | 0.5 | Float |
|  | **gestation** | Length of pregnancy (year) | 0.7692 | Float |

## 5.2. eventDebut

**Name:** debut

**Interdependency**

Formation

Debut

Birth

Formation MSM

MSM

FSW

Female

**Hazard function**



**Parameters**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Symbol | Name | Comment | Default | Type |
| 1/h | debut\_age | lower limit of sexual debut age | 15 | Float |

## 5.3. eventFormation

**Name:** formation

**Interdependency**

Sero-

discordant

Conception

MTCT

Hetersexual transmission

Dissolution

Formation

Debut

Pregnant female

Female

HIV test

**Hazard function**



**Parameters**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Symbol | Name | Comment | Default | Type |
|  | baseline\_factor |  |  |  |
|  | male\_current\_relations\_factor |  |  |  |
|  | female\_current\_relations\_factor |  |  |  |
|  | current\_relations\_difference\_factor |  |  |  |
|  | mean\_age\_factor |  |  |  |
|  | age\_difference\_factor |  |  |  |
|  | community\_difference\_factor |  |  |  |
|  | transaction\_sex\_factor |  |  |  |
|  | preferred\_age\_difference |  |  |  |
|  | last\_change\_factor |  |  |  |

## 5.4. eventDissolution

**Name:** dissolution

**Interdependency**

Sero-

discordant

Conception

HIV transmission

Formation

Dissolution

**Hazard function**



**Parameters**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Symbol | Name | Comment | Default | Type |
|  | baseline\_factor |  |  |  |
|  | male\_current\_relations\_factor |  |  |  |
|  | female\_current\_relations\_factor |  |  |  |
|  | current\_relations\_difference\_factor |  |  |  |
|  | mean\_age\_factor |  |  |  |
|  | age\_difference\_factor |  |  |  |
|  | community\_difference\_factor |  |  |  |
|  | transaction\_sex\_factor |  |  |  |
|  | preferred\_age\_difference |  |  |  |
|  | last\_change\_factor |  |  |  |

## 5.5. eventFormationMSM

**Name:** formation\_MSM

**Interdependency**

MSM transmission

Dissolution MSM

Formation MSM

Debut

HIV test

**Parameters**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Symbol | Name | Comment | Default | Type |
|  | baseline\_factor |  |  |  |
|  | current\_relations\_factor |  |  |  |
|  | current\_relations\_difference\_factor |  |  |  |
|  | mean\_age\_factor |  |  |  |
|  | age\_difference\_factor |  |  |  |
|  | community\_difference\_factor |  |  |  |
|  | preferred\_age\_difference |  |  |  |
|  | last\_change\_factor |  |  |  |

## 

## 5.6. eventDissolutionMSM

**Name:** dissolution\_MSM

**Interdependency**

Dissolution MSM

Formation MSM

MSM transmission

**Parameters**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Symbol | Name | Comment | Default | Type |
|  | baseline\_factor |  |  |  |
|  | current\_relations\_factor |  |  |  |
|  | current\_relations\_difference\_factor |  |  |  |
|  | mean\_age\_factor |  |  |  |
|  | age\_difference\_factor |  |  |  |
|  | community\_difference\_factor |  |  |  |
|  | preferred\_age\_difference |  |  |  |
|  | last\_change\_factor |  |  |  |

## 

## 5.7. eventTransmission

**Name:** HIV\_transmission

**Interdependency**

MTCT

HIV introduction

AIDS mortality

Heterosexual transmission

HIV test

Sero-

discordant

Formation

Pregnant female or

MSM Breastfeeding female

MSM transmission

**Hazard function**



**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| infectiousness | 3 cells |  |  |
| -infectiousness{2,3} | possibility per sex HIV stage I (%) | 3.2 | Float |
| -infectiousness{3,3} | possibility per sex HIV stage II (%) | 0.35 | Float |
| -infectiousness{4,3} | possibility per sex HIV stage III (%) | 1.52 | Float |
| AIDS\_mortality\_distribution | 2 cells |  |  |
| -AIDS\_mortality\_distribution{2,2} | Weibull shape parameter of HIV survival time | 2.25 | Float |
| -AIDS\_mortality\_distribution{2,3} | Weibull scale parameter of HIV survival time | 11 | Float |
| infectiousness\_decreased\_by\_condom |  | 0.8 | Float |
| infectiousness\_decreased\_by\_ARV |  | 0.96 | Float |
| infectiousness\_increased\_during  \_conception |  | 2 | Float |
| CD4\_distribution\_at\_infection | 4 cells |  |  |
| -CD4\_distribution\_at\_infection{2,1} | Baseline CD4 count | 600 | Float |
| -CD4\_distribution\_at\_infection{2,2} | CD4 increase with age  (per year) | 5 | Float |
| -CD4\_distribution\_at\_infection{2,3} | Gender difference | 40 | Float |
| -CD4\_distribution\_at\_infection{2,4} | Not used |  |  |
| sexual\_behaviour\_parameters | cells |  |  |
| -sexual\_behaviour\_parameters{2,1} | Coital frequency at relationship initiation (per week) | 3 | Float |
| -sexual\_behaviour\_parameters{2,2-7} | Not used |  | Float |
| -sexual\_behaviour\_parameters{2,1} | Exponential coital frequency decrease with time | 1 | Float |

## 5.8. eventTransmissionMSM

**Name:** HIV\_transmission\_MSM

**Interdependency**

MSM transmission

Sero-

discordant

HIV test

AIDS mortality

Formation MSM

Heterosexual transmission

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| infectiousness | 3 cells |  |  |
| -infectiousness{2,3} | possibility per sex HIV stage I (%) | 3.2 | Float |
| -infectiousness{3,3} | possibility per sex HIV stage II (%) | 0.35 | Float |
| -infectiousness{4,3} | possibility per sex HIV stage III (%) | 1.52 | Float |
| AIDS\_mortality\_distribution | 2 cells |  |  |
| -AIDS\_mortality\_distribution{2,2} | Weibull shape parameter of HIV survival time | 2.25 | Float |
| -AIDS\_mortality\_distribution{2,3} | Weibull scale parameter of HIV survival time | 11 | Float |
| infectiousness\_decreased\_by\_condom |  | 0.8 | Float |
| infectiousness\_decreased\_by\_ARV |  | 0.96 | Float |
| infectiousness\_increased\_during  \_conception |  | 2 | Float |
| CD4\_distribution\_at\_infection | 4 cells |  |  |
| -CD4\_distribution\_at\_infection{2,1} | Baseline CD4 count | 600 | Float |
| -CD4\_distribution\_at\_infection{2,2} | CD4 increase with age  (per year) | 5 | Float |
| -CD4\_distribution\_at\_infection{2,3} | Gender difference | 40 | Float |
| -CD4\_distribution\_at\_infection{2,4} | Not used |  |  |
| sexual\_behaviour\_parameters | cells |  |  |
| -sexual\_behaviour\_parameters{2,1} | Coital frequency at relationship initiation (per week) | 3 | Float |
| -sexual\_behaviour\_parameters{2,2-7} | Not used |  | Float |
| -sexual\_behaviour\_parameters{2,1} | Exponential coital frequency decrease with time | 1 | Float |

## 5.9. eventConception

**Name:** conception

**Interdependency**

Not pregnant

Antenatal care

Formation

Conception

Sexually active HIV+ mother

Birth

MTCT

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| constant\_fertility\_parameter | Fertility rate if not read from data file | 2.2 | Float |
| fertility\_rate\_from\_data\_file |  | 0 | Logical |
| fertility\_rate\_reference\_file | Name of fertility data file | ‘none’ | String |

## 5.10. eventANC

**Name:** antenatal\_care

**Interdependency**

HIV test

Antenatal care

Conception

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| attendance | 2x3 cells |  |  |
| -attendance{2,2} | Percentage women attending early ANC | 55 | Float |
| -attendance{2,3} | Percentage women attending late ANC | 55 | Float |
| -attendance{2,4} | Percentage women never attending ANC | 10 | Float |
| -attendance{3,2} | Time of early ANC (weeks) | 22 | Float |
| -attendance{3,3} | Time of late ANC (weeks) | 32 | Float |
| -attendance{3,4} | NA | ‘None’ | NA |

## 

## 5.11. eventTest

**Name:** HIV\_test

**Interdependency**

ARV treatment

ANC

HIV test

Formation

Formation MSM

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| CD4\_baseline\_for\_ARV | 1x5 cells |  |  |
| - CD4\_baseline\_for\_ARV{2,2} | Current threshold | 350 | Float |
| - CD4\_baseline\_for\_ARV{2,3} | Current time | ’31-Dec-2013’ | Date |
| - CD4\_baseline\_for\_ARV{2,4} | Current coverage (percentage) | 50 | Float |
| - CD4\_baseline\_for\_ARV{2,5} | Up-scaling target time | ’31-Dec-2015’ | Date |
| - CD4\_baseline\_for\_ARV{2,6} | Up-scaling target coverage | 65 | Float |
| Option\_B\_coverage | Positive mothers receiving Option B (percentage) | 95 | Float |
| monitoring\_frequency | Frequency of CD4 monitoring (per year) | 2 | Float |
| longterm\_relationship\_threshold | Threshold of long-term relationship (year) | 0.25 | Float |

## 5.12. eventARV

**Name:** ARV\_treatment

**Interdependency**

ARV stop

ARV treatment

HIV test

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| ARV\_program\_start\_time | Time of ARV programme implementation since simulation starts (year) | 2 | Float |
| average\_delay\_after\_AIDS | Average time from AIDS symptoms to ARV initiation (year) | 1/12 | Float |
| life\_time\_extension\_by\_ARV | 2 cells |  |  |
| -ife\_time\_extension\_by\_ARV{2,1} | Multiplier of remained surivival time | 2.25 | Float |
| -ife\_time\_extension\_by\_ARV{2,2} | Weibull shape parameter | 4 | Float |

## 5.13. eventARVstop

**Name:** ARV\_stop

**Interdependency**

ARV stop

ARV treatment

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| drop\_out\_rate | ARV dropout rate per year | 0.05 | Float |
| life\_time\_extension\_by\_ARV | 2 cells |  |  |
| -ife\_time\_extension\_by\_ARV{2,1} | Multiplier of remained surivival time | 2.25 | Float |
| -ife\_time\_extension\_by\_ARV{2,2} | Weibull shape parameter | 4 | Float |

## 5.14. eventARVintervention

**Name:** ARV\_intervention

**Interdependency**

HIV test

ARV intervention

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| ARV\_expansion\_strategies | n x 4 cells |  |  |
| -ARV\_expansion\_strategies{i,1}\* | Target subpopulation |  | String |
| -ARV\_expansion\_strategies{i,2} | Implementation date |  | Date |
| -ARV\_expansion\_strategies{i,3} | CD4 threshold |  | Float |
| -ARV\_expansion\_strategies{i,4} | Coverage in target subpopulation (%) |  | Float |

\* Options for target subpopulation include:

‘all HIV+’

‘pregnant women’

‘female sex workers’

‘sero-discordant couples’

‘aged 50+’

‘non-breastfeeding’ (mothers)

‘multi-partners’

## 5.15. eventBehaviourChange

**Name:** behaviour\_change

**Interdependency:** Open to modifications

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| behaviour\_changes | n x 6 cells |  |  |
| -behaviour\_changes{i,1} | Name of the behaviour change | ‘condom usage’ | String |
| -behaviour\_changes{i,2} | Whether implemented | True | Logical |
| -behaviour\_changes{i,3} | Start date |  | Date |
| -behaviour\_changes{i,4} | End date |  | Date |
| -behaviour\_changes{i,5} | Change rate (0-1) |  | Float |
| -behaviour\_changes{i,6} | Coverage (0-1) |  |  |

## 5.16. eventFSW

**Name:** FSW

**Interdependency**

Formation

Debut

FSW

Dissolution

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| baseline\_factor |  |  | Float |
| time\_factor |  |  | Float |
| age\_factor |  |  | Float |
| baseline\_factor\_stop\_working |  |  | Float |
| time\_factor\_stop\_working |  |  | Float |
| maximal\_number\_of\_fsw | Limitation of FSW in the population |  | Integer |

## 5.17. eventMTCT

**Name:** MTCT

**Interdependency**

MTCT

Conception

Heterosexual transmission

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| probability\_of\_MTCT | 2 cells |  |  |
| - probability\_of\_MTCT{2,2} | Cumulative prenatal MTCT probability | 0.25 | Float |
| - probability\_of\_MTCT{3,2} | Cumulative MTCT probability | 0.5 | Float |
| infectiousness\_decreased\_by\_ARV |  | 0.9 | Float |
| probability\_of\_breastfeeding |  | 0.9 | Float |
| HIV\_positive\_infants\_survival\_time | 2 cells |  |  |
| -HIV\_positive\_infants\_survival\_time{2,1} | Weibull scale parameter | 5 | Float |
| -HIV\_positive\_infants\_survival\_time{2,2} | Weibull shape parameter | 1 | Float |

## 5.18. eventCircumcision

**Name:** male\_circumcision

**Interdependency**

Circumcision

Heterosexual transmission

MSM transmission

Birth

Boy

MSM

**Hazard function**



**Parameters**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Symbol | Name | Comment | Default | Type |
|  | Cauchy\_scale\_parameter |  | 1 | Float |
|  | Cauchy\_peak\_age |  | 40 | Float |

## 5.19. eventMortality

**Name:** non\_AIDS\_mortality

**Interdependency**

Birth

Mortality

**Hazard function**



**Parameters**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Symbol | Name | Comment | Default | Type |
|  | Weibull\_scale\_parameter | For males |  | Float |
|  | Weibull\_shape\_parameter |  |  | Float |
|  | gender\_difference |  | 5 | Float |

## 5.20. eventAIDSmortality

**Name:** AIDS\_mortality

**Hazard function**



**Interdependency**

Heterosexual transmission

AIDS Mortality

MTCT

MSM transmission

**Parameters**

Survival time after HIV infection is calculated by HIV transmission events (eventTransmission, eventTransmissionMSM, eventMTCT).

## 5.21. eventIntroduction

**Name:** HIV\_introduction

**Interdependency**

HIV introduction

**Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Comment | Default | Type |
| number\_of\_introduced\_HIV |  |  | Integer |
| period\_of\_introduced\_HIV | 2 cells |  |  |
| -period\_of\_introduced\_HIV{2,1} | Start time of HIV introduction (year) |  | Float |
| -period\_of\_introduced\_HIV{2,2} | End time of HIV introduction (year) |  | Float |

# 6. Supplementary functions

A number of supplementary functions developed and stored in /lib folder.

## 6.1. Calibration functions

## 6.2. Facilitating functions

Facilitating functions that are called by event functions during simulation are managed by /lib/spTools.m.

## 6.3. Output functions

# 7. Appendix

# 8. Index

[antenatal care](#_5.10._eventANC)

# References