

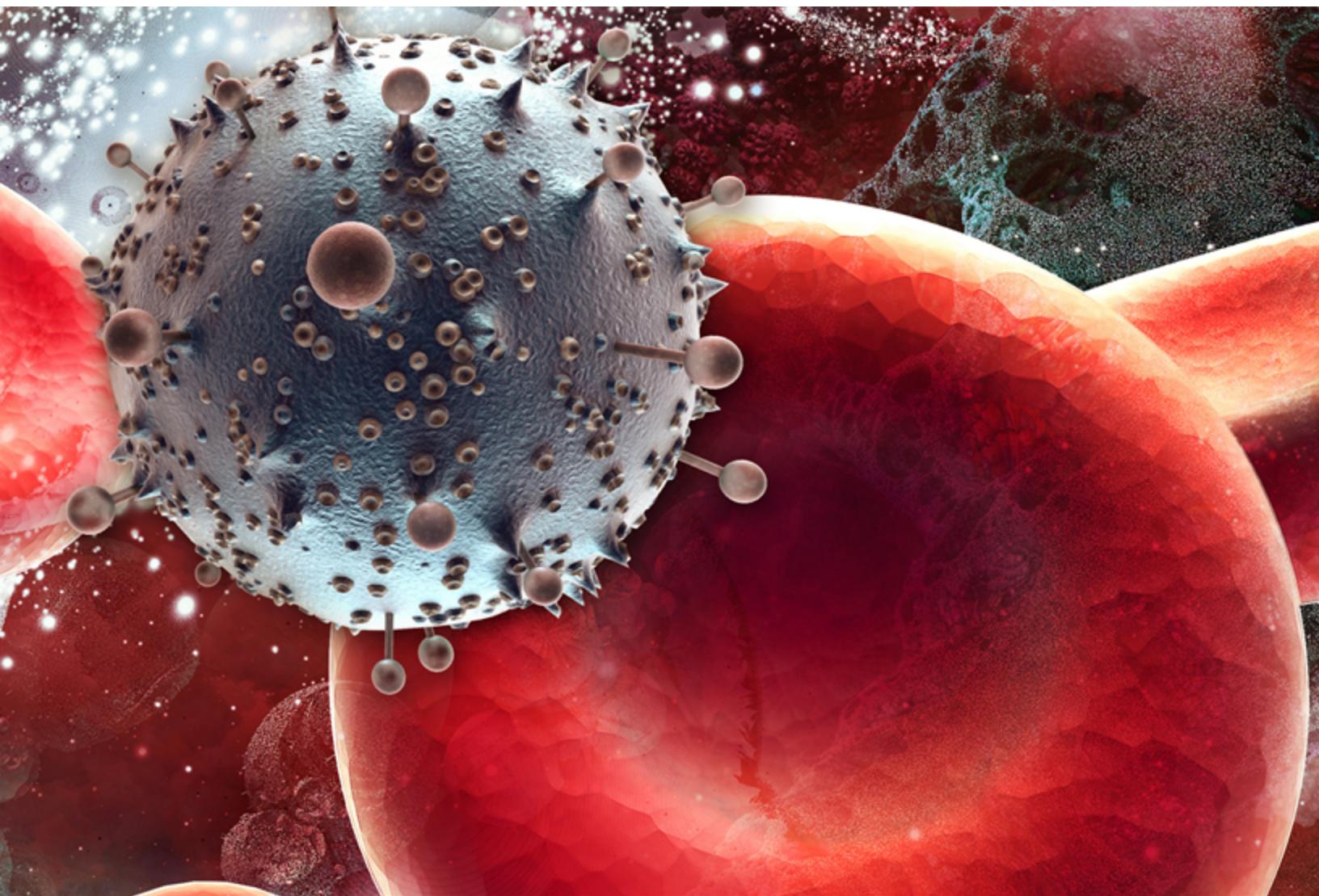
STI and HIV Model Introduction

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These HIV and STI tutorials were created for the EMOD QuickStart v2.0. Later versions of the QuickStart are not completely compatible with these tutorials as installation and some of the demographics, configuration and intervention parameters have been changed. IDM continues to improve our EMOD documentation for training and research, and new and updated STI and HIV tutorial information will be added to our new documentation [site](#). As the EMOD documentation is hosted on our new site most of the links in the PDF will not work. If you have any questions or need additional information, please contact support@idmod.org.

Table of Contents

What's New in EMOD v2.0?	1
STI Overview	1
HIV Overview	1
HIV Tutorial 1: STI Network Model	3
1-a. Welcome to STI_SIM	3
1-b. The Age of Sexual Debut	9
1-c. Choice of Sex Partner Age	12
1-d. Relationship Types and Durations	17
1-e. Concurrency: Independent Behavior across Relationship Type	19
1-f. Concurrency: Correlated Behavior across Relationship Types	24
1-g. Choice of Sex Partner Age by Relationship Type	28
1-h. Risk Groups	29
1-i. Coital Frequency and Coital Dilution with Multiple Partnerships	34
HIV Tutorial 2: HIV-Specific Biology	36
2-a. Setting Up to Study Disease Progression (Baseline_Disease_Progression)	36
2-b. Survival Time for Children	39
2-c. Survival Time for Adults	43
2-d. CD4 Count, WHO Stage, and Symptomatic Presentation	47
2-e. Heterogeneity in CD4 Count at the Time of HIV Seroconversion and Death	51
2-f. Survival Time on ART	53
2-g. Reconstitution of CD4 Count during Antiretroviral Therapy	58
2-h. Evolution of CD4 Count during Treatment Interruption and Re-Initiation	60
HIV Tutorial 3: Transmission	63
3-a. Sexual Transmission: Base Infectivity and Multipliers by Gender and Age	63
3-b. Effect of Voluntary Male Medical Circumcision on Sexual Transmission	65
3-c. Effect of Antiretroviral Therapy on Sexual Transmission	68
3-d. Effect of Condom Usage on Sexual Transmission	72

3-e. Impact of Co-infections on Sexual Transmission	75
3-f. PrEP and Vaccines	76
3-g. Vertical Transmission	78
HIV Tutorial 4: Health Care	80
4-1. Structure and Syntax of Health Care Interventions	80
4-1-a. Campaign Events: Controlling "When" and "Where"	82
4-1-b. Event Coordinator: Controlling "Who"	83
4-1-c. Intervention: Controlling "What" and "Why"	83
4-1-d. Categorizing Stages of Health Care with Cascade State	86
4-1-e. Using cascade state to control future health seeking	87
4-2. Building Blocks of a Health Care System	91
4-2-1. Standard Interventions	92
4-2-1-a. Antiretroviral Therapy (ART)	92
4-2-1-b. Voluntary Male Medical Circumcision (VMMC)	92
4-2-1-c. Prevention of Mother to Child Transmission	93
4-2-1-d. STI Co-Infection and STI Treatment	94
4-2-1-e. Condom Usage	94
4-2-2. Diagnostics	95
4-2-2-a. Testing for HIV	95
4-2-2-b. Measuring CD4 count	96
4-2-2-c. Determining ART Eligibility	97
4-2-3. Decisions	101
4-2-3-a. Random Choice	101
4-2-3-b. Making Decisions According to Most Recent CD4 Count	101
4-2-3-c. Making Decisions According to Calendar Time	102
4-2-3-d. Making Decisions According to Current Age	104
4-2-3-e. Making Decisions According to Individual's Sexual Debut Status	105
4-2-4. Delays	105
4-2-4-a. Distributions of delay time	105

4-2-4-b. Delay with expiration and Cascade State	106
4-2-4-c. Restricting multiple entries with a muxer	107
4-3. Sub-Saharan Africa epidemic model with transmission and health care	108
4-3-1. Initializing HIV and Co-Infections	110
4-3-2. Voluntary male medical circumcision (VMMC)	111
4-3-3. Prevention of Mother-to-Child Transmission (PMTCT)	112
4-3-4. Overview of Antiretroviral Treatment (ART)	116
4-3-5. Testing	118
4-3-5-a. Symptom-Driven Testing	119
4-3-5-b. Pediatric Testing	120
4-3-5-c. Antenatal Testing	121
4-3-5-d. Routine/Voluntary HIV Testing and Counseling	122
4-3-6. Staging	129
4-3-7. Linking to Care	131
4-3-7-a. Linking to pre-ART	132
4-3-7-b. Linking to ART	133
4-3-8. Pre-ART	134
4-3-9. ART	136
HIV Tutorial 5: Intervention Examples	140
5-1. Voluntary Medical Male Circumcision (VMMC)	140
5-1-a. One-Time VMMC Campaign	140
5-1-b. One-Time Age-Targeted VMMC Campaign	142
5-1-c. Continuous Availability of VMMC for Adults and Infants	143
5-1-d. Age-Triggered VMMC	145
5-1-e. VMMC Driven by Existing Levels of Testing	146
5-1-f. Expansion of HIV Testing and VMMC	147
5-2. Treatment Eligibility	152
5-2-a. Configuring Expansion of Treatment Guidelines	152
5-2-b. Impact of Expanded Guidelines on Retention	154

5-2-c. Impact of Expanded Guidelines on Linkage	157
5-2-d. Age-Targeted Treatment	158
5-3. HIV Testing	160
5-3-a. One-Time Testing Campaign	160
5-3-b. Changing Existing Testing Patterns: Regular Annual Testing	162
5-3-c. Community-Based Testing	164
5-3-d. Community-Based Testing and Staging	166
5-3-e. Community-Based Testing and Staging with Delayed Presentation	167
5-4. Retention	170
5-4-a. Complex Rate of Retention on ART: Dependence on Time, CD4 Count, and Demographics	171
5-4-b. Point-of-Care CD4 Testing	172
5-4-c. Gradual Roll-Out of PoC CD4 Testing	173
5-4-d. 90% Linkage After Diagnosis	174
5-5. Re-Initiation of Care	176
5-5-a. Outreach to Re-Initiate Those Who Become Lost to Care	176
5-5-b. Outreach to Re-Initiate Those Already Lost to Care	177
5-6. Delays in Receiving Care	178
5-6-a. Removing Delays in Health Care Access	178
5-6-b. Removing Delays and Ensuring Successful Linkage to Care	179
5-7. HIV Prophylaxis	180
5-7-a. Uniform Efficacy	180
5-7-b. Heterogeneous efficacy or adherence	181
5-7-c. Long-acting product for HIV prophylaxis	183
Appendix A: Output File Descriptions	185
Age and Gender-Stratified HIV Epidemic	186
ART Initiation and Discontinuation	188
HIV Mortality	189
HIV Disease Progression	192

Health Events and Interventions	196
Formation of Relationships	198
Dissolution of Relationships	202
Transmission of disease within relationships	204
Coital Acts	208
Age-Stratified Epidemic Information	210
Age-Stratified Demographic Information	211
Diagnostic Outputs for Software Developers	213
Appendix B: Scripts for Plotting Model Results	215
InsetChart Channel Viewer	216
Prevalence, Incidence, Mortality, and Number on ART	217
Population by Age	218
Log of Events and Interventions Applied to Individuals	219

What's New in EMOD v2.0?

EMOD v2.0 now includes transmission in a person-to-person contact network, available as a generic sexually transmitted infection ([STI Overview](#)) and with the specific biology and health care system associated with human immunodeficiency virus ([HIV Overview](#)).

This new functionality is illustrated in a series of scenarios/tutorials:

- [HIV Tutorial 1: STI Network Model](#)
- [HIV Tutorial 2: HIV-Specific Biology](#)
- [HIV Tutorial 3: Transmission](#)
- [HIV Tutorial 4: Health Care](#)
- [HIV Tutorial 5: Intervention Examples](#)

Currently, the STI and HIV models do not support migration, multi-node or multi-core simulations.

STI Overview

The STI model enables person-to-person transmission of disease, which is distinct from the vector-borne, airborne, or waterborne transmission routes also available in EMOD.

The STI contact network enables users to configure up to three relationship types with different durations, gender-specific levels of concurrency, age patterns of formation, and preference functions. Partnership preference can select for partners with similar or different risk behavior, STI infection status, and sociodemographic groupings that can be used represent geographic location, race, socioeconomic status, and other factors. Concurrency and levels of co-infection can also be configured independently for each risk group.

The balance of "supply and demand" of partners is handled using a feed-forward algorithm that dynamically adjusts the rates of relationship formation as the population structure changes. Feed-forward can be disabled during the simulation to allow future patterns of relationship formation to change in response to demographic shifts in the population.

These capabilities are demonstrated in [HIV Tutorial 1: STI Network Model](#).

HIV Overview

The HIV-specific implementation of the STI network model includes co-factors and interventions affecting transmission, disease progression on and off therapy, and detailed and time-variable linkage and

retention along the care continuum. The HIV tutorials and sample input files are aimed at modeling generalized epidemics in sub-Saharan Africa.

[HIV Tutorial 2: HIV-Specific Biology](#) demonstrates the disease-specific biological factors in EMOD v2.0 that influence HIV transmission and progression.

[HIV Tutorial 3: Transmission](#) demonstrates the model's configuration and assumptions around HIV transmission, including the effect of disease stage, male circumcision, co-infections, condom usage, anti-retroviral therapy, and prophylaxis.

[HIV Tutorial 4: Health Care](#) demonstrates configuration of the health care system to distribute HIV services for prevention and treatment. It describes an approach to creating complex health care systems by linking together simple building blocks such as health-seeking triggers, diagnostics, and decisions based on time, sociodemographic group, health status, and medical history. The structure and syntax of the individual building blocks is provided. Then, a fully configured system of HIV services is demonstrated, and each component of the system is described in detail. These include PMTCT, VMMC, and ART with routine testing, event-driven testing, historical changes in eligibility, and patterns of retention and re-initiation of care.

[HIV Tutorial 5: Intervention Examples](#) illustrates how users can project many improvements to HIV prevention and treatment programs, as well as emerging technologies such as long-acting HIV prophylaxis.

HIV Tutorial 1: STI Network Model

EMOD is a modeling framework that supports multiple modes of disease transmission. One of these is person-to-person transmission through a network of relationships. In a contact network, there is a specific transmitter and recipient of every transmission event. To organize the network, individuals form one or more relationships that are remembered over time.

Preference for partners is configurable through the model's input files. Inside the model, the "supply and demand" for types of partners is balanced by a pair formation algorithm (PFA) that, if desired, can dynamically adjust the rates of relationship formation in each demographic category to produce a constant mixing pattern, even with demographic changes in the population. Alternatively, the dynamic adjustments can be turned off to allow mixing patterns to change in response to demographic changes.

You will learn how to configure and measure the mixing pattern in the population, and how to adjust the structure of the network by controlling factors such as sexual debut, levels of concurrency, and relationship types and durations.

All of the examples given will be for heterosexual relationships. Same-sex relationships are not yet included in 2.0 release, although the model is intended to be extensible to support same-sex relationships in future releases.

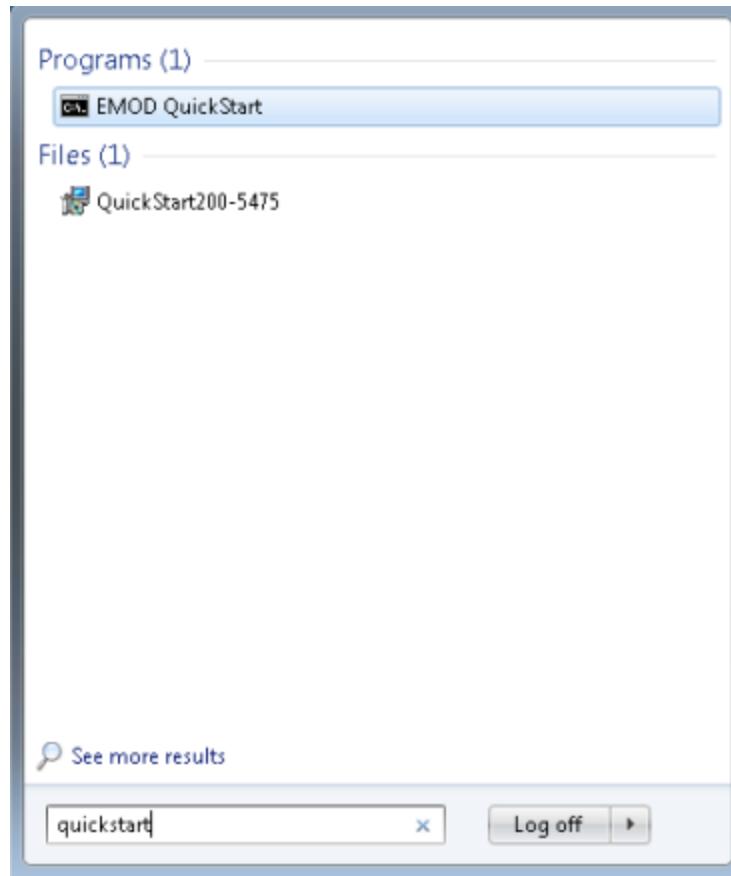
1-a. Welcome to STI_SIM

The files for this scenario are located in the directory: C:\Users\<user-name>\Ap-pData\Local\EMOD\QuickStart\STIAndHIV\01_STI_Network\A_Welcome_to_STI_SIM.

This scenario explains how to enable network transmission in EMOD, the input files required to run the model, and the output files that can be produced.

As with all of the scenarios/tutorials, a set of input and output files for this demonstration is provided with the Quick Start, available for download at www.idmod.org/software. After installing the Quick Start, use Windows Explorer to open the directory:

To find the directory, first locate the folder where the Quick Start has been installed. One way to do this is to open the windows Start menu, type the word "quickstart". Then click on the program EMOD Quick Start under the Programs list, like in the example below:



This will open the Quick Start directory in a command line window. If you prefer to use Windows Explorer, type "start ." -- the word "start" followed by a space and a period -- and press Enter, like in the example below:

```
EMOD QuickStart
Microsoft Windows [Version 6.1.7601]
Copyright (c) 2009 Microsoft Corporation. All rights reserved.

C:\Users\IDMGuest\AppData\Local\EMOD\QuickStart\v2.0.0>start .
```

This will open up the directory in an Windows Explorer window.

Alternatively, you can navigate to the Quick Start directory in Windows Explorer, starting with the drive or partition (usually C:) where the Quick Start was installed:

```
C:\Users\<YourUsername>\AppData\Local\EMOD\QuickStart\v2.0.0
```

Depending on your computer settings, you may not be able to directly navigate to the AppData directory. In this case, you can try the following:

- Navigate to C:\Users\<YourUsername>
- Update the path in the Address Bar to C:\Users\<YourUsername>\AppData and press enter.

This should open the AppData directory so that you can navigate to the Quick Start folder.

Once in the Quick Start folder, navigate to the folder for this scenario:

Scenarios\STIAndHIV\01_STI_Network\A_Welcome_to_STI_SIM

To enable network transmission, a parameter must be set in the config.json input file, which is one of the three [input files](#) provided for this tutorial: config.json, campaign.json, and a simple demographics file that provides a constant birth rate and mortality at a fixed age. All three files are written in JavaScript object notation syntax, or JSON, and can be modified using a text editor or an online JSON editor such as <http://codebeautify.org/jsonviewer> or <https://www.jsoneditoronline.org/>.

The parameter to enable network transmission is `Simulation_Type`. In this scenario, it is set to the string “`STI_SIM`”.

Parameter	Values	Descriptions
<code>Simulation_Type</code>	<code>STI_SIM</code>	Sets the simulation type. This is a required parameter that determines which disease biology and transmission modality to apply, and which parameter categories are valid for the simulation. <code>STI_SIM</code> supports generic disease progression including susceptible, exposed, infected, and recovered (immune) disease states.

To run the model, launch the EMOD Quick Start, navigate to the directory where the Quick Start was installed, and open the folder:

\EMOD\QuickStart\Scenarios\STIAndHIV\01_STI_Network\A_Welcome_to_STI_SIM

Double-click the file:

runEmod.cmd

A command window will open, report on the status of the model as it is running, and close when the model is finished running.

Alternatively, if you downloaded and compiled the EMOD source code, you can [run the model through the command line](#):

..\..\..\..\Eradication\x64\Release\Eradication.exe -C config.json -I ..\..\..\InputFiles -O output\

The previous command line assumes that you have compiled the release version of EMOD source. If you compiled the debug version, change *Release* to *Debug*.

After running the model, several files will be written to the output directory. The files are briefly described in the following table. To enable creation of each output file, set the config.json parameter to 1. To disable creation of the file, set the config.json parameter to 0.

The table only includes the reports used for this scenario. For a complete list of reports available for STI and HIV simulations, see [Appendix A](#). For additional details see the [Data Output Files](#) page in the File Format Layout Descriptions area of the online documentation.

Filename	Enable via config.json parameter	Description
RelationshipStart.csv	Report_Relationship_Start	<p>Detailed information about each relationship, evaluated at the time of relationship formation</p> <p>Includes the relationship type, start time, scheduled end time, and detailed information about each participant (ID, gender, age, infection status, circumcision status for males, co-infections, and number of active, recent, and lifetime relationships).</p>
RelationshipEnd.csv	Report_Relationship_End	<p>Detailed information about each relationship, evaluated at the time of relationship dissolution.</p> <p>Includes the relationship type, start time, scheduled end time, actual end time (which may differ from the scheduled end time, e.g., due to the death of a partner), participant IDs, and ages at the time of dissolution.</p>

Filename	Enable via config.json parameter	Description
<u>TransmissionReport.csv</u>	Report_Transmission	<p>Detailed information about each transmission event, evaluated at the time of disease transmission.</p> <p>Includes the time/date of transmission and information about the transmitter and recipient (age, gender, current and lifetime number of relationships, infection stage, circumcision status for males, co-infections, and disease-specific biomarkers if applicable).</p>
<u>RelationshipConsummated.csv</u>	Report_Coital_Acts	<p>Detailed information about each coital act.</p> <p>Includes time, relationship and participant IDs, whether a condom was used, and each participant's age, gender, infection status, circumcision status, co-infection status, and treatment status.</p>
<u>BinnedReport.json</u>	Enable_Demographics_Report	<p>Age-stratified records (in 5-year age bins) of the population size, number of infections, number of new infections, and disease-related deaths over time.</p>
<u>DemographicsSummary.json</u>	Enable_Demographics_Report	<p>Age-stratified records (in 5-year age bins) of the population size, number of births, number of non-disease deaths (those not associated with the disease being modeled), gender ratio, and other demographic summary statistics.</p>
<u>InsetChart.json</u>	Enable_Default_Report	<p>Information about the simulation at each time step, customized for model development (compared to other output files that are more tailored for scientific research)</p>

The scenarios in the STI and HIV tutorials include examples of how to analyze the model outputs in a variety of scripting languages, including Python, R, Matlab, and Mathematica.

The CSV output files can be opened in Microsoft Excel. For age-stratified and other categorized outputs, it is useful to aggregate records using the PivotChart feature in Excel, or using your preferred data analysis software.

For the JSON output files, many software packages offer tools to import JSON data. For example, this scenario includes a Python script, `plotAllCharts.py`, that can be used to plot all of the data in the `InsetChart.json` output file.

In the EMOD-HIV tutorials, scripts are provided to generate the plots used for each of the simulations. The scripts are located in each scenario's directory.

In addition to the scenario-specific scripts, the `Scripts` and `Scripts/HIV` directories contain common scripts for plotting basic model outputs such as prevalence, incidence, mortality, antiretroviral treatment, population size by age, and the health care interventions received by individuals.

`Scenarios\Scripts`

or

`Scenarios\Scripts\HIV`

The scripts are duplicated in R and Python, with the exception of the inset chart viewer, which is provided only in Python. The R and Python versions produce graphs with the same data content, but slightly different aesthetics such as line colors. R scripts save an image in png format to a folder named "figs", whereas python uses matplotlib to produce an on-screen figure.

A brief summary of each of the generic scripts is provided in the following table. For more information, please refer to [Appendix B](#).

Filename	Purpose	Input Arguments
<code>plotAllCharts.py</code>	Plot all channels from the <code>InsetChart.json</code> file	Path to <code>InsetChart.json</code> and a descriptive title. See InsetChart Channel Viewer .
<code>plotHIVSummary_15_49.{py,R}</code>	Plot HIV incidence, prevalence, mortality, and ART coverage by gender for ages 15-49.	Path to <code>ReportHIVByAgeAndGender.csv</code> . See Prevalence, Incidence, Mortality, and Number on ART . For an example of <code>ReportHIVByAgeAndGender.csv</code> , see Scenario 2-h .

Filename	Purpose	Input Arguments
plotEventRecorder.{py,R}	Plot events that are broadcast during a simulation.	Path to ReportEventRecorder.csv. See Population by Age . For an example of ReportEventRecorder.csv, see Scenario 4-1-e .
plotBinnedPopulation.{py,R}	Plot the population by age group over time.	Path to BinnedReport.json. See Log of Events and Interventions Applied to Individuals .

Congratulations! You've just run your first STI_SIM.

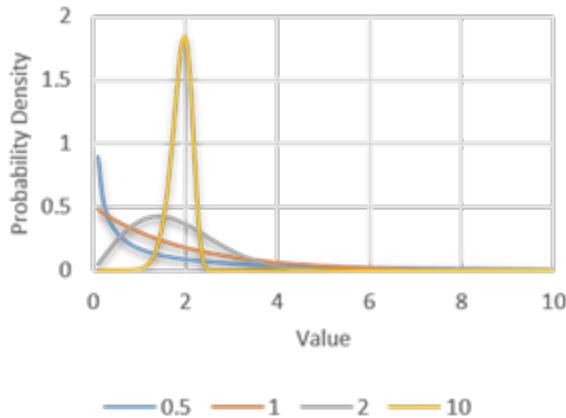
1-b. The Age of Sexual Debut

The files for this scenario are located in the directory Scenarios\STIAndHIV\01_STI_Network\B_Sexual_Debut

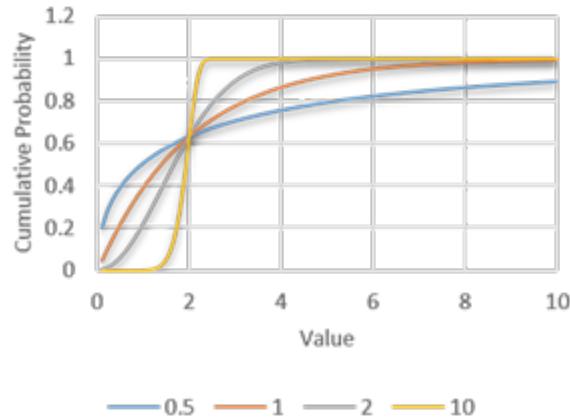
Individuals are eligible to enter relationships only after reaching the age of sexual debut. The age of sexual debut is randomly drawn for each individual from a Weibull distribution.

Weibull distributions are used often in EMOD and require two parameters. The shape parameter governs the shape of the density function. When the shape parameter is equal to 1, it is an exponential distribution. For shape parameters above 1, it forms a unimodal (hump-shaped) density function. As the shape parameter becomes large, the function forms a sharp peak.

**Weibull Probability Density
Scale = 2, Varying Shape**

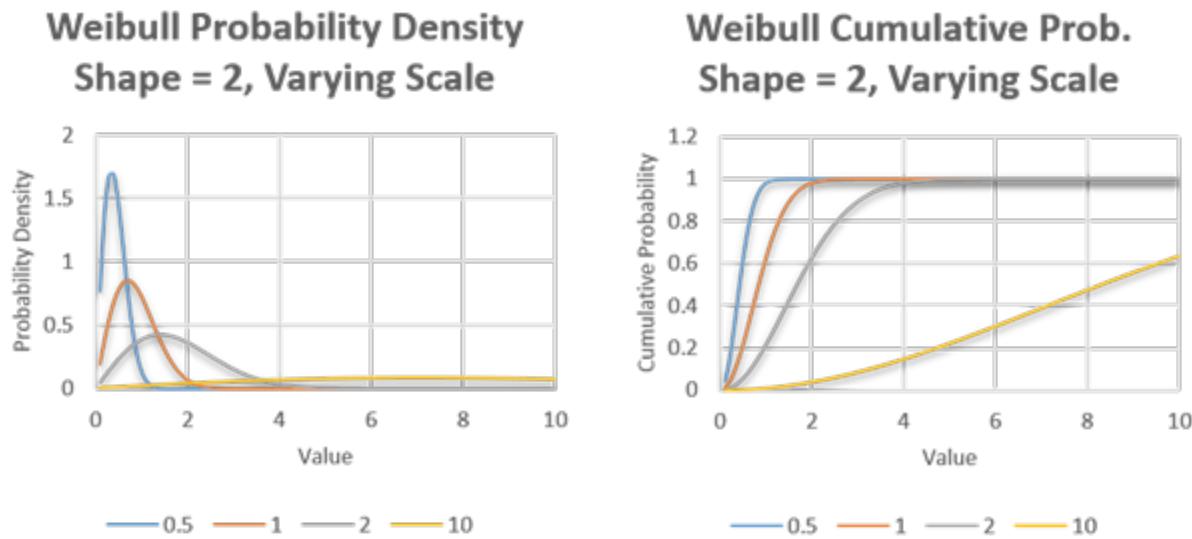


**Weibull Cumulative Prob.
Scale = 2, Varying Shape**



The inverse of the shape parameter is sometimes referred to here as the “heterogeneity” of the distribution ($\text{heterogeneity} = 1/\text{shape}$), because it can be helpful to think about the degree of heterogeneity of draws from the distribution, especially for hump-shaped functions with heterogeneity values between 0 and 1 (i.e., shape parameters greater than 1).

A second parameter shifts the distribution from left to right, and is called the scale parameter:



When heterogeneity is small (i.e., the shape parameter is large), the scale parameter sets the location of the sharp peak. The scale parameter is related to the median of the distribution by the equation:

$$\text{Median} = \text{Scale} \times (\ln(2))^{1/\text{Shape}} = \text{Scale} \times (\ln(2))^{\text{Heterogeneity}}$$

so that when heterogeneity is close to zero, the median is close to the scale parameter.

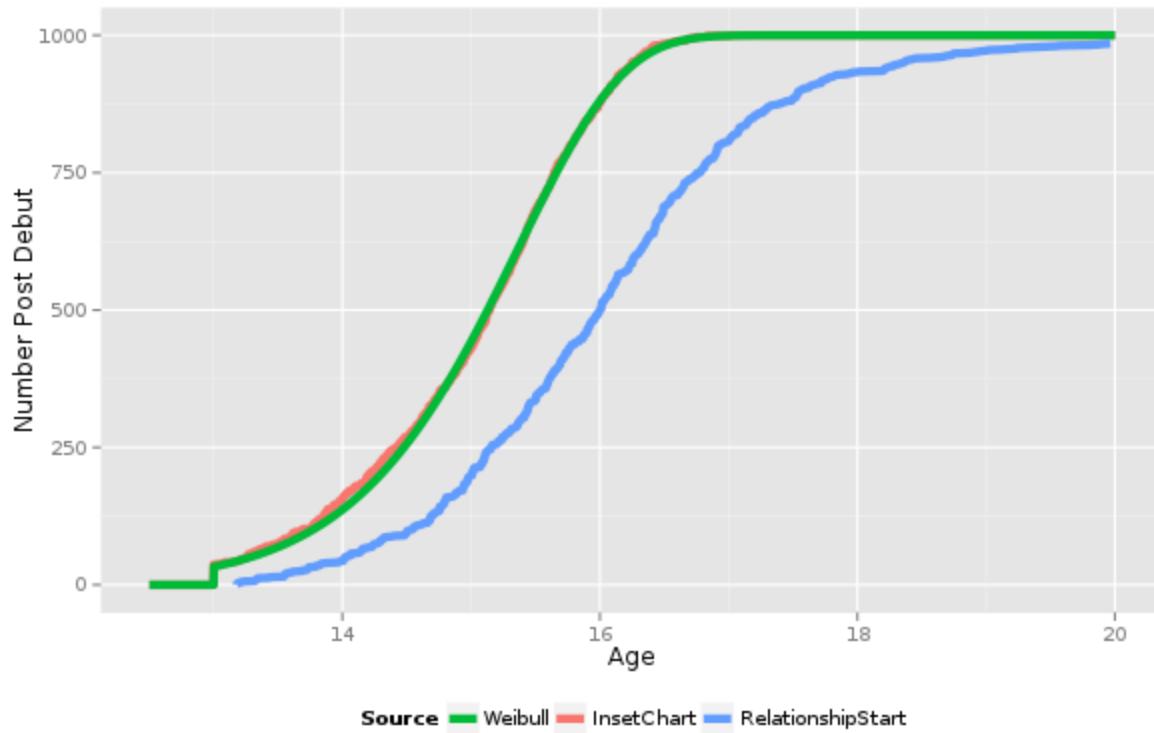
To familiarize yourself with the Weibull distribution, explore the Excel spreadsheet called Weibull.xlsx in the figures directory for this scenario:

Scenarios\STIAndHIV\01_STI_Network\A_Welcome_to_STI_SIM\figs

To define the distribution of age of sexual debut, three parameters are specified: the Weibull heterogeneity parameter, the Weibull scale parameter, and the minimum possible age of sexual debut. The first two parameters can be set to different values for males and females. The third parameter prevents debut ages lower than a specific value, even if the Weibull distribution has some mass below that value. These parameters are located in the config.json input file, and are tabulated below:

Parameter	Value	Range	Units	Description
Sexual_Debut_Age_Male_Weibull_Scale	16.946729660034	[0,50]	Years	Scale of Weibull for male debut age.
Sexual_Debut_Age_Male_Weibull_Heterogeneity	0.05	[0.02,3.40282e+38]	None	Heterogeneity of Weibull for male debut age.
Sexual_Debut_Age_Female_Weibull_Scale	15.919654846191	[0,50]	Years	Scale of Weibull for female debut age.
Sexual_Debut_Age_Female_Weibull_Heterogeneity	0.05	[0.02,3.40282e+38]	None	Heterogeneity of Weibull for female debut age.
Sexual_Debut_Age_Min	13	[0.02,3.40282e+38]	Years	Minimum debut age.

To demonstrate the effect of these parameters, the demographics file for this scenario creates a cohort of 1000 individuals born on a specific date, and the config.json file contains the parameter settings tabulated above. The plot below shows the age of sexual debut, as well as the age at which the individuals form their first relationship.



The green curve shows the expected left-truncated Weibull distribution of ages at sexual debut, calculated from the input parameters. The red curve shows the number of individuals who have reached sexual debut, from the “Post-Debut Population” channel of the InsetChart.json output file. As expected, the red curve closely matches the green curve, including the lack of sexual debut ages below the Sexual_Debut_Age_Min of 13.

The blue curve shows the age of the first relationship from the [RelationshipStart.csv](#) output file. Sexual debut determines eligibility for forming a relationship, but there is a lag time between eligibility and actual formation of a first relationship determined by the pair formation rates. Here, the first relationship begins an average of 1 to 2 years after the age of sexual debut.

See [1d. Relationship types and durations](#) for more about relationship formation.

1-c. Choice of Sex Partner Age

The previous scenario explained how individuals become eligible to form relationships for the first time, and showed a lag between eligibility and actual formation of the first relationship. This scenario explains what takes place between eligibility and formation of a relationship, and how the choice of partners is made.

EMOD allows you to configure the mixing patterns in the population by prescribing the proportion of relationships that should occur between different categories of partners. The populations of the two categories are not necessarily equal, and proportion of partners specified to have a given pair of categories

is not always proportional to the populations of those categories. To compensate for this, the model uses a feed-forward algorithm called a Pair Formation Algorithm (PFA) to dynamically adjust the rates of relationship formation in order to balance “supply and demand.” The mathematics of this algorithm have been published elsewhere¹, as well the resulting age patterns of HIV transmission².

The prescribed mixing patterns are provided as input to the model in a [demographics file](#). You can find this scenario’s demographics files, along with the other demographics files used in the EMOD tutorials, in the directory:

Scenarios\InputFiles

The demographics file deals with many aspects of the population, including fertility, mortality, and sub-populations for heterogeneities such as risk behavior or access to health care. To make it easier to swap out different partner preference patterns without having to edit a complex demographics file, the partner preferences can be provided as a separate file that is [layered over the baseline demographics file](#).

In this scenario, a simple demographics file is provided, called uniform_demographics.json. The partnership preferences layer is provided as a separate file called PFA_Transitory_2x2.json. To tell the model to use these files, list them under the array “Demographics_Filenames” in config.json. The base filename should be listed first, followed by the overlay:

```
"Demographics_Filenames": ["uniform_demographics.json", "PFA_Transitory_2x2.json"],
```

Because PFA_Transitory_2x2.json is listed second, it will be layered over the base file uniform_demographics.json. This means that the files are merged, but if a field is specified in both the base and the overlay file, the content of the overlay file overrides the content of the base file.

The uniform_demographics.json base demographics file included with this tutorial creates a population of 10,000 individuals with a fixed (population-independent) birth rate. The initial population age distribution is uniform (configured by setting AgeDistributionFlag to 1) between the ages of zero (configured by AgeDistribution1) and 55 years (20,075 days, configured with AgeDistribution2). To maintain the uniform population structure, the mortality rate goes from zero to 100% per day at the age of 55. In the excerpt below, the mortality rate is specified independently for males and females by adding a second "gender" axis with the categories "male=0,female=1". However, the mortality assigned to each gender is identical in this example. There is no geographic substructure, so only a single geographic loc-

¹Klein DJ. Relationship formation and flow control algorithms for generating age-structured networks in HIV modeling. 2012 IEEE 51st Annual Conference on Decision and Control (CDC). 2012. p. 1041-6.

²Bershteyn A, Klein DJ, Eckhoff PA. Age-dependent partnering and the HIV transmission chain: a microsimulation analysis. J R Soc Interface. 2013 Nov 6;10(88):20130613.

ation or node is specified. Note that multiple nodes (spatial heterogeneity with distributed computing) are not supported in the current release of EMOD-HIV.

```
{
  ...
  [
    ...
    {
      ...
      "NodeAttributes": {
        ...
        "InitialPopulation": 10000,
        "BirthRate": 0.0000548
      },
      "IndividualAttributes": {
        ...
        "AgeDistributionFlag": 1,
        "AgeDistribution1": 0,
        "AgeDistribution2": 20075,
        ...
      },
      "MortalityDistribution": {
        ...
        "NumDistributionAxes": 2,
        "AxisNames": [ "gender", "age" ],
        "AxisUnits": [ "male=0,female=1", "years" ],
        "AxisScaleFactors": [ 1, 365 ],
        "NumPopulationGroups": [ 2, 3 ],
        "PopulationGroups": [ [ 0, 1 ], [ 0, 55, 55 ] ],
        "ResultUnits": "deaths per day",
        "ResultScaleFactor": 1,
        "ResultValues": [ [ 0, 0, 1 ], [ 0, 0, 1 ] ]
      }
    }
  ]
}
```

Here, the overlay file is used to categorize types of partners, and to specify the proportion of couples that should be formed between each pair of categories. Factors such as infection status and risk group are inherently categorical, but ages must be categorized into age “bins” of a specified width. Analogous to the process of creating a histogram, the edges between the age bins are specified in increasing order. Age bins are created between each sequential pair of edges. In addition, a bin is created for all individuals younger than the lowest edge, and a separate bin is created for all individuals older than the highest edge.

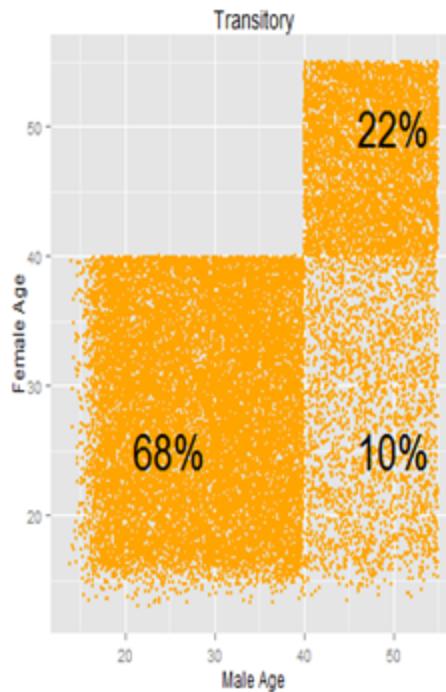
In pfa_transitory_2x2.json, only one edge is specified for each gender at the age of forty. This creates two age bins/categories for each gender: individuals younger than forty, and those older than forty. The total number of bins for each gender is set to 2, and the age of the first bin is set to 40. Because each

gender is only divided into two groups, the Years_Between_Bin_Edges_* parameters are not used in this example.

```
"Pair_Formation_Parameters_TRANSITORY" :  
{  
    "Number_Age_Bins_Male" : 2,  
    "Number_Age_Bins_Female" : 2,  
    "Age_of_First_Bin_Edge_Male" : 40,  
    "Age_of_First_Bin_Edge_Female" : 40,  
    "Years_Between_Bin_Edges_Male" : 25,  
    "Years_Between_Bin_Edges_Female" : 25,  
    "Assortivity" :  
    {  
        "Group" : "NO_GROUP"  
    },  
    "Joint_Probabilities" :  
    [  
        [ 0.7, 0.0],  
        [ 0.1, 0.2]  
    ]  
},
```

The preference matrix specifies that 70% of relationships should be between males under forty and females under forty; 20% be between males over forty and females over forty; 10% be between males over forty and females under forty, and none should be between males under forty and females over forty.

The ages of both partners are recorded in RelationshipStart.csv and can be plotted to verify that the age pattern at the time of relationship formation is close to the prescribed mixing pattern. In the figure below, each dot represents the age of the male and female partner for each newly formed relationship.



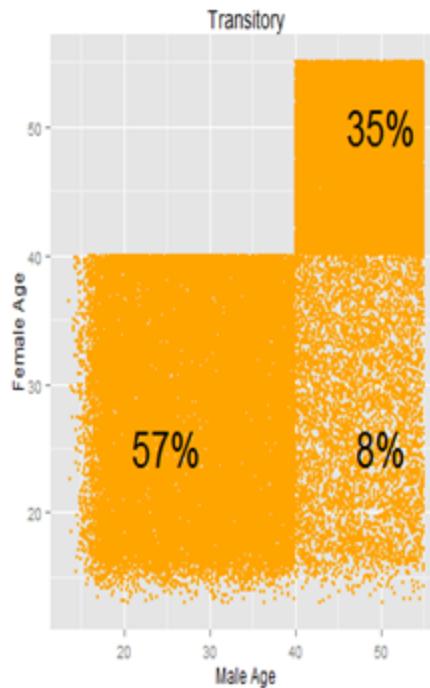
The number of relationships actually formed in each category is close but not identical to the prescribed preferences. This is because the desired partner type is not always available at the time of pair formation. In this case, the algorithm will either pair the individual with whoever is available, or it will have the individual wait in a queue until the next round of pair formation.

The decision between waiting and choosing who is available is determined by the parameter `PFA_Cum_Prob_Selection_Threshold`. When some categories of potential partners are unavailable, the parameter determines the minimum level of preference for the available partners required for the individual to choose among whoever is available, rather than wait.

In the provided config.json file, the `PFA_Cum_Prob_Selection_Threshold` is set to zero, meaning that when a chosen type of partner is not available, any partner for whom the individual has a nonzero preference can be chosen instead.

```
"PFA_Cum_Prob_Selection_Threshold": 0,
```

One way that desired partner types can become unavailable is if the rate of relationship formation for the different individuals is set to a very high number. For example, if the config.json parameter `Transitory_Forecast_Rate_Heterosexual1` is increased from once per 100 days to once per day, then the PFA frequently runs out of the desired partner type, and the age mixing pattern drifts away from the prescribed distribution:



Another potential reason why the actual mixing patterns in the model can differ from the configured ones is that the dynamic feed-forward adjustment of pair formation rates has been disabled. The pair formation algorithm (PFA) dynamically adjust the relationship formation rates to fit the configured mixing patterns, but only up until a specified time. The time is set by the config.json parameter PFA_Burnin_Duration_In_Days :

```
PFA_Burnin_Duration_In_Days": 5475
```

This parameter sets the number of days, since the start of the simulation, over which the PFA will dynamically adjust the pair formation rates. After this period of time, the rates are no longer adjusted, allowing the patterns of relationship formation to change in response to demographic shifts in the population.

1-d. Relationship Types and Durations

The previous scenario demonstrated age mixing for just one relationship type (transitory). In fact, the STI and HIV models support three relationship types: transitory, informal, and marital. The mixing patterns and rates of formation demonstrated earlier can be configured independently for each relationship type. In addition, each relationship type can be assigned a different average duration. These are fully configurable, but as a guide to get started, some recommended settings for the relationship durations and mixing patterns are:

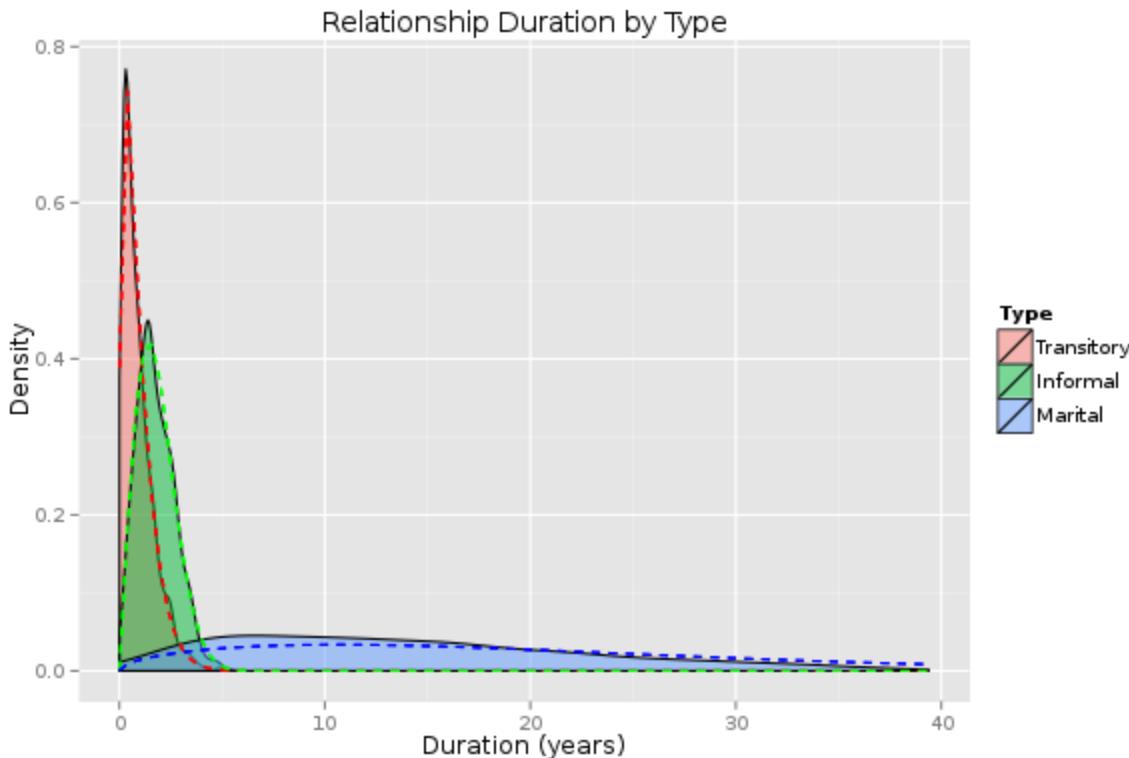
Relationship Type	Intended Duration	Participant Age	Age Gaps
Transitory	Short, about 1 year	Young, often under 20 years	Small, men tend to be older by a year or two.
Informal	Medium, 1-3 years	Intermediate, primarily 20-30 years	Intermediate
Marital	Long, 10+ years	Older, typically over 30 years of age	Large, men tend to be about 5 years older

The relationship durations are Weibull-distributed. See [Scenario 1b](#) for details about how to configure a Weibull distribution. The values below have been set so that the median length of the transitory, informal, and marital relationships comes out to 0.9, 1.8, and 20 years, respectively. For more information on the ranges for these parameters, see the [simulation parameters](#).

Parameter	Value	Units	Description
Relationships_Transitory_Weibull_Scale	0.95677477	Years	Weibull scale parameter to determine relationship duration for transitory-type relationships.
Relationships_Transitory_Weibull_Heterogeneity	0.83333333	None	Level of heterogeneity expressed as the inverse of the Weibull shape parameter for transitory-type relationships.
Relationships_Informal_Weibull_Scale	2.03104913	Years	Weibull scale parameter to determine relationship duration for informal-type relationships.
Relationships_Informal_Weibull_Heterogeneity	0.5	None	Level of heterogeneity expressed as the inverse of the Weibull shape parameter for informal-type relationships.
Relationships_Marital_Weibull_Scale	22.1544552	Years	Weibull scale parameter to determine relationship duration for marital-type relationships.
Relationships_Marital_Weibull_Heterogeneity	0.66666667	None	Level of heterogeneity expressed as the inverse of the Weibull shape parameter for marital-type relationships.

These distributions govern the duration that is assigned to a relationship when it is formed. The duration is used to calculate the scheduled end time of the relationship. Sometimes relationships dissolve earlier than this scheduled end time: for example, if a participant dies. This will lead to an actual end time that is sooner than the scheduled end time.

The start time, scheduled end time, and actual end time of each relationship is recorded in the output file [RelationshipEnd.csv](#). The figure below shows how the Weibull distributions compare to the actual durations of the relationships:



As expected, relationships are slightly shorter than their expected durations due to factors such as mortality. This is most pronounced for marital relationships because they are longer, and because they tend to be composed of older individuals (who, in this disease-free example, are affected by background mortality).

1-e. Concurrency: Independent Behavior across Relationship Type

The model can be configured to allow individuals to have multiple relationships simultaneously. Concurrency is controlled by "flags" for each relationship type that determine if an individual is capable of seeking additional relationships when already participating in a relationship of that type. For example, a person who lacks an extra-marital "flag" cannot add an additional relationship while participating in a marital relationship. If an individual is participating in multiple types of relationships, then a "flag" is required for each type in order to enable further concurrent relationships. Thus, an individual who is

simultaneously in a transitory and a marital relationship can only enter additional relationships if they have both the `extra_transitory` and `extra_marital` flags.

The probability of receiving a “flag” is configurable for each relationship type, gender, and demographic/risk group. In this example, these values are applied uniformly to the population without stratifying by risk or sociodemographic group. The following parameters are configured so that a small fraction of men and a large fraction of women receive these flags:

Parameter	Value	Range	Units	Description
Prob_Extra_Transitory_Relationship_Male	0.2	[0,1]	None	Probability of a male receiving the <code>extra_transitory</code> flag
Prob_Extra_Transitory_Relationship_Female	0.8	[0,1]	None	Probability of a female receiving the <code>extra_transitory</code> flag
Prob_Extra_Informal_Relationship_Male	0.2	[0,1]	None	Probability of a male receiving the <code>extra_informal</code> flag
Prob_Extra_Informal_Relationship_Female	0.4	[0,1]	None	Probability of a female receiving the <code>extra_informal</code> flag
Prob_Extra_Marital_Relationship_Male	0.1	[0,1]	None	Probability of a male receiving the <code>extra_marital</code> flag
Prob_Extra_Marital_Relationship_Female	0.1	[0,1]	None	Probability of a female receiving the <code>extra_marital</code> flag

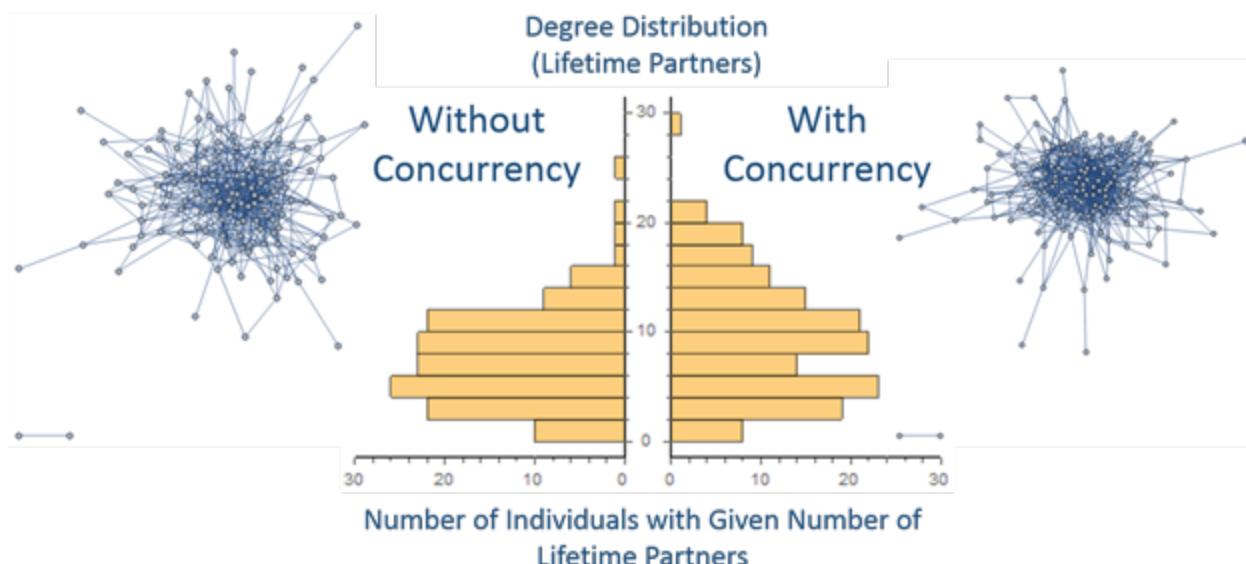
In addition to setting the probability of enabling concurrent relationships, the model also limits the total number of relationships of each type that an individual can participate in at the same time. These can also be configured differently by risk group or other sociodemographic group, although in this example, they are uniformly applied to the population. The following parameters enable men who receive a flag to engage in several relationships, whereas women who receive the flag have a maximum of two relationships per type:

Parameter	Value	Range	Units	Description
Max_Simultaneous_Transitory_Relationships_Males	4	[0,10]	Relationships	Maximum number of concurrent transitory relationships for males.

Parameter	Value	Range	Units	Description
Max_Simultaneous_Transitory_Relationships_Females	2	[0,10]	Relationships	Maximum number of concurrent transitory relationships for females.
Max_Simultaneous_Informal_Relationships_Males	3	[0,10]	Relationships	Maximum number of concurrent informal relationships for males.
Max_Simultaneous_Informal_Relationships_Females	2	[0,10]	Relationships	Maximum number of concurrent informal relationships for females.
Max_Simultaneous_Marital_Relationships_Males	2	[0,10]	Relationships	Maximum number of concurrent marital relationships for males.
Max_Simultaneous_Marital_Relationships_Females	2	[0,10]	Relationships	Maximum number of concurrent marital relationships for females.

Note that an individual can be in no more than 9 simultaneous relationships at any point in time. This limitation is enforced by requiring the per-gender sums of the above parameters to be less than 10.

Enabling concurrency increases the average number of simultaneous partners, and over the course of the simulation, also increases the average number of lifetime partners. The figure below shows the degree distribution of a network of 100 individuals with concurrency disabled and enabled:



It is interesting to note that, despite the increase in concurrency and number of lifetime partners, the overall size of the connected component of the network remains similar. Numerous factors influence the network connectivity, including the population size and structure and the configured formation rates, durations, and mixing patterns for each relationship type. This mix of factors determines the extent to which “serial monogamy” is sufficient to connect the network.

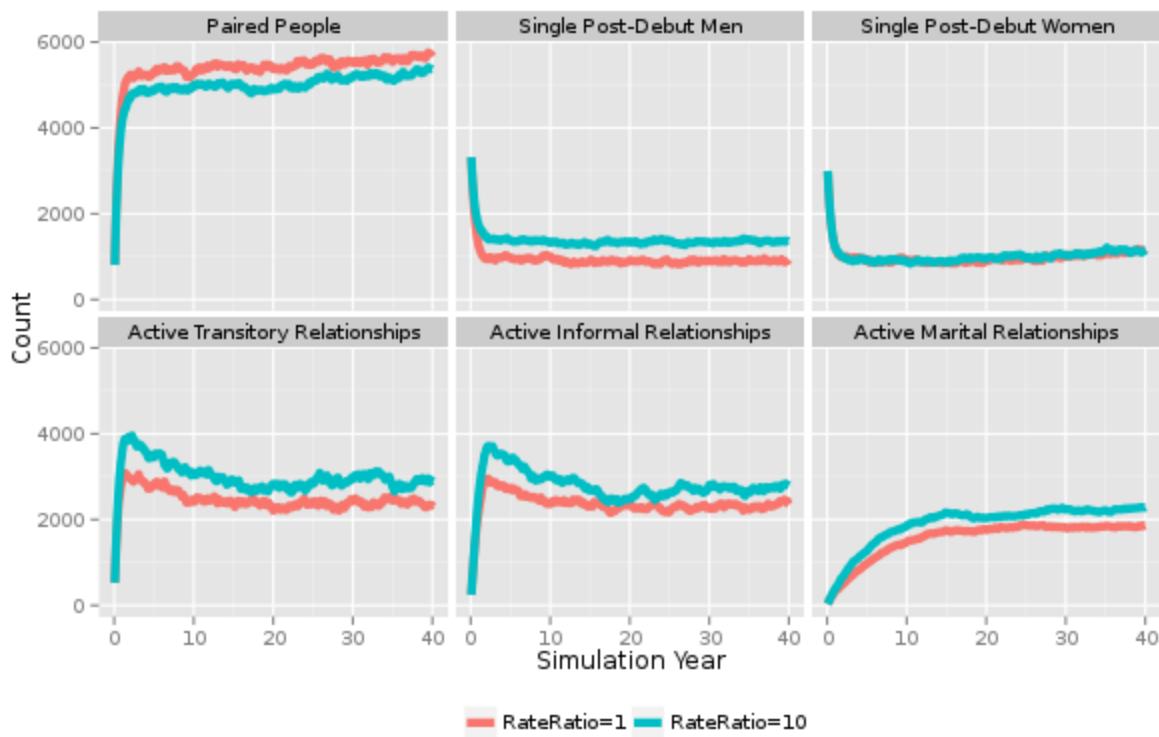
Although the configuration parameters allow high levels of concurrency, the actual levels of concurrency at any given time are considerably lower. That is because the extra-relational flags only create the potential for individuals to add relationships, but depending on the formation rate and mixing pattern, actual formation may not occur. This is similar to the way that sexual debut occurs earlier than actual formation of the first relationship.

The model offers a way to control the proportion of “potential concurrency” that is realized. The rate of formation of relationships can be modified specifically for individuals who received a concurrency-enabling flag. These parameters, separately configurable by gender, are:

```
"Extra_Relational_Rate_Ratio_Female": 1,  
"Extra_Relational_Rate_Ratio_Male": 1,
```

Individuals who have a concurrency flag for a given relationship type will seek relationships of that type at an increased rate, whereas others will seek relationships of that type at a decreased rate. The rates are adjusted to that ratio of the increased to decreased rates is equal to the configured rate ratio parameter, by gender, and so that the expected number of relationships formed on each time step is unchanged from a rate ratio of 1.

To demonstrate the rate ratio parameter, the figure below shows several network statistics from the InsetChart.json output file comparing rate ratios of 1 and 10. From the figure, you can see that the RateRatio=10 scenario results in fewer paired people, more single post-debut men, and more active relationships overall.

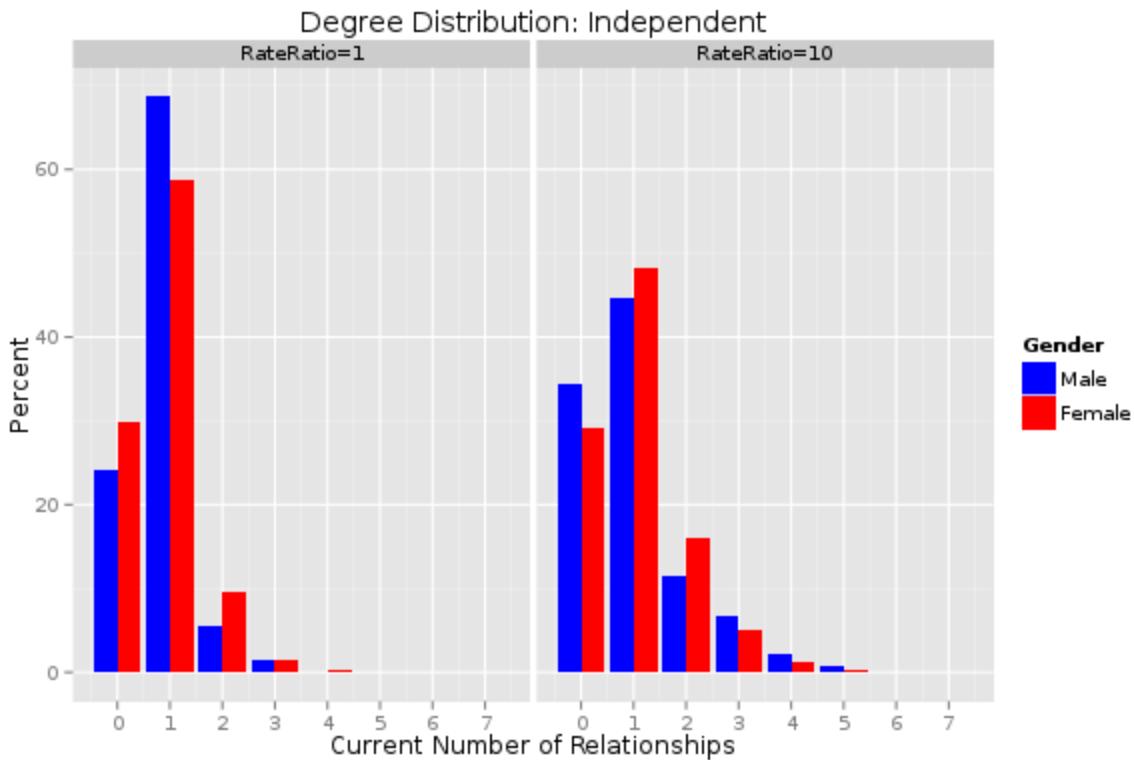


The total number of paired people decreases because relationships are concentrated in the subset of individuals who have the extra-relational flags. The number of single post-debut individuals, and men in particular due to the configuration of this scenario, increases for similar reasons.

The mathematics of the model ensure that a given number of relationship-eligible individuals will always form the same number of relationships, regardless of the rate ratio. Yet, in the bottom row of the figure above, you can see that more transitory, informal, and marital relationships increased were formed when the rate ratio was raised from 1 to 10. This is because raising the rate ratio effectively increased the number of relationship-eligible individuals.

Why did this happen? Consider an individual who has only the extra-transitory flag. With the rate ratio parameter set to a large value like 10, the individual will have an increased tendency to form transitory relationships, and a decreased tendency to form informal and marital relationships. Thus, there is an elevated probability that the individual will enter a transitory-type relationship. This elevated probability in turn increases the expected number of relationships that the individual can enter before becoming effectively blocked from entering additional relationships by an informal or marital relationship.

Another way to see the effect of the rate ratio parameter is to look at distribution of the number of relationships that individuals have at a specific point in time. This statistic is also known as the degree distribution and the point prevalence of concurrency. The following figure compares the degree distribution for rate ratio values of 1 (left) and 10 (right).



Setting rate ratio to 10 leads to fewer individuals participating in exactly one relationship, and more individuals with no relationships or with multiple relationships.

To give the user control over the speed of adding concurrent relationships, the minimum number of days between adding subsequent relationships is a configurable parameter. This parameter causes any subsequent additions of relationships to be spaced apart by at least a specified number of days. Dissolution of the relationship releases any constraint on time until addition of a new one. The parameter allows users to configure risk behavior involving a high but lagged propensity to add new partners.

Parameter	Value	Range	Units	Description
Min_Days_Between_Adding_Relationships	0	[0,365]	Days	Minimum number of days between considering additional relationships, for those that are eligible for concurrency based on extra-relational flags and maximums.

1-f. Concurrency: Correlated Behavior across Relationship Types

In the previous scenario, the maximum allowable number of concurrent partners in some relationship types were set to high values. Yet, even after setting the rate ratio parameter to 10, few individuals achieve their maximum simultaneous allowable number of relationships.

This is due to the fact that the concurrency flags were handed out independently by relationship type. This makes it unlikely for an individual to independently receive all three extra-relational flags. Without a flag for a particular type of relationship, joining that relationship prohibits the addition of any further relationships (of any type).

To greater concentrate risk in a subset of the population, EMOD offers a way to distribute extra-relational flags in a correlated way. To enable correlated concurrency, set the parameter `Extra_Relational_Flag_Type` to "Correlated" in the config.json file.

```
"Extra_Relational_Flag_Type": "Correlated",
```

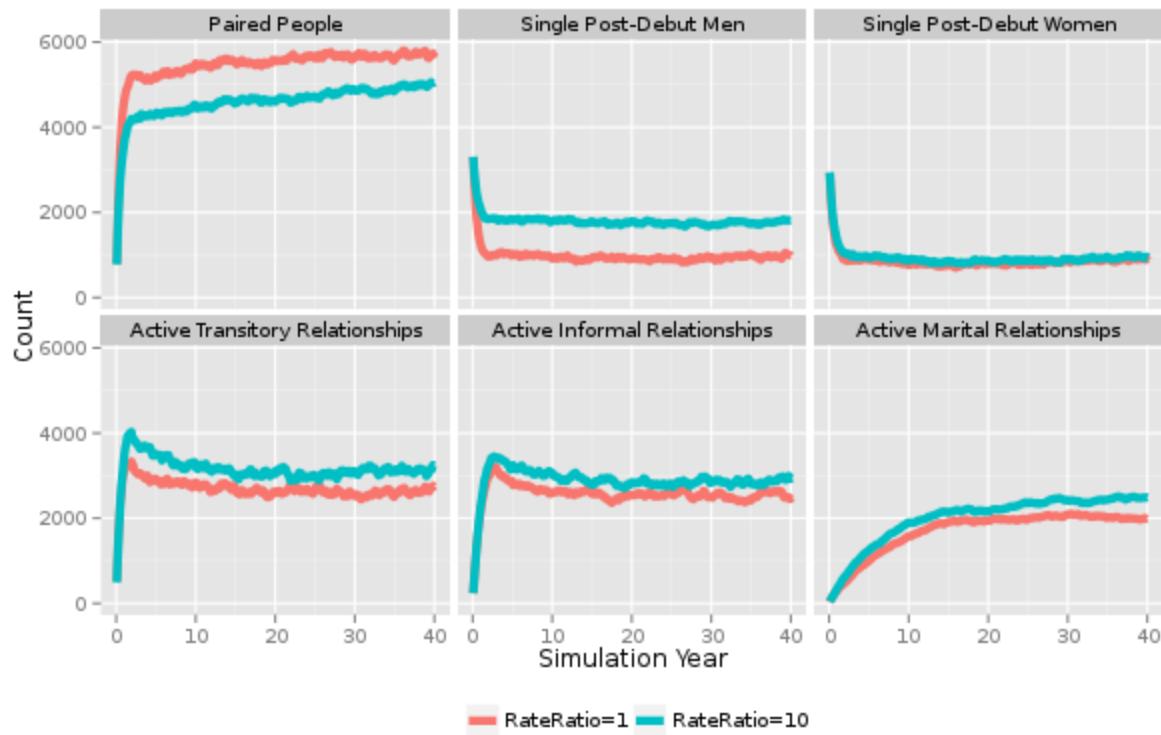
When correlated extra-relational flags are enabled, the extra-transitory flag is handed out randomly, as before, but the extra-informal flag is only provided to those who possess an extra-transitory flag, and the extra-marital flag is only provided to those who possess an extra-informal flag.

Because extra-transitory flags are given out in the same manner regardless of correlation, the associated parameter name does not change. However, the parameter names associated with correlated extra-informal and extra-marital probability are different:

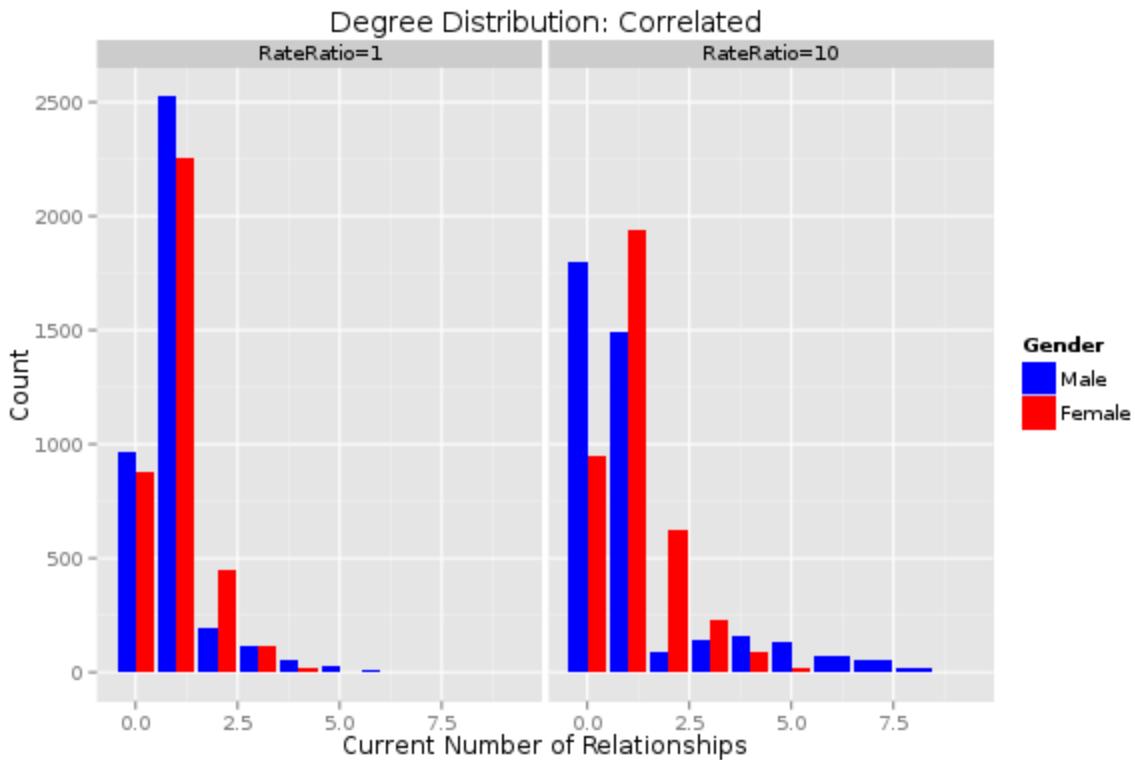
```
"Prob_Extra_Informal_Given_Extra_Transitory_Male": 1,  
"Prob_Extra_Informal_Given_Extra_Transitory_Female": 0.5,  
"Prob_Extra_Marital_Given_Extra_Informal_Male": 0.5,  
"Prob_Extra_Marital_Given_Extra_Informal_Female": 0.25
```

These parameter values result in the same number of individuals possessing the flags as in the independent [Scenario 1e](#), but here the flags are concentrated in a smaller number of individuals.

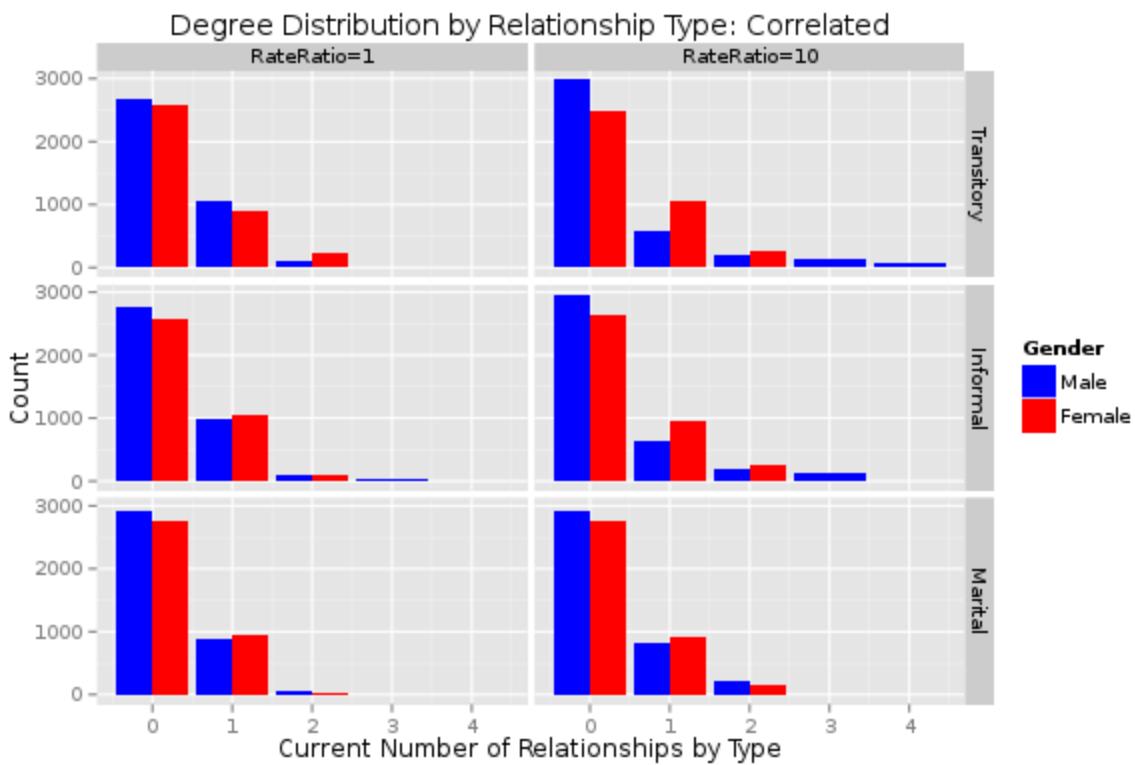
Network statistics from the inset chart have a similar trend to the independent method, but the impact of increasing the rate ratio parameter from 1 to 10 is magnified, as shown in the figure below.



The next figure shows the degree distribution by gender, as before. When the rate ratio is increased to 10, the shift away from monogamous partnerships is amplified compared to the independent method because individual possessing multiple concurrency flags are less likely to get blocked by a relationship for which they are unwilling to seek additional relationships.



Finally, the last figure below shows how the degree distribution varies by gender, relationship type, and rate ratio. For the RateRatio=10 configuration, the men who have 2-4 transitory partnerships are also likely to have multiple informal and marital partnerships, due to the correlated distribution of extra-relational flags.



1-g. Choice of Sex Partner Age by Relationship Type

By now, you have learned about the pair formation algorithm (PFA) for configuring mixing patterns and about the three relationship types with their recommended (but fully configurable) age ranges and durations. In the following example, this scenario demonstrate how to configure more complex mixing patterns by relationship type using published data.

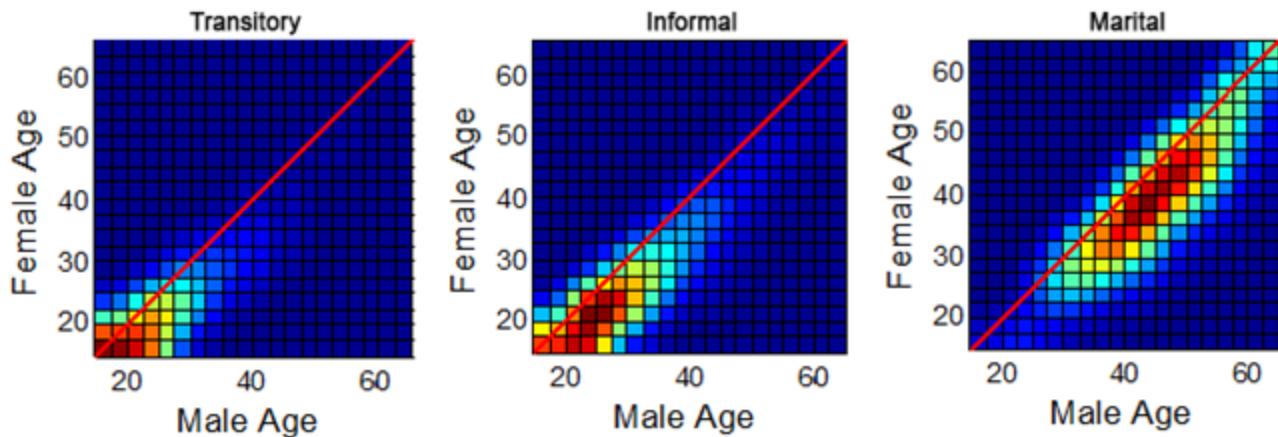
The mixing patterns demonstrated below were published by Ott et al.¹ based on relationship questionnaires conducted at the Africa Centre for Health and Population Studies in Kwazulu-Natal, South Africa. The researchers asked individuals to identify up to three current partners, and recorded both the interviewee's age and the partners' ages.

To create the demographics overlay file included with this scenario (PFA_overlay.json), the published mixing patterns were distributed over 2.5-year age bins (as the published summary data was in 5-year bins), smoothed using a Gaussian kernel, and shifted back in age by half of the average relationship duration to reflect the average age at formation, rather than at reporting of an existing relationship.

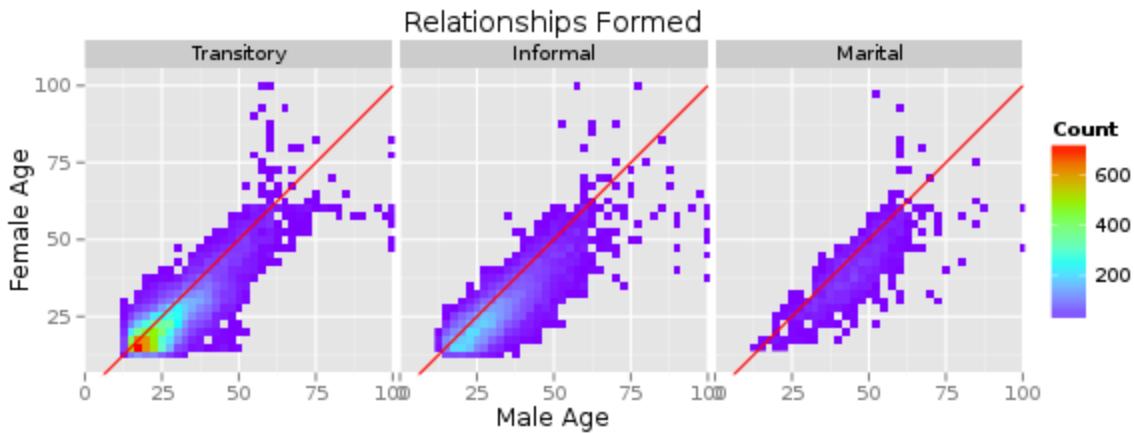
The resulting mixing patterns by relationship type are shown below. Transitory relationships (referred to in Ott et al.'s publication as 'Casual Partners') tend to include younger individuals who are closer in age.

¹Ott MQ, Bärnighausen T, Tanser F, Lurie MN, Newell M-L. Age-gaps in sexual partnerships: seeing beyond "sugar daddies." AIDS. 2011 Mar;25(6):861-3.

Marital relationships (referred to as ‘Husbands/Wives’) tend to include older individuals with men approximately five years older than women. Informal partnerships (referred to as ‘Current Partners’) lie between transitory and marital in these characteristics.



The model forms relationships with these mixing patterns using a method that has been published elsewhere¹. The resulting age patterns of HIV transmission have been published also², and have been generated below from the included simulation files.



1-h. Risk Groups

In addition to mixing patterns by age, EMOD also allows the user to specify partner preference by any [IndividualProperty](#), which can be used to represent factors such as HIV risk, geography, socioeconomic group, accessibility to health care, and quality of health care.

¹Klein DJ. Relationship formation and flow control algorithms for generating age-structured networks in HIV modeling. 2012 IEEE 51st Annual Conference on Decision and Control (CDC). 2012. p. 1041-6.

²Bershteyn A, Klein DJ, Eckhoff PA. Age-dependent partnering and the HIV transmission chain: a microsimulation analysis. J R Soc Interface. 2013 Nov 6;10(88):20130613.

This scenario will demonstrate how to apply this feature to configure mixing between HIV risk groups. Recall that risk groups are an [Individual Property](#) with a demographic distribution that is set in the demographics file. In this example, the demographics file RSA_Demographics_With_RiskGroup.json is configured to assign 20% of the population to the HIGH risk group, and 80% to the LOW risk group, as follows:

```
"IndividualProperties": [
  {
    "Property": "Risk",
    "Values": [ "LOW", "HIGH" ],
    "Initial_Distribution": [ 0.8, 0.2 ],
    ...
  }
]
```

An overlay file for the demographics file is provided, called PFA_overlay_risk_assortivity.json. This file adds to the age-mixing pattern from the previous example by additionally configuring preference by risk group. As with age mixing, risk group preference is independently configurable for each relationship type. In this example, transitory relationships are configured so that individuals prefer partners of the opposite risk group 80% of the time; informal relationships are formed with equal preference for either risk group, and marital relationships are formed with an 80% preference for the same risk group (high with high, low with low):

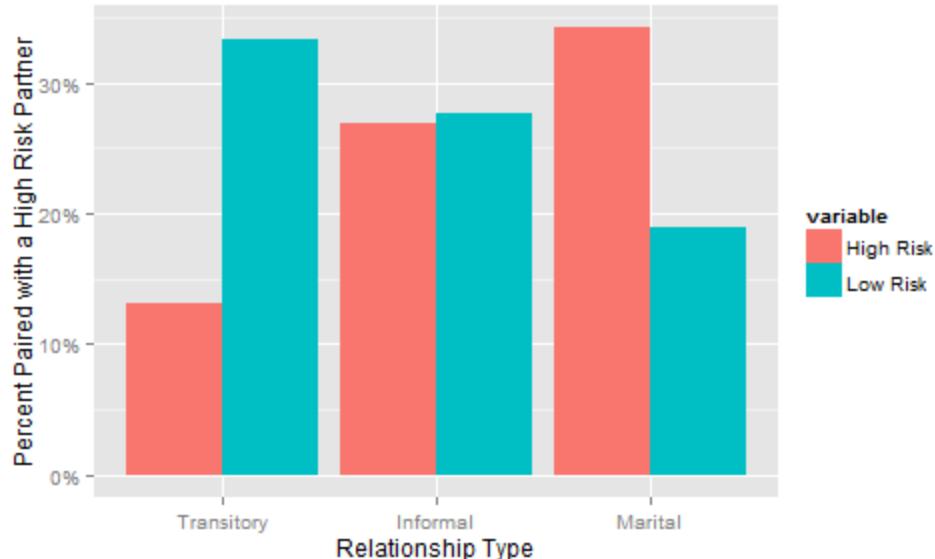
```
...
"Society" : {
  "Pair_Formation_Parameters_TRANSITORY" :
  {
    "Assortivity" :
    {
      "Group" : "INDIVIDUAL_PROPERTY",
      "Property_Name" : "Risk",
      "Axes" : [ "LOW", "HIGH" ],
      "Weighting_Matrix_RowMale_ColumnFemale" :
      [
        [
          [ 0.2, 0.8 ],
          [ 0.8, 0.2 ]
        ]
      ]
    }
  },
  "Pair_Formation_Parameters_INFORMAL" :
  {
    ...
  }
}
```

```

        [ 0.5, 0.5 ],
        [ 0.5, 0.5 ]
    ]
}
},
"Pair_Formation_Parameters_MARITAL" :
{
...
{
...
[
    [ 0.8, 0.2 ],
    [ 0.2, 0.8 ]
]
}
}
}
...

```

To illustrate the preferential pairing by risk group, this plot shows the proportion of individuals whose partner is in the high-risk group, stratified by the individual's risk group and the relationship type. When there is no preference by risk group, it is expected that high-risk and low-risk individuals would be equally likely to choose high-risk partners. As expected, this is the case for the informal relationships, where the preference has been configured as 50-50, or neutral in terms of risk group preference.



The plot shows that for informal relationships, both high-risk and low-risk individuals formed relationships with high-risk partners 27% of the time. Recall that, in the demographics file, the population

was configured to consist of 20% high-risk individuals. So why was the percentage of relationships with high-risk individuals greater than 20%?

The reason is that, in this example, concurrency is configured to be higher for high-risk individuals than for low-risk individuals. Recall that the parameters for risk behavior, such as concurrency, can be set independently by risk group using the `STI_Network_Params_By_Property` section of `config.json`. In this example, they are set as follows:

```
"STI_Network_Params_By_Property": {
    "Individual_Property_Name": "Risk",

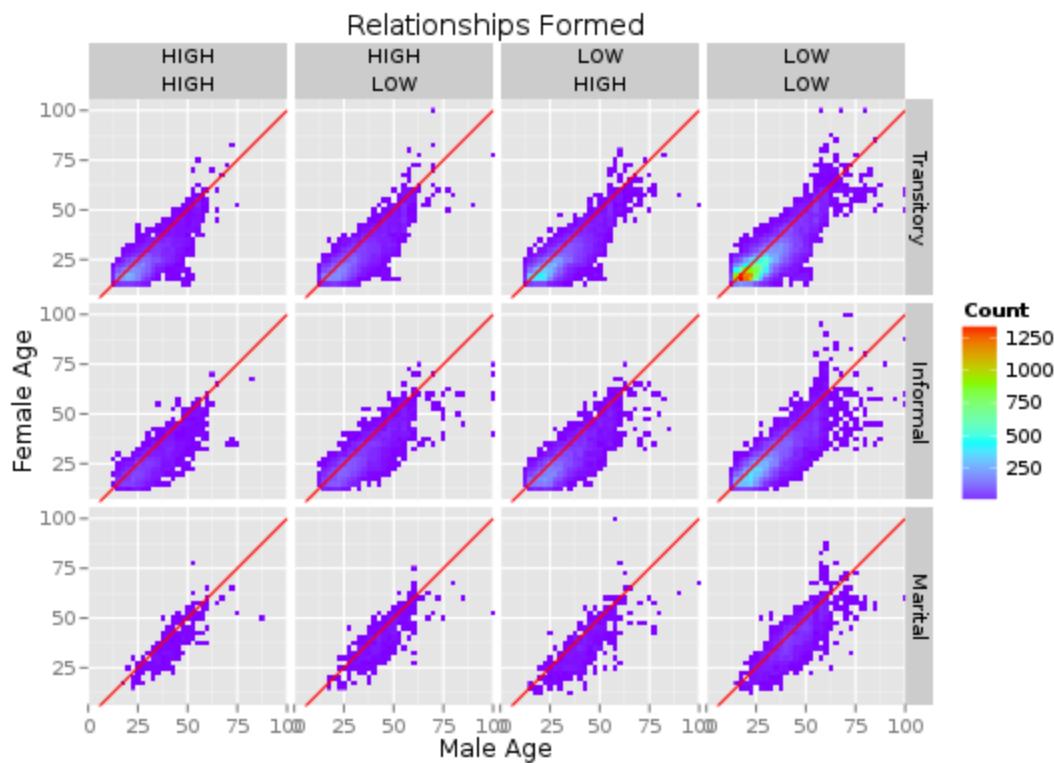
    "HIGH": (
        "Extra_Relational_Flag_Type": "Correlated",
        ...
        "Max_Simultaneous_Informal_Relationships_Males": 3,
        ...
        "Prob_Extra_Transitory_Relationship_Female": 0.8,
        "Prob_Extra_Transitory_Relationship_Male": 0.2
    },

    "LOW": {
        "Extra_Relational_Flag_Type": "Independent",
        ...
        "Max_Simultaneous_Informal_Relationships_Males": 2,
        ...
        "Prob_Extra_Transitory_Relationship_Female": 0.15,
        "Prob_Extra_Transitory_Relationship_Male": 0.25
    }
},
```

Thus, the number of relationships involving high-risk individuals is out of proportion to their population. More generally, the proportion of relationships formed will not always match the proportion of preference for the partner type, because the "supply" of a given type will not always match the "demand." This is especially true when preferences are imbalanced (e.g., if the preference matrix is not symmetric across the diagonal) or if many categories of preferences are specified.

When both age-based and risk/property-based preferences are provided (as in this example), the age-based preferences override property-based preferences. In other words, the model first groups individuals by age to create the desired age-mixing patterns, then stratifies the age categories by risk to attempt to form the desired risk-mixing patterns. If a desired risk category is empty, then a different individual of the desired age is substituted.

The figure below shows the mixing patterns from this example stratified by all of the relevant categories: age, gender, risk group, and relationship type.



In this example, belonging to a risk group influences only risk behavior (concurrency) and partner preference. To create correlations between partner preference and other factors, such as access to health care, you can use different [IndividualProperty](#) to assign partner preference. Some of the Individual Property names used in EMOD include Risk, Geographic, Accessibility, Place, and QualityOfCare.

In addition, sero-sorting for HIV infection status can be configured. The preference for HIV status can be based on the individual's actual infection status, based on whether the individual has ever tested HIV positive, (i.e., their status lagged by the time since their last test), or by the individual's self-perception of status (positive, negative, or unknown) which is initialized as unknown and can be updated upon HIV testing with a probability that is configurable for each testing intervention. (Configuration of HIV testing and knowledge of status is discussed in Scenario 5.)

Lastly, in HIV_SIM, sero-sorting can be performed on the basis of STI co-infections such as HSV-2. This is not to be confused with sero-sorting based on STI status in a generic STI_SIM. The table below shows the groups that can be used to configure partner preferences, according to the type of simulation being run.

NO_GROUP	STI_SIM	Use only age mixing; no other preferences are applied.
STI_INFECTION_STATUS	STI_SIM only	For STI_SIM only, matching is based on whether the individual is infected by the STI.

NO_GROUP	STI_SIM	Use only age mixing; no other preferences are applied.
INDIVIDUAL_PROPERTY	STI_SIM or HIV_SIM	Preference based on Individual Properties. Examples include Risk, Geographic, Accessibility, Place, and QualityOfCare.
STI_COINFECTION_STATUS	STI_SIM or HIV_SIM	Use the STI co-infection flag to determine matching.
HIV_INFECTED_STATUS	HIV_SIM only	Matching is based on IsInfected() status - is their body infected
HIV_TESTED_POSITIVE_STATUS	HIV_SIM only	Matching is based on the EverTestedHIVPositive() - once they tested positive this always returns true
HIV_RECEIVED_RESULTS_STATUS	HIV_SIM only	Matching is based on the last test results received - Have to be tested and results received, can be unknown

1-i. Coital Frequency and Coital Dilution with Multiple Partnerships

The frequency of coital acts, in units of acts per day, is independently configurable for each relationship type. For example, setting the parameters to 0.33 will cause all relationships to be consummated once per three days on average.

```
"Coital_Act_Rate_Informal": 0.33,
"Coital_Act_Rate_Marital": 0.33,
"Coital_Act_Rate_Transitory": 0.33,
```

The timing of coital acts is random, (i.e., the time until the next coital act is exponentially distributed with the configured rate), so that it is not guaranteed that exactly 3 days will elapse between coital acts. When multiple coital acts occur in the same timestep, as determined by a draw from a Poisson distribution, they are accounted for using Bernoulli statistics with the associated transmission probability for each of the individual coital acts. Transmission is described in detail in [HIV Tutorial 3 Transmission](#).

When an individual participates in multiple partnerships simultaneously, the model can incorporate coital dilution, i.e., a change in the frequency of coital acts as a result of having multiple partnerships. This capability is enabled by setting the config.json parameter `Enable_Coital_Dilution` to 1.

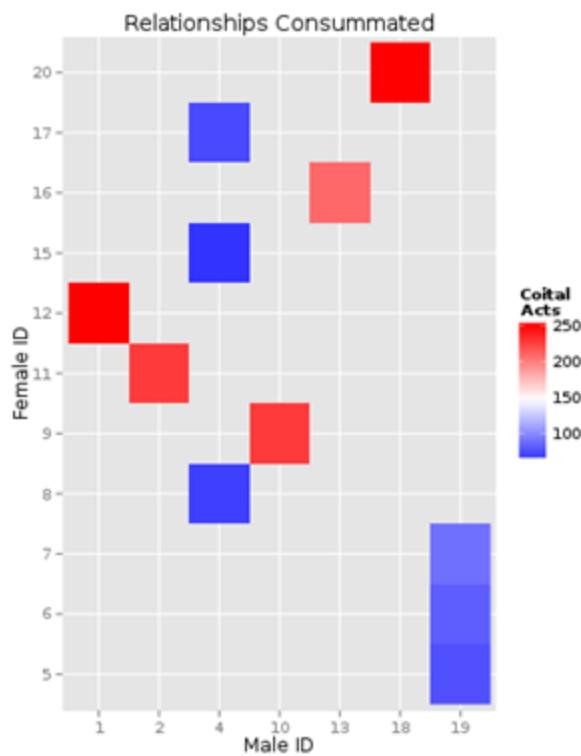
The reduction in coital dilution is independently configurable for individuals with two, three, or more than three partners. When the two participants in a relationship have different numbers of partners, then the reduction factor from the person with more partners is applied.

```
"Enable_Coital_Dilution": 1,
"Coital_Dilution_Factor_2_Partners": 0.5,
"Coital_Dilution_Factor_3_Partners": 0.33,
"Coital_Dilution_Factor_4_Plus_Partners": 0.25,
```

Coital dilution can be observed by recording each coital act to the output file [RelationshipsConsummated.csv](#). It is not recommended to produce this file when modeling large population sizes, because the file size can become very large. To produce the file, set the config.json parameter Report_Coital_Acts to 1:

```
"Report_Coital_Acts": 1
```

The figure below shows the number of relationships consummated between different partners. Relationships in which both participants have only one partner (red) have more coital acts than those in which one or both partners have multiple relationships (blue).



HIV Tutorial 2: HIV-Specific Biology

The HIV model adds within-host HIV biology to the transmission modality of the STI person-to-person contact network. The purpose of modeling within-host HIV biology is to produce transmission rates, mortality rates, and evolution of biomarkers such as CD4 count specific to HIV-infected individuals according to factors such as their age, disease state, co-infections, use of antiretroviral therapy, and other factors.

This scenario illustrates HIV-specific mortality and evolution of CD4 counts in untreated individuals and in individuals receiving antiretroviral therapy.

To focus on disease progression within an individual host, transmission is disabled in these scenarios.

2-a. Setting Up to Study Disease Progression (Baseline_Disease_Progression)

To illustrate the natural history of HIV progression without treatment, infections are initialized in specific age groups of a population so you can observe CD4 counts and mortality over time.

To start with a simple example, a cohort of 10,000 newborn individuals with no additional births, non-disease deaths, or transmission of disease is set up. Then the individuals are infected at different ages using the [OutbreakIndividual](#) intervention.

Here is how you can set up a simple cohort in the simulation configuration file (config.json):

Parameter	Value	Description
Simulation_Type	HIV_SIM	Sets the simulation type. This is a required parameter. It determines which disease biology and transmission modality to apply, and which parameter categories are valid for the simulation.
Base_Population_Scale_Factor	0.01	Scales the initial population size. When this parameter is set to 1 with the included demographics file, the population size is 10,000.
Base_Year	2000	This sets the starting year of the simulation, which can be between 1800 and 2100.
Simulation_Duration	37000	Sets the duration of the simulation in days. We'll have it last just over 100 years.

Parameter	Value	Description
Demographics_Filename	newborn_cohort_demographics.json	This parameter loads a simple demographics file similar to the one introduced in the generic SIR model from the first release of EMOD. For this scenario, the demographics file only provides the initial population size and specifies that all individuals should be initialized at age zero.
Age_Initialization_Distribution_Type	DISTRIBUTION_SIMPLE	Setting the Age_Initialization_Distribution_Type to DISTRIBUTION_SIMPLE allows you to choose from EMOD's built-in simple age distributions. In the demographics file, you can now choose AgeDistributionFlag = 0 to initialize everyone at the same age (which is set, in days, by AgeDistribution1), or you can choose AgeDistributionFlag = 1 to have initial ages uniformly distributed between two bounds (set, in days, by AgeDistribution1 and AgeDistribution2).
Enable_Birth	0	Since this simulation is modeling a cohort, new births are disabled.
Death_Rate_Dependence	NONDISEASE_MORTALITY_OFF	Turns off non-disease mortality.
Base_Infectivity	0	Sets the baseline transmission rate (before multiplication by factors such as co-infection, circumcision, etc.)

Setting the parameter `Base_Infectivity` is all that is needed to disable transmission because `Base_Infectivity` multiplies all factors affecting sexual transmission. Mother-to-child transmission (MTCT) is handled separately, but because births are disabled for the purpose of demonstration, there is no chance for MTCT to occur in this simplified example.

The campaign.json file controls when the cohort becomes infected using the OutbreakIndividual intervention. For example, suppose you want half of the individuals to become infected at age 20, and the remaining half to become infected at age 30. Because everyone was born in the year 2000, a simple way to do this is to control the year when the infections are initialized, using the parameter "Start_Year", and the proportion of the population to be infected, using the parameter Demographic_Coverage. In the included campaign.json file, half of individuals are infected in the year 2020, like this:

```

"Start_Year": 2020,
...
"Event_Coordinator_Config":
{
    ...
    "Target_Demographic": "Everyone",
    "Demographic_Coverage": 0.5,
    ...
}

```

The remaining half of the cohort is infected in the year 2030 by applying a second outbreak with a demographic coverage of 1.0. Because individuals cannot become doubly infected, this will result in all remaining uninfected individuals becoming infected.

```

"Start_Year": 2030,
...
"Event_Coordinator_Config":
{
    ...
    "Target_Demographic": "Everyone",
    "Demographic_Coverage": 1.0,
    ...
}

```

Of course, it's not always the case that all individuals in the model are the same age. It's possible to target an intervention to a specific age and gender by changing "Target_Demographic": "Everyone" to "Target_Demographic": "ExplicitAgeRangesAndGender". For this particular example, if you to create to target the age range of 19 to 21 (in years), the effect would be the same as the previous example, since everyone is 20 years old in the year 2020:

```

"Start_Year": 2020,
...
"Event_Coordinator_Config":
{
    "Target_Demographic": "ExplicitAgeRangesAndGender",
    "Target_Age_Min": 19,
    "Target_Age_Max": 21,
    "Target_Gender": "All",
    "Demographic_Coverage": 0.5,
    ...
}

```

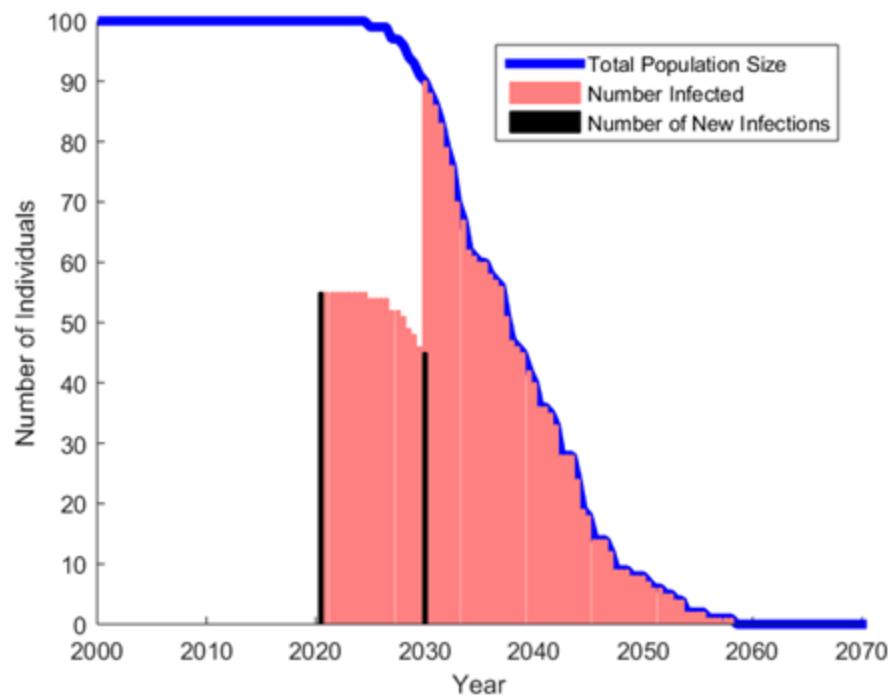
Yet another way to target half of the population in this example is to target 100% of only one gender with the 2020 infections, and to target everyone or the opposite gender with the 2030 infections:

```

"Start_Year": 2020,
...
"Event_Coordinator_Config":
{
    "Target_Demographic": "ExplicitAgeRangesAndGender",
    "Target_Age_Min": 19,
    "Target_Age_Max": 21,
    "Target_Gender": "Male",
    "Demographic_Coverage": 1.0,
    ...
}

```

All of these should produce similar results, with about fifty individuals becoming infected in 2020 and the other fifty in 2030. To see this in Matlab, you may use the included script Scenario2a.m and obtain the following:



Although the model was configured to run for 100 years, the cohort has died out after 65 years.

Congratulations! You've just learned how to set up a cohort in the model! You are now ready to look at the age-dependence of survival in the model, [2-b. Survival Time for Children](#).

2-b. Survival Time for Children

In the model, children can become infected with HIV via mother-to-child vertical transmission if they are born to HIV-infected mothers. The parameters to enable mother-to-child transmission are described in

[Scenario 3-g](#), and interventions to prevent mother-to-child transmission are described in [Scenario 4-2-1c](#). However, for the sake of demonstrating HIV progression in children, [OutbreakIndividual](#) creates infections in infants instead of using mother-to-child transmission.

Without treatment, progression of HIV disease in infants is generally more rapid than in adults, and can be further sub-divided into rapid progressors and slower progressors following a model published by Ferrand et al.¹:

$$S(t) = \alpha e^{-\beta t} + (1 - \alpha)2^{-(\frac{t}{\mu})^s}$$

The proportion of children who are rapid progressors, α , is configured by the parameter `HIV_Child_Survival_Rapid_Progressor_Fraction`. Rapid progressors have an exponentially distributed survival time with decay rate β configured by the parameter `HIV_Child_Survival_Rapid_Progressor_Rate`. Slower progressors have a Weibull-distributed survival time with shape parameter s configured by `HIV_Child_Survival_Slow_Progressor_Shape` and scale parameter μ configured by `HIV_Child_Survival_Slow_Progressor_Scale`. The Weibull distribution is a generalized form of the exponential distribution that is specified by two parameters, one for shape, the other for scale. [Scenario 1-b](#) described this distribution in detail and provides an Excel tool for understanding how the parameters influence the shape of the distribution.

The Weibull survival function is applied to all individuals younger than the threshold to be considered a child, which is also configurable using the parameter `HIV_Age_Max_for_Child_Survival_Function`.

Parameter	Value	Description
<code>HIV_Child_Survival_Rapid_Progressor_Fraction</code>	0.57	The proportion of HIV-infected children who are rapid HIV progressors.
<code>HIV_Child_Survival_Rapid_Progressor_Rate</code>	1.52	The exponential decay rate, in years, describing the distribution of HIV survival for children who are rapid progressors.

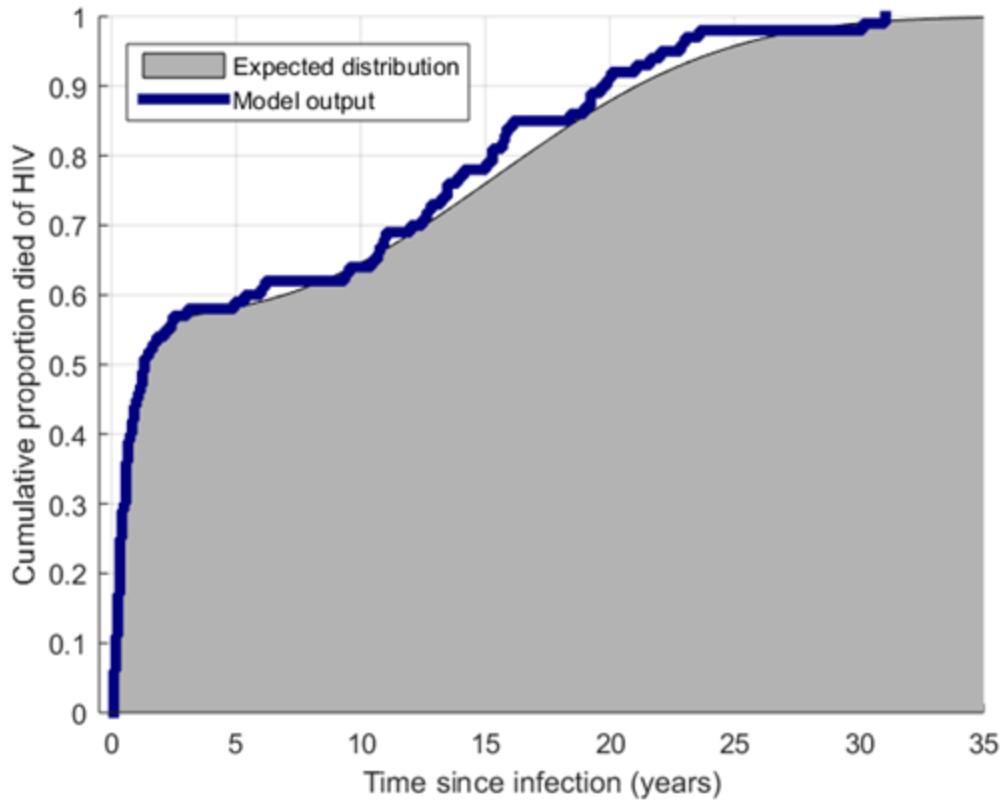
¹Ferrand RA, Corbett EL, Wood R, et al. AIDS among older children and adolescents in Southern Africa: projecting the time course and magnitude of the epidemic. AIDS 2009; 23:2039-2046.

Parameter	Value	Description
HIV_Child_Survival_Slow_Progressors_Shape	2.7	The Weibull shape parameter describing the distribution of HIV survival for children who are slower progressors.
HIV_Child_Survival_Slow_Progressors_Scale	16.0	The Weibull scale parameter describing the distribution of HIV survival for children who are slower progressors.
HIV_Age_Max_for_Child_Survival_Function	15	Individuals infected at ages younger than HIV_Age_Max_for_Child_Survival_Function use the child survival function. Older individuals use the adult age-dependent survival function. When this parameter is set above zero and below the age of sexual debut, model results are not sensitive to this parameter value because there is no mechanism for children to become infected between infancy and sexual debut.

Compare the expected distribution of child survival to the actual survival times in our simulated cohort. The output file [HIVMortality.csv](#) contains a line for every HIV-associated mortality event in the model, including the number of years from infection to death. This output file is enabled by setting the parameter Report_HIV_Mortality to 1.

Parameter	Value	Description
Report_HIV_Mortality	1	Set to 1 to create the output file HIVMortality.csv, or 0 to suppress this output file.

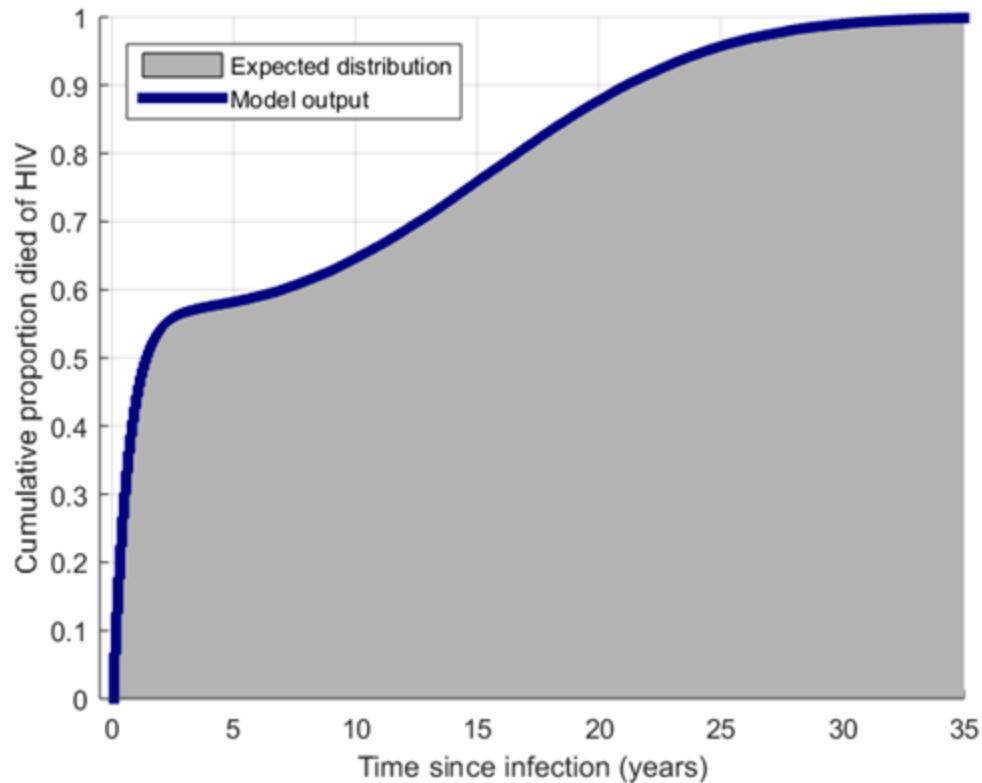
After the simulation runs (a few seconds), you can open the output file HIVMortality.csv and create a plot of the Years_since_infection column (using your preferred software, such as Excel, R, Python, Matlab, etc.). Here's how the result compares to the expected distribution of child mortality when the run-Emod.cmd and included plotting scripts are run:



The histogram is noisy because only 100 individuals are in the simulation. You can reduce the noise by increasing the population size from 100 individuals to something larger such as 100,000 individuals, by increasing the `Base_Population_Scale_Factor` from 0.01 to 10. With this larger population size, on a 2.6 GHz PC with 16 GB RAM, the simulation will take approximately one minute to run.

Parameter	Value	Description
<code>Base_Population_Scale_Factor</code>	10	Scales the initial population size. When this parameter is set to 1 with the included demographics file, the population size is 10,000.

The survival distribution can now be compared to the expected distribution with less noise:



Note that the HIV simulation type does not support Monte Carlo weighting of individuals in the population, so every individual is explicitly simulated in the model.



Do not modify the parameters `Individual_Sampling_Type` or `Base_Individual_Sample_Rate` in the tutorials. Monte Carlo weighting of individuals is not supported for the STI or HIV simulation types.

Congratulations! You've learned how to analyze and modify pediatric AIDS survival in the model.

2-c. Survival Time for Adults

Survival time with untreated HIV infection depends on the age of the individual at the time of infection. At infection, survival time is drawn from a Weibull distribution with shape parameter κ and scale parameter λ . The scale parameter λ is allowed to vary linearly with age as follows:

$$\lambda = \text{HIV_Adult_Survival_Scale_Parameter_Intercept} + \text{HIV_Adult_Survival_Scale_Parameter_Slope} * \text{Age (in years)}.$$

Because survival time with HIV becomes shorter with increasing age, `HIV_Adult_Survival_Scale_Parameter_Slope` should be set to a negative number.

Although the scale parameter for survival time declines with age, it cannot become negative. To avoid negative survival times at older ages, an additional parameter, `HIV_Age_Max_for_Adult_Age`

`Dependent_Survival`, determines the age beyond which HIV survival is no longer affected by further aging.



If you change the age-dependence of HIV survival using the `HIV_Adult_Survival_*` parameters, and have set `HIV_Adult_Survival_Scale_Parameter_Slope` to a negative number, make sure that the value for `HIV_Age_Max_for_Adult_Age_Dependent_Survival` is less than or equal to the ratio between `HIV_Adult_Survival_Scale_Parameter_Intercept` and the absolute value of `HIV_Adult_Survival_Scale_Parameter_Slope`.

The simulation parameters below have been set using a trend in age-dependence of survival from an analysis by Todd et al.¹, for which data in older individuals were very sparse. The chosen value of `HIV_Adult_Survival_Scale_Parameter_Slope` (-0.2717) would have caused survival time to become negative at age 77, so the `HIV_Age_Max_for_Adult_Age_Dependent_Survival` must be set to an age less than 77.

Parameter	Value	Description
<code>HIV_Adult_Survival_Scale_Parameter_Slope</code>	-0.2717	<p>At the time of infection, survival time is drawn from a Weibull distribution with a scale parameter that can vary linearly with age as follows:</p> $\text{HIV_Adult_Survival_Scale_Parameter_Intercept} + \text{HIV_Adult_Survival_Scale_Parameter_Slope} * \text{Age(in years)}$ <p>Because survival with HIV becomes shorter with increasing age, this parameter is normally set to a negative number.</p>
<code>HIV_Adult_Survival_Scale_Parameter_Intercept</code>	21.182	<p>At the time of infection, survival time is drawn from a Weibull distribution with a scale parameter that can vary linearly with age as follows:</p> $\text{HIV_Adult_Survival_Scale_Parameter_Intercept} + \text{HIV_Adult_Survival_Scale_Parameter_Slope} * \text{Age(in years)}$. This parameter sets the y-intercept of the line.
<code>HIV_Adult_Survival_Shape_Parameter</code>	2	<p>At the time of infection, survival time is drawn from a Weibull distribution with this scale parameter.</p>

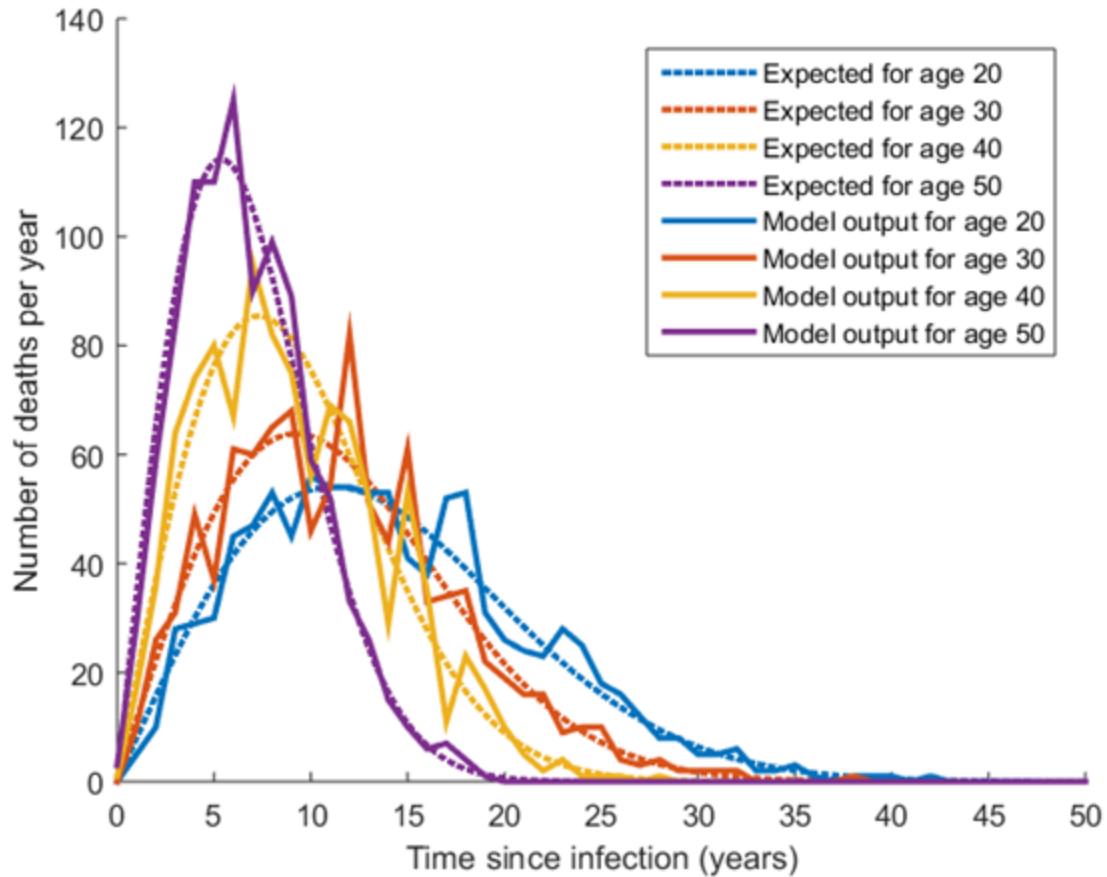
¹Todd J, Glynn JR, Marston M, et al. Time from HIV seroconversion to death: a collaborative analysis of eight studies in six low and middle-income countries before highly active antiretroviral therapy. AIDS 2007; 21:S55-S63
10.1097/01.aids.0000299411.75269.e8.

Parameter	Value	Description
HIV_Age_Max_for_Adult_Age_Dependent_Survival	70	Extrapolation of this linear decline to high values of age can lead to negative values of λ , which are not valid. To avoid negative λ values, a maximum age is set using the parameter HIV_Age_Max_for_Age_Dependent_Survival. All individuals infected at ages greater than HIV_Age_Max_for_Age_Dependent_Survival use the survival distribution corresponding to the age set by HIV_Age_Max_for_Age_Dependent_Survival. HIV incidence in many scenarios will be relatively low in these age groups, so model results are usually not highly sensitive to this parameter value.

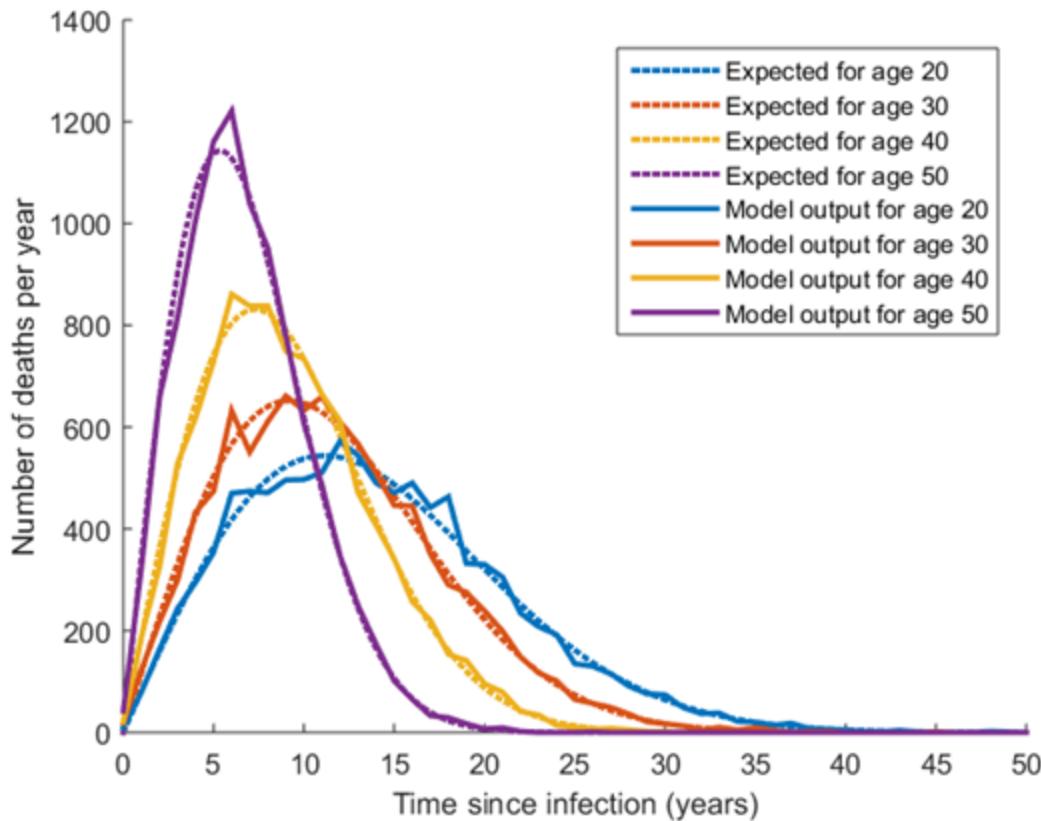
To demonstrate the age-dependence of adult survival, the Outbreak intervention is used to infect approximately equal numbers of adults at different ages.

In the cohort setup described in [Scenario 2-a](#), individuals appear as newborns in the year 2000. Now in Scenario 2c, the included campaign.json file infects a random 1/4th of individuals in the year 2020, 1/4th of the individuals in the year 2030, 1/4th of the individuals in the year 2040, and the remaining 1/4th of individuals in the year 2050. This will infect approximately equal numbers of individuals at ages 20, 30, 40, and 50.

By enabling the output file [HIVMortality.csv](#) (i.e., with Report_HIV_Mortality set to 1), you can observe the distribution of mortality for each age group. This allows us to compare the distribution of survival time by age to the expected Weibull distribution.



For less noise, you can increase the `Base_Population_Scale_Factor` from 0.4 to 4, in order to raise the population size from 4,000 to 40,000 individuals (approximately 10,000 per age group). The simulation runs in less than one minute on a 2.6 GHz laptop computer with 16 GB of RAM.. With the larger population size, it is easier to see that the survival curves match the expected distributions:



Congratulations! You've just learned to analyze and modify age-dependent HIV survival in the model.

2-d. CD4 Count, WHO Stage, and Symptomatic Presentation

This scenario demonstrates how CD4 count and WHO stage progress in the model over the course of an untreated HIV infection, as well as how the model represents the time that a person might be driven to appear for healthcare due to AIDS-related symptoms.

CD4 count is initialized at a value that is selected from a Weibull distribution, and declines with a trend that is linear in square-root of CD4 count to a final value that is also configurable from a Weibull distribution. WHO stage advances from 1 to 4 with Weibull-distributed transition times, and is associated with declining bodyweight, per the WHO clinical staging definitions available here: . As you will see in the next scenario, both CD4 count and WHO stage influence the individual's survival after ART initiation.

To examine CD4 counts and WHO stages over the course of HIV infections, you can log each individual's state at each timestep to the output file [ReportHIVInfection.csv](#).



It is not recommended to enable the ReportHIVInfection.csv output file when running large populations. Because this file logs the state of each individual at each timestep, the output file can be very large.

To create ReportHIVInfection.csv, set the parameter Report_HIV_Infection to 1. Check that the population size of the simulation is not too large. This example uses 100 individuals. It is also possible to restrict the time window over which model outputs are logged to ReportHIVInfection.csv (for example, only logging these states over the course of one year). This example logs the entire 100-year duration of the simulation.

Parameter	Value	Description
Report_HIV_Infection	1	Set to 1 to create the output file ReportHIVInfection.csv, or 0 to suppress this output file. The file causes every infected individual to log information about their disease progression at every timepoint. You can enable this later in the tutorial to demonstrate CD4 progression.
Report_HIV_Infection_Start_Year	2000	The simulation year when infections begin to be logged in the ReportHIVInfection.csv file. This parameter is only required if Report_HIV_Infection is set to 1.
Report_HIV_Infection_Stop_Year	2100	The simulation year when infections cease to be logged in the ReportHIVInfection.csv file. This parameter is only required if Report_HIV_Infection is set to 1.

WHO stage is assumed to also progress in proportion to an individual's assigned survival time, but has added randomness to account for variability in HIV symptoms (and resulting ART eligibility) over a range of CD4 counts. Following a model by Johnson et al¹, progression across WHO stage categories is divided into Weibull-distributed durations over the interval of survival, using the Weibull parameters tabulated below:

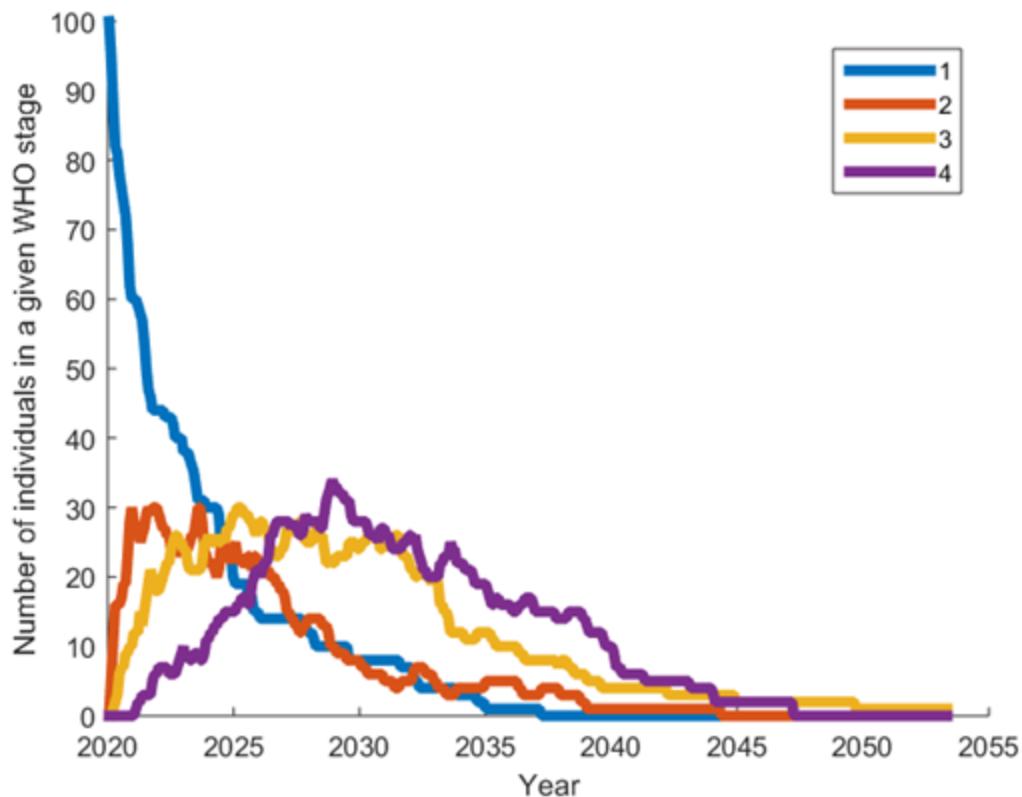
WHO Stage Transition	Shape	Scale
1 to 2	0.9664	0.26596
2 to 3	0.9916	0.19729
3 to 4	0.9356	0.34721

WHO stage is generally considered an integer of 1, 2, 3, or 4. To provide additional information about how close an individual is to advancing to the next WHO stage, the model linearly interpolates between

¹Johnson LF, Dorrington R. Modelling the demographic impact of HIV/AIDS in South Africa and the likely impact of interventions. Demographic Research 2006; 14:541-574.

transitions of WHO stage. For example, if an individual advances from WHO stage 1 to WHO stage 2 over the course of 100 days, the WHO stage on the 90th day will be 1.9. To obtain the expected integer value of WHO stage, the output should be rounded down.

For the current 100-individual example, here is a histogram of the number of individuals in each WHO stage (after rounding down), generated by running runEmod.cmd and the provided plotting script:



Additional information about WHO stage, including its relationship to bodyweight and survival on ART, can be found in [Scenario 2-f](#).

In addition to WHO clinical staging, the model independently draws the time at which an individual may present for care due to AIDS-related symptoms. The time between symptomatic presentation and (untreated) AIDS-related death is assumed to be Weibull-distributed. The two Weibull parameters can be set in config.json. The parameters below would configure a unimodal (hump-shaped) distribution with a mean of 1.5 years (and a median of 1.4 years):

```
"Days_Between_Symptomatic_And_Death_Weibull_Heterogeneity": 0.5,
"Days_Between_Symptomatic_And_Death_Weibull_Scale": 618.341625,
```

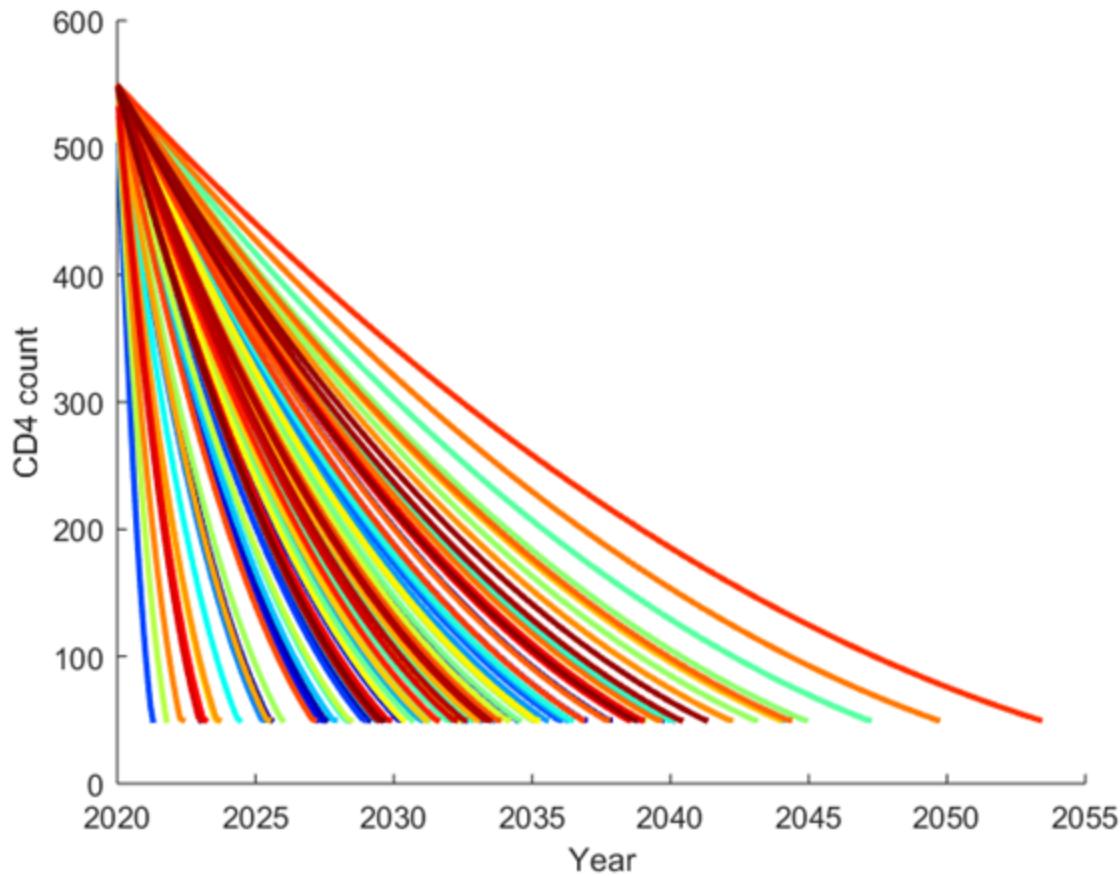
Upon infection or ART discontinuation, the individuals draw from the configured Weibull distribution to determine the time between symptomatic presentation and untreated AIDS-related death. The duration

is subtracted from the AIDS-related death date (described in the previous scenario) to determine the time of symptomatic presentation. Small values lead to symptomatic presentation close to the time of AIDS-related death. Large values lead to symptomatic presentation well before AIDS-related death. If the drawn time is longer than the total survival time, then the total survival time is used (i.e., symptomatic presentation occurs immediately upon infection). The date of symptomatic presentation has no direct impact on clinical progression; however, it can be used to configure health-seeking behavior. For examples of healthcare triggered by symptomatic presentation, see Scenarios [4-1-c](#) and [4-3-5-a](#).

CD4 count during untreated HIV infection is assumed to decline such that the square root of CD4 count varies linearly between a starting and an ending CD4 count. This assumption of sqrt-linear decline does not include the rapid and complex dynamics of CD4 counts during early HIV infection and during late-stage AIDS.

The time required to decline from the starting to the ending CD4 count corresponds to the survival time assigned to that individual, which in turn determines the slope of the CD4 decline. The survival time for untreated infection is used to determine the CD4 slope, even if that person will later initiate ART and survive for longer than the time used to compute the slope.

The model includes configurable levels of heterogeneity of the starting and ending CD4 count, which will be described in the next scenario. For this scenario, everyone's starting and ending CD4 count is the same, so that only the slope in CD4 count varies among individuals. We'll do this by making sure the heterogeneity in starting CD4, (CD4_Post_Infection_Weibull_Heterogeneity) and the heterogeneity in ending CD4 (CD4_At_Death_LogLogistic_Heterogeneity) are both set to zero. If you set the starting CD4 count to 550 and the ending CD4 count to 50, the CD4 decline patterns will look like this:



Congratulations! You've learned how to use ReportHIVInfection.csv to monitor CD4 and WHO stage progression. You are now ready to add more realistic distributions of CD4 count.

2-e. Heterogeneity in CD4 Count at the Time of HIV Seroconversion and Death

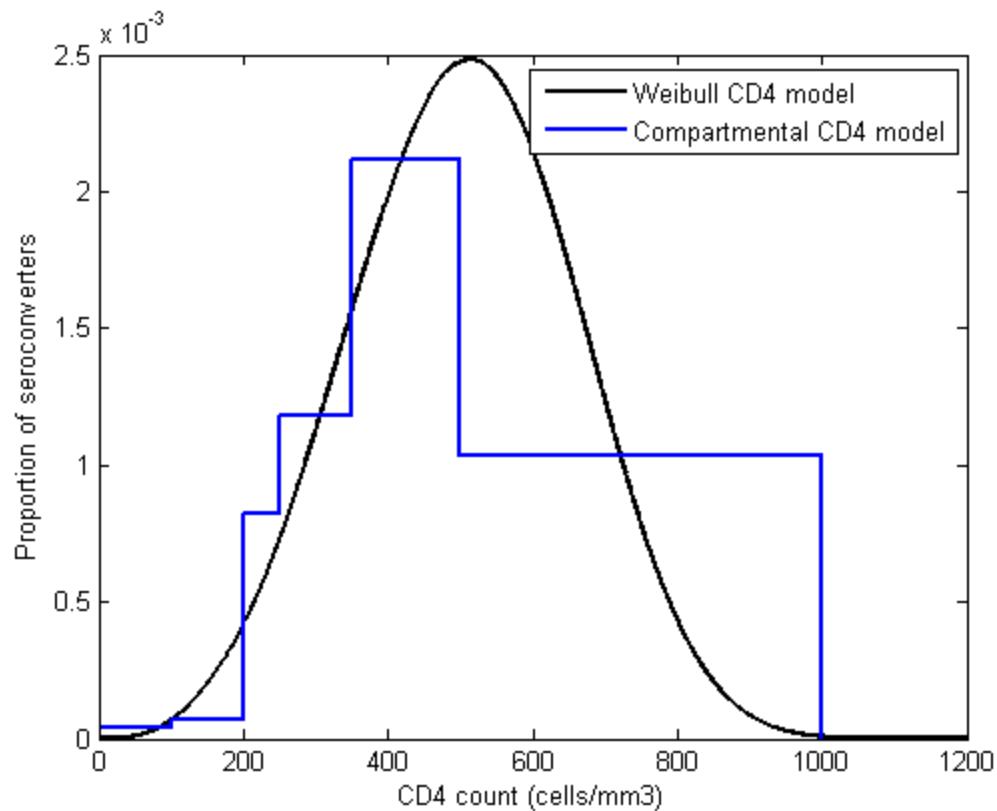
The initial CD4 count at the time of HIV infection can be made heterogeneous in the model by setting the CD4_Post_Infection_Weibull_Heterogeneity parameter to a value greater than zero. This parameter is equal to the inverse of the Weibull shape parameter. Very small values of heterogeneity are equivalent to very large values of the Weibull shape parameter, creating a sharp peak near the value set by CD4_Post_Infection_Weibull_Scale. When CD4_Post_Infection_Weibull_Heterogeneity is equal to zero, the initial CD4 count will be always be set to the value of CD4_Post_Infection_Weibull_Scale.

Similarly, heterogeneous final CD4 count can be configured by setting CD4_At_Death_LogLogistic_Heterogeneity to a value greater than zero, which sets the scale parameter for a log-logistic distribution.

Parameter	Value	Description
CD4_Post_Infection_Weibull_Scale	560.43	The Weibull scale parameter for the distribution of initial CD4 count at the time of HIV infection. All individuals will adopt this initial CD4 count when CD4_Post_Infection_Weibull_Heterogeneity is set to zero.
CD4_Post_Infection_Weibull_Heterogeneity	0.2756	The inverse of the Weibull shape parameter for the distribution of initial CD4 count at the time of HIV infection. When this parameter is set to zero, there is no heterogeneity in initial CD4, so all individuals will adopt the initial CD4 count set by CD4_Post_Infection_Weibull_Scale.
CD4_At_Death_LogLogistic_Scale	2.96	The log-logistic scale parameter for the distribution of CD4 count at the time of HIV-associated death. All individuals will adopt this CD4 count when CD4_At_Death_LogLogistic_Heterogeneity is set to zero.
CD4_At_Death_LogLogistic_Heterogeneity	0.70	The inverse of the log-logistic shape parameter for the distribution of CD4 count at the time of HIV-associated death. When this parameter is set to zero, there is no heterogeneity in CD4 at death, so all individuals will adopt the final CD4 count set by CD4_At_Death_LogLogistic_Scale.

The parameter values below are fit to a compartmentalized CD4 count distribution that resulted from a recent meta-analysis of CD4 progression by Mangal et al¹. Here is a comparison of the published compartmental model's initial CD4 distribution to that of the Weibull distribution with the listed parameters:

¹ Mangal TD. Joint Estimation of HIV Progression and Survival: A Pooled Analysis of 25 Countries. Conference on Retrovirology and Opportunistic Infections. Seattle, WA, 2015.



Using [ReportHIVInfection.csv](#), you can now plot the CD4 trajectories of our 100 individuals with heterogeneous initial and final CD4 counts by running runEmod.cmd and the provided plotting script.

2-f. Survival Time on ART

Now that you have examined survival and progression of untreated individuals, you can look at the impact of ART on survival. This example demonstrates survival with continuous ART. In the next section, you can see how to configure patterns of discontinuation and return to care, and their effect on survival.

It is important to note that interpreting clinical cohort data for survival on ART is challenging because only a fraction of deaths and inter-clinic transfers among those enrolled in the clinic are reported to the clinic^{1,2}. “Loss to follow-up” can encompass a combination of discontinuation of care due to death, death due to discontinuation of care, temporary discontinuation of care at the facility, and silent transfers

¹Rachlis B, Ochieng D, Geng E, Rotich E, Ochieng V, Maritim B, et al. Evaluating outcomes of patients lost to follow-up in a large comprehensive care treatment program in western Kenya: JAIDS Journal of Acquired Immune Deficiency Syndromes. 2014 Dec;1.

²Geng EH, Odony TA, Lyamuya RE, Nakiwogga-Muwanga A, Diero L, Bwana M, et al. Estimation of mortality among HIV-infected people on antiretroviral treatment in east Africa: a sampling based approach in an observational, multisite, cohort study. The Lancet HIV. 2015 Mar;2(3):e107-16.

with resumption of care at another facility¹. Demographic surveillance sites can gather information about deaths in the community through household surveys, but still face challenges due to refusal of HIV testing², mobility of populations (which is associated with silent transfers), and challenges in linking records between community surveys and clinics. Some of the best evidence on ART-associated survival comes from links between clinical records and highly complete vital registration. For generalized HIV epidemics, these links are available in only limited regions because they generally require unique patient identifiers.

In the model, survival time on ART is assumed to follow a Weibull proportional hazards model published by May et al³, with the IeDEA Southern Africa collaboration, with hazard ratios applied according to gender, age, CD4 count at initiation of ART, WHO stage at initiation of ART, and body weight at initiation of ART. Body weight is assumed to be linked to WHO stage progression, with linearly declining body weight between each WHO stage transition, as follows:

WHO Stage Transition	Body Weight
At time of infection	65 kg
1 to 2	62 kg
2 to 3	57 kg
3 to 4	50 kg
4 until death	40 kg

The base-case is defined as males age <40 with WHO stage 1-2, and follows a Weibull distribution for survival (in years) with shape parameter 0.34 and scale parameter 123.83. Hazard rates are applied either proportionally to a value (CD4 count and weight) or categorically (gender, age category, and WHO stage).

The continuously variable hazard ratios are tabulated below.

¹Meyer-Rath G, Over M, Klein D, Bershteyn A. The Cost and Cost-Effectiveness of Alternative Strategies to Expand Treatment to HIV-Positive South Africans. Center for Global Development. 2015 Apr 23.

²McGovern ME, Bärnighausen T, Salomon JA, Canning D. Using interviewer random effects to remove selection bias from HIV prevalence estimates. BMC Medical Research Methodology. 2015 Feb 5;15(1):8.

³May M, Boulle A, Phiri S, et al. Prognosis of patients with HIV-1 infection starting antiretroviral therapy in sub-Saharan Africa: a collaborative analysis of scale-up programmes. The Lancet 2010; 376:449-457.

Category	Hazard Ratio Base	Hazard Ratio Multiplier
Body Weight at Initiation	21.1	0.93 per kg
CD4 at Initiation	1.32	0.9925/cell/uL up to 350 cells/uL

The reduction in hazard of death per increase in CD4 count is capped at a CD4 count of 350 cells/uL, such that individuals initiating at CD4 counts greater than 350 cells/uL receive the same CD4-related hazard adjustment as those with a CD4 count of 350 cells/uL. In other words, the model currently makes a conservative assumption of the health benefit of initiating at CD4 counts greater than 350 cells/uL is identical to that of initiating at exactly 350 cells/uL. Evidence about the clinical benefit of initiation at higher CD4 counts will soon become available and may necessitate revision of these assumptions¹.

The categorical hazard ratios are tabulated below:

Category	Value	Hazard Ratio
Gender	Female	0.68
Age	>40 Years	1.43
WHO Stage	3 or 4	2.71

You can see the effect of each of these factors by providing ART to individuals at different ages and times. As you'll learn in the next few scenarios, it's also possible to target ART by CD4 count and other factors. This particular scenario is designed as follows:

- Half of individuals become infected at age 20, in the year 2020.
- Of these, half receive ART one year later, in the year 2021 (if they survive to that time).
- The rest receive ART ten years later, in 2030 (if they survive to that time).
- The remaining uninfected individuals become infected at age 50, in the year 2050.
- All of them receive ART one year later, in the year 2051 (assuming they survive to that time).

To distribute ART to the desired sub-populations, the [ARTBasic](#) intervention is added to the campaign.json file with the desired Start_Year and target population. For example, to provide ART to half of the individuals who are infected in the year 2021, the following is added to the campaign.json file:

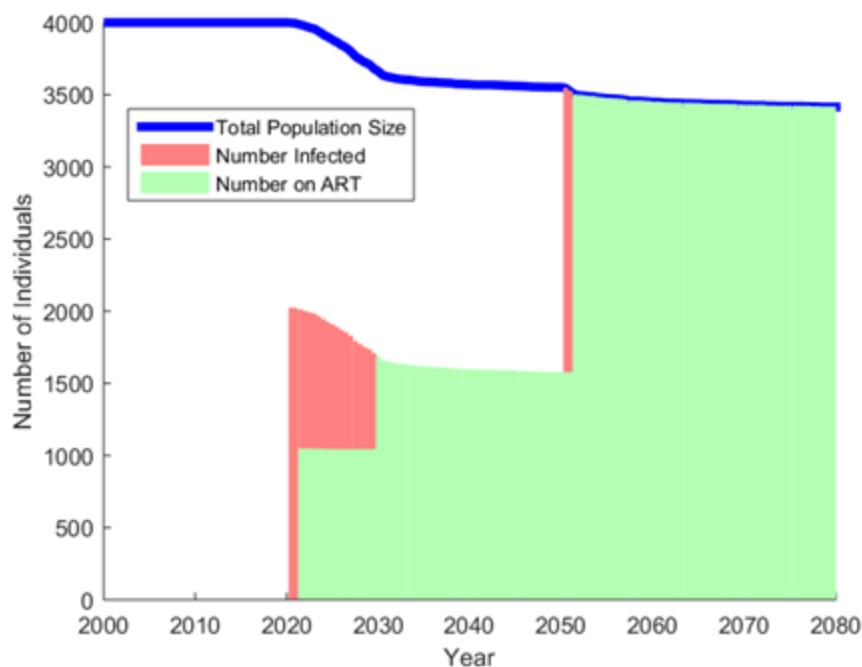
¹Babiker AG, Emery S, Fätkenheuer G, Gordin FM, Grund B, Lundgren JD, et al. Considerations in the rationale, design and methods of the Strategic Timing of AntiRetroviral Treatment (START) study. Clin Trials. 2013;10(10):S5-36.

```

"Start_Year": 2021,
...
{
  ...
  "Target_Demographic": "Everyone",
  "Demographic_Coverage": 0.5,
  ...
  {
    "class": "ARTBasic"
  }
}

```

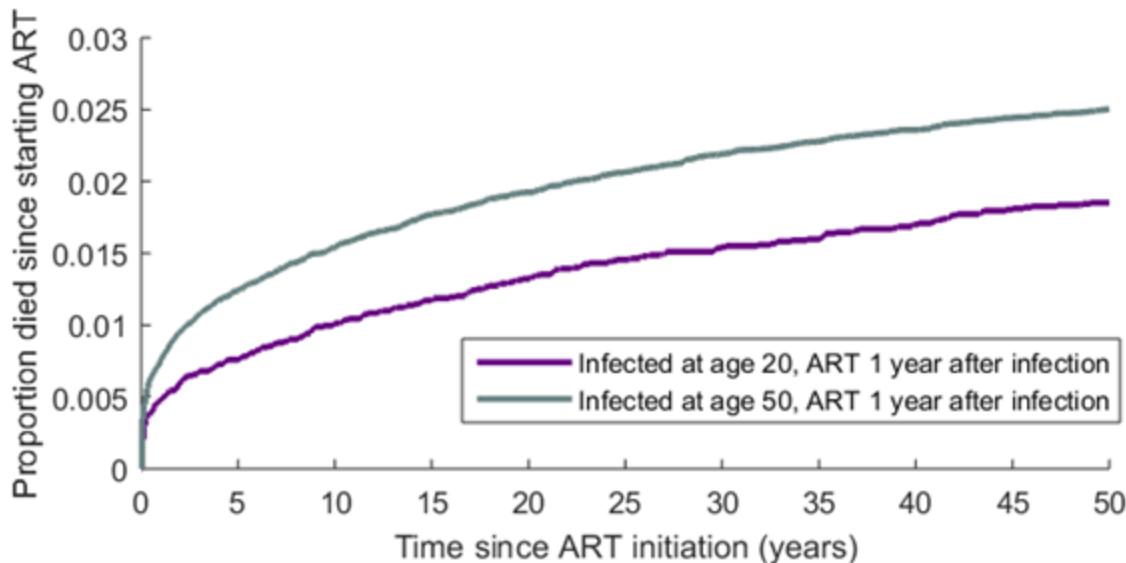
Similar blocks are added to provide ART in 2030 and 2041 to all infected individuals at those times (a Demographic_Coverage of 1.0). The pattern of population size, number infected, and number on ART will look like this:



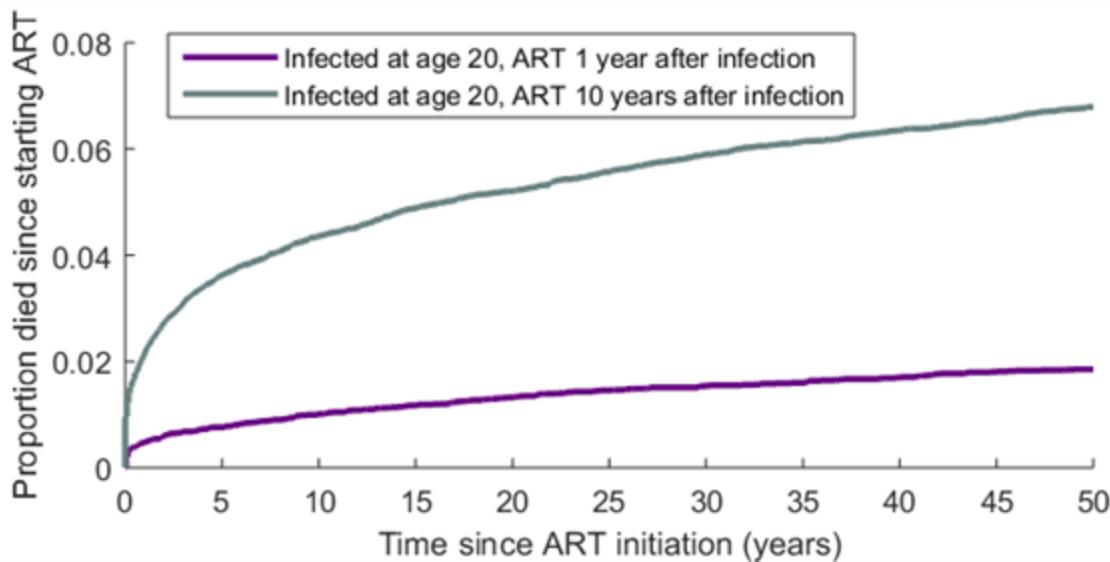
It's clear that mortality on ART is much lower than off ART. The model would have to be run with a large population size to see substantial numbers of people dying on ART. You can see what the outcome will look like with a population of 3 million people, which takes several minutes to run.

The expected outcome is that mortality should be lower among 20-year-olds than among 50-year-olds, and lower among those initiating ART after 1 year compared to after 5 years, and lower among women than men. To see this, aggregate the rows of [HIVMortality.csv](#) to select different sub-populations.

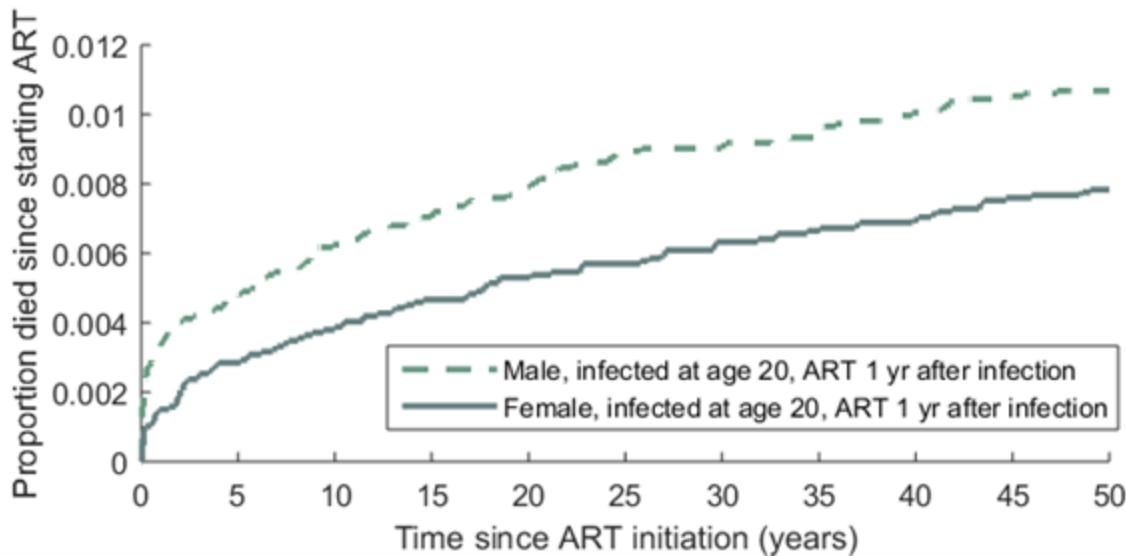
Here is a comparison of survival on ART among 20-year-olds and 50-year-olds, each initiated on ART one year after becoming infected. Deaths prior to ART initiation are not included.



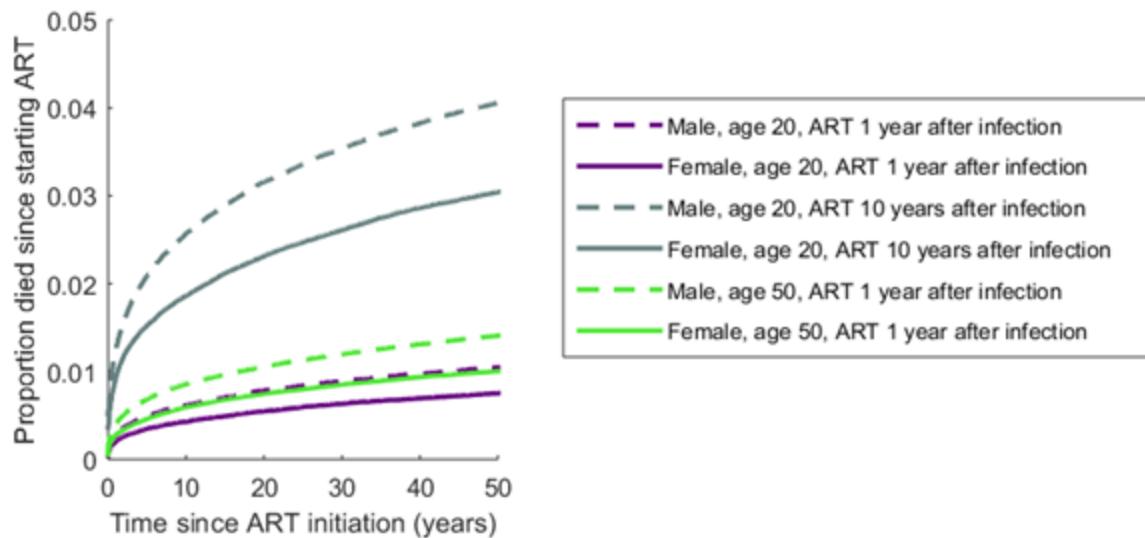
Here is a comparison of survival among the 20-year-olds initiated on ART one year after infection, compared to those initiated on ART ten years after infection. Deaths prior to ART are not included.



Here is a comparison of survival on ART between men and women, aggregated over the different ages and duration of infection prior to ART initiation:



The curves can be made smoother by increasing the population size. For the figure below, the population size was increased from 50,000 to 500,000 individuals.

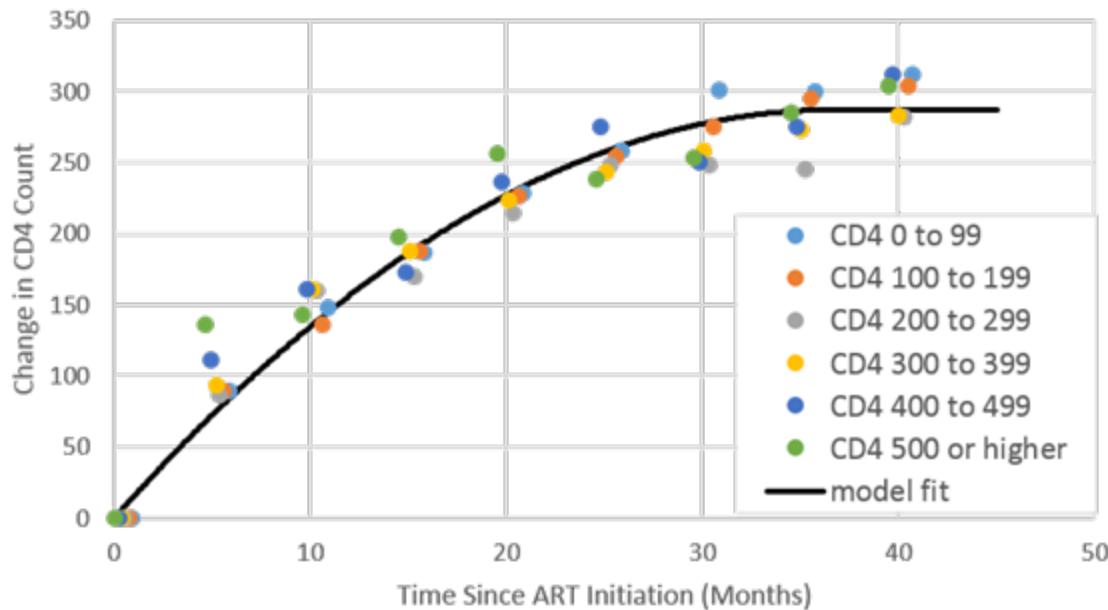


2-g. Reconstitution of CD4 Count during Antiretroviral Therapy

An analysis of CD4 counts after ART initiation in the Swiss HIV Cohort showed that the absolute changes in CD4 from baseline is consistent over the first few years of ART, independently of the baseline CD4 count at ART initiation. For example, a patient starting at a CD4 count of 100 cells/uL, on average, reconstitutes to 200 cells/uL in the same time that a patient starting at 200 cells/uL reconstitutes to 300 cells/uL.

The figure below shows the average change in CD4 count from pre-initiation levels for groups of patients initiating in different CD4 count categories, published by Kaufmann et al. The chart shows the absolute change in CD4 count (difference between current CD4 and CD4 at initiation) over time since

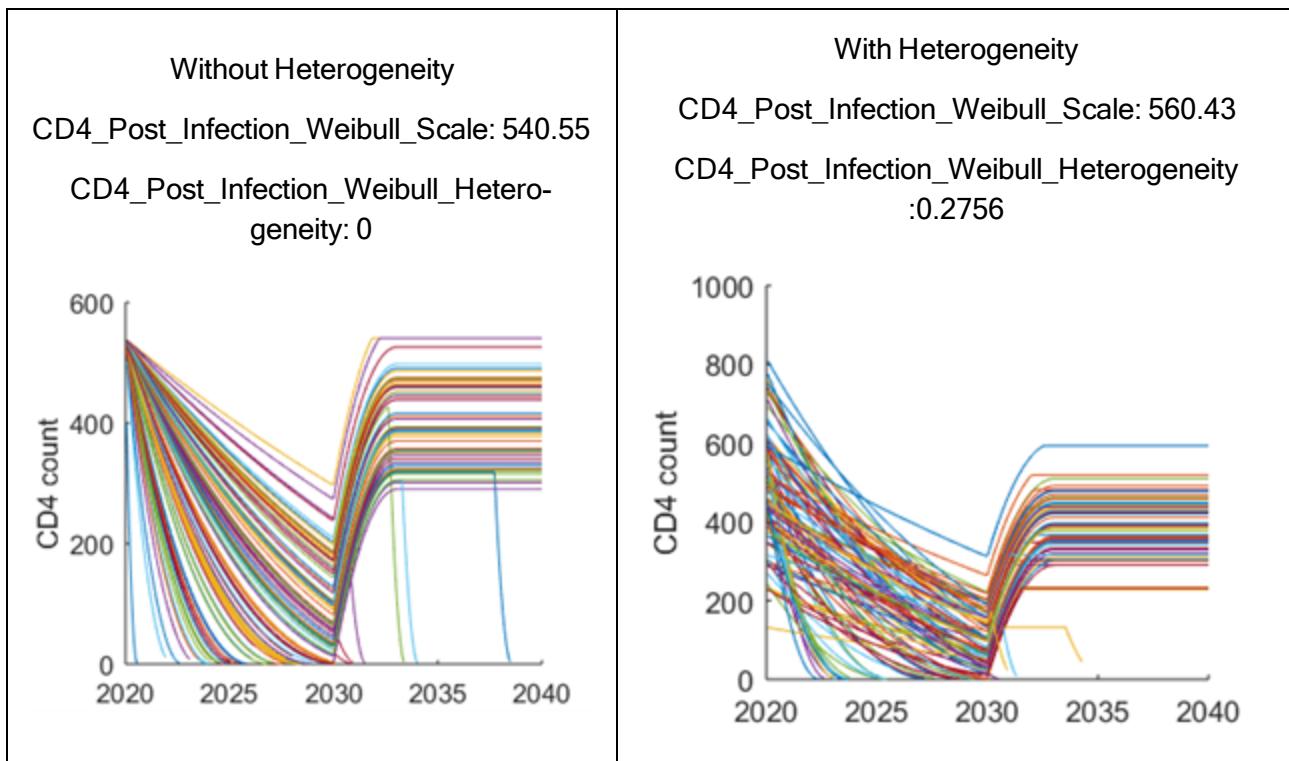
ART initiation. The colors indicate the category of CD4 count at ART initiation. The reconstitution rate fits a quadratic increase that saturates over three years, shown in black.



The equation for the CD4 count increase over the first three years is:

$$\text{CD4 count increase} = 15.584 \times \text{months since initiation} - 0.2113 \times \text{months since initiation}^2$$

Reconstitution of ART can be demonstrated using a setup similar to the previous scenario, with individuals infected and initiated on ART at a specific time. The figures below show the CD4 trajectories of 100 individuals initiated onto ART five years after infection. The trajectories are shown without heterogeneity in initial CD4 count (left), and with heterogeneity (right). Individuals who fail ART experience CD4 decline over nine months prior to death. The parameter values for CD4 heterogeneity are provided, so that you can modify them in the included config.json file.



2-h. Evolution of CD4 Count during Treatment Interruption and Re-Initiation

CD4 counts decline when treatment is interrupted and reconstitute when ART is resumed. To calculate the survival time upon discontinuation of ART, the model first determines what the survival time would have been for a newly infected individual at the age when discontinuation occurred. Survival is then adjusted to account for potentially low CD4 count at the time of ART discontinuation, as follows, up to a maximum of 100% of the "newly infected" survival time:

$$\% \text{ survival time applied at ART discontinuation} = \frac{\text{CD4 at ART discontinuation}}{\text{CD4 at infection}}$$

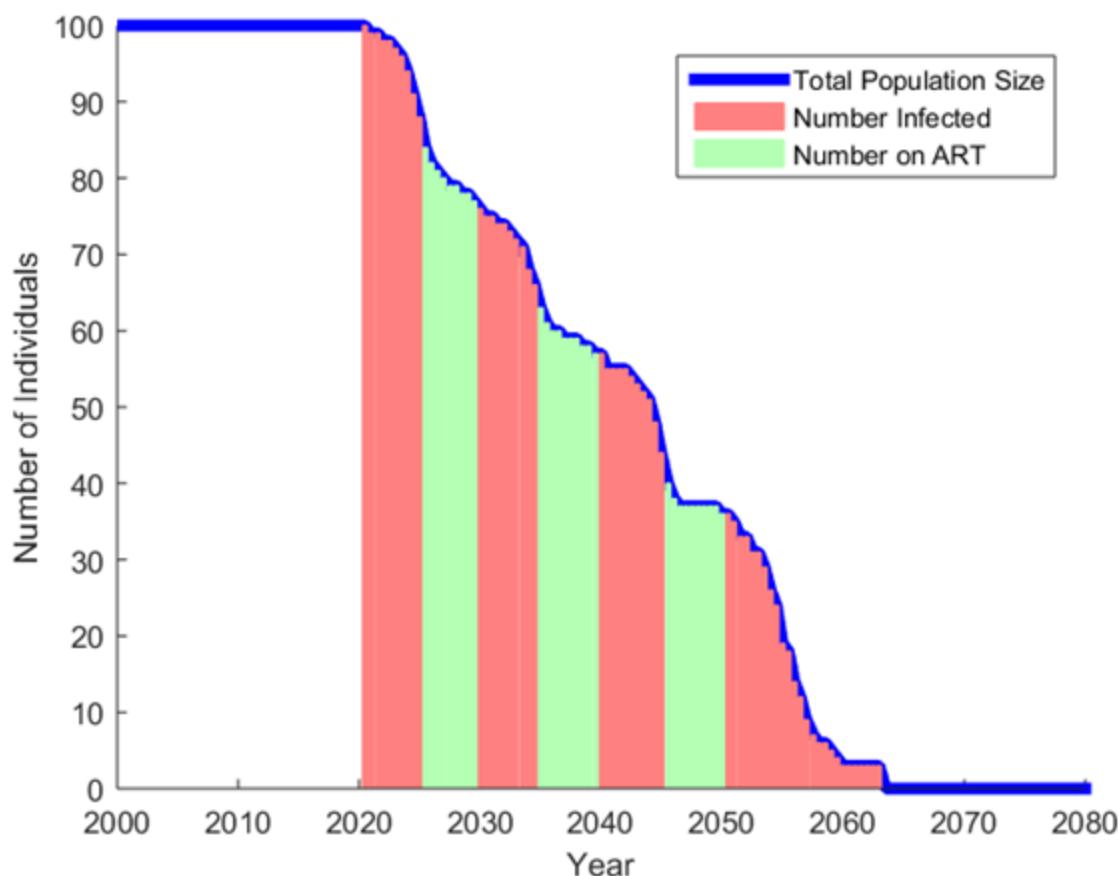
The slope of CD4 decline is therefore comparable to that of a newly infected individual, but the infection is "fast-forwarded" proportionally to the loss of CD4 count relative to a newly infected individual.

Upon re-initiation of ART, survival time is drawn from the survival distribution corresponding to the individual's updated CD4 count and age at the time of re-initiation. Recall from [Scenario 2-f](#) that mortality rates on ART were modeled as Weibull distributions with a shape<1, producing a "super-exponential" mortality curve (one with a probability density function that declines more rapidly than an exponential distribution). This produces an elevated mortality rate soon after ART initiation, and a lower mortality rate as time on ART increases. Discontinuation and re-initiation of ART produces higher mortality rates than continuous ART by repeatedly exposing the individual to this high early mortality rate.

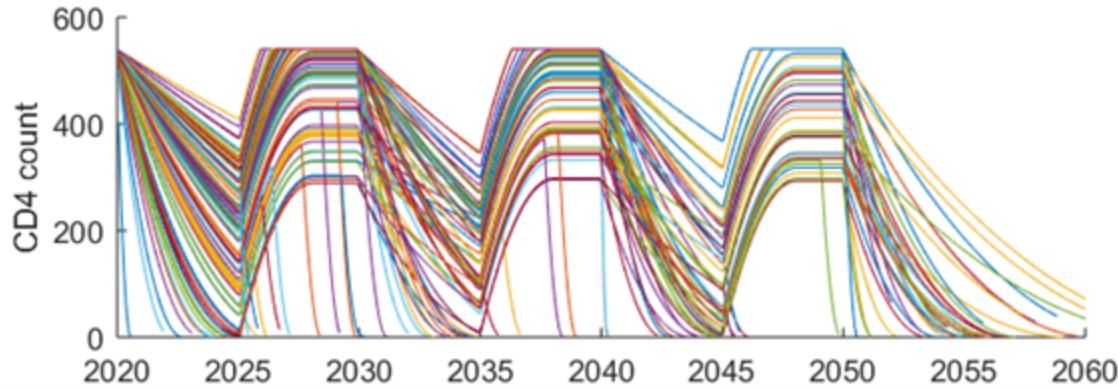
Interruption of ART can be achieved with the [ARTDropout](#) intervention. The syntax for ARTDropout is similar to that of [ARTBasic](#). For example, to trigger ART interruption in all individuals currently on ART in the year 2025, the campaign file should include:

```
"Start_Year": 2025,  
...  
{  
    ...  
    "Target_Demographic": "Everyone",  
    "Demographic_Coverage": 1.0,  
    ...  
{  
    "class": "ARTDropout"  
}
```

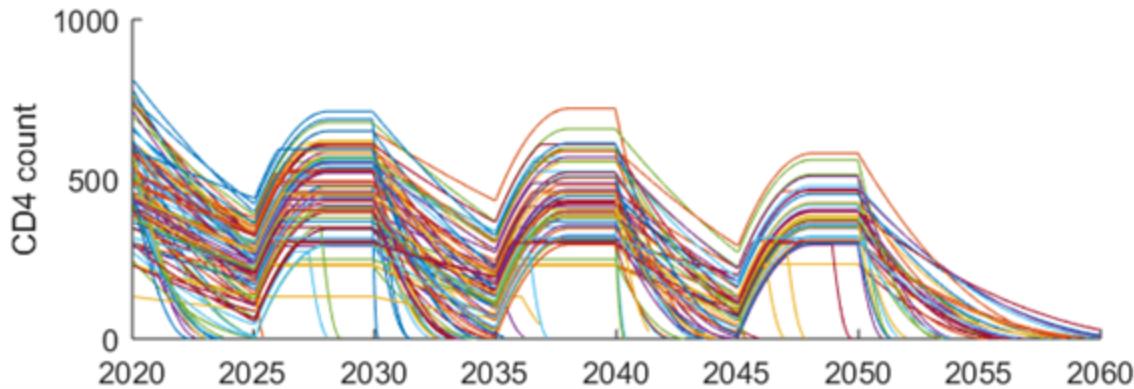
To demonstrate CD4 evolution during ART interruptions, the included campaign file creates a cohort of ART-infected individuals and who are cycled on and off ART every ten years. As before, the population size, number infected, and number on ART can be obtained from the [ReportHIVByAgeAndGender.csv](#) output file. (For additional details on configuring this report, see [HIVByAgeAndGender Report File](#) in the File Format Layout Descriptions section of the online documentation.)



and the CD4 trajectories in the cohort can be obtained from [ReportHIVInfection.csv](#). It is easiest to see the pattern by first disabling heterogeneity in the initial CD4 count, as you did in the previous scenario:



before enabling heterogeneity to see the full spectrum of possible CD4 trajectories:



Congratulations! You have completed the tutorial on HIV biology in EMOD v2.0!

HIV Tutorial 3: Transmission

In EMOD, the probability of transmission is calculated for each discordant coital act or each childbirth. (Parenteral transmission of HIV is not included in v2.0 of EMOD-HIV.) This tutorial demonstrates the different factors that influence the probability of HIV transmission.

3-a. Sexual Transmission: Base Infectivity and Multipliers by Gender and Age

Factors that influence the transmission rate all multiply a base rate, which is set by the parameter `Base_Infectivity`. When running `STI_SIM` and `HIV_SIM`, the interpretation of `Base_Infectivity` is the probability of transmission when none of the transmission multipliers apply to a particular coital act (or when all multipliers are set to 1).

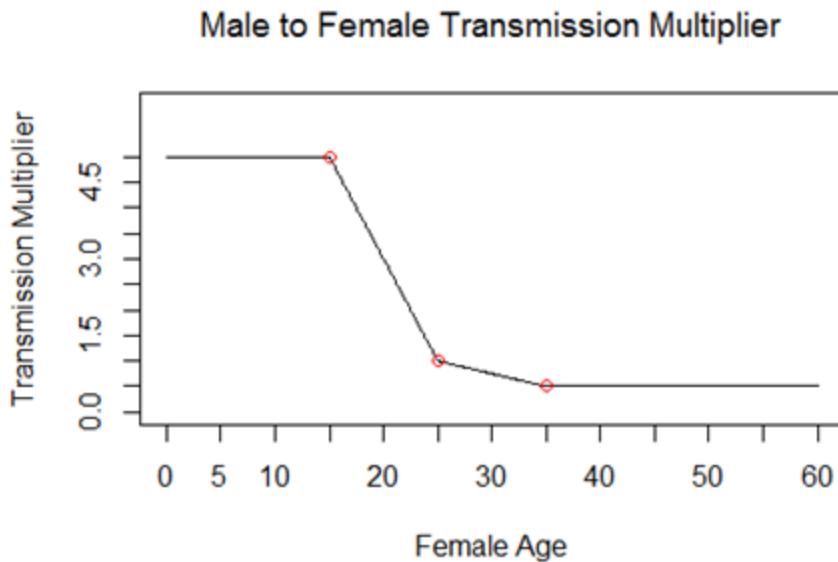
In this example, the `Base_Infectivity` is set to 1 transmission per 1000 coital acts:

```
"Base_Infectivity": 0.002,
```

The rate of male-to-female heterosexual transmission can be configured to be different than the rate of female-to-male heterosexual transmission. This gender bias in transmission can also be varied according to the age of the female partner. Both the gender and age multipliers on transmission are configured through a pair of matched arrays in the `config.json` file:

```
"Male_To_Female_Relative_Infectivity_Ages": [ 15, 25, 35 ],  
"Male_To_Female_Relative_Infectivity_Multipliers": [ 5, 1, 0.5 ],
```

The lengths of these two arrays must be equal, so that each multiplier has a corresponding age. To remove age dependence, put just one value in each array. When multiple values are provided, the multiplier on the probability of transmission is linearly interpolated between the specified ages. Ages do not have to be integer values. Ages younger than the youngest specified age are assigned the value for the youngest specified age. Likewise, ages older than the oldest specified age are assigned the value for the oldest specified age.



The transmission rate can also be configured to be heterogeneous among individuals, with a multiplier on infectiousness sampled from a Weibull distribution. The multiplier is assigned to each individual at birth and will be applied to every infection in that individual's lifetime (which is not relevant for most HIV modeling use cases, but may be important for modeling a hypothetical HIV cure with potential for re-infection). The heterogeneity is disabled by setting the heterogeneity parameter to zero. When heterogeneity is set to zero, transmission rates are all multiplied by the mean parameter of the Weibull, so make sure to set it to 1 if you are not using this feature:

```
"Heterogeneous_Infectiousness_Weibull_Heterogeneity": 0,  
"Heterogeneous_Infectiousness_Weibull_Scale": 1,
```

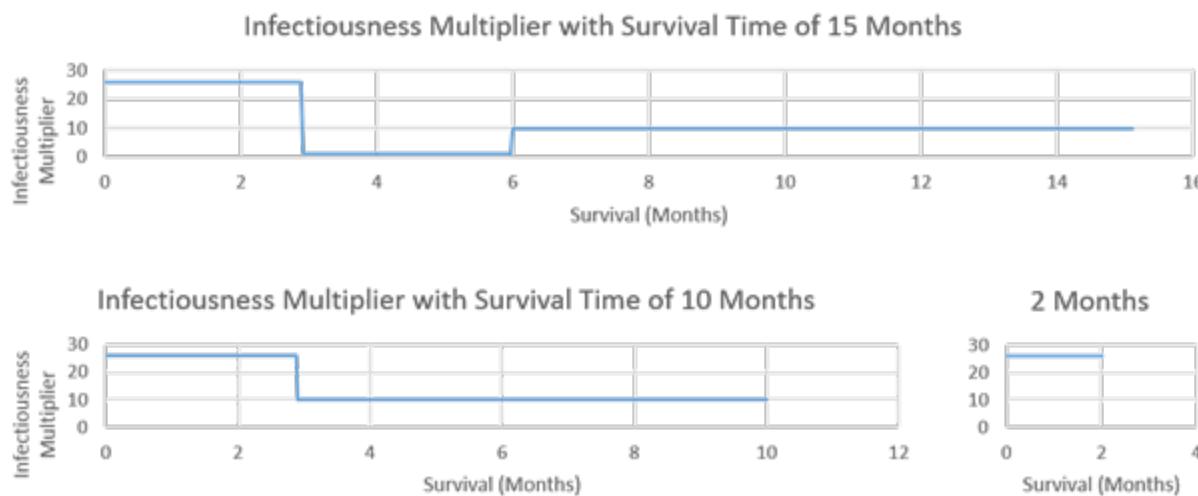
For more about Weibull distributions and tools for plotting and calculating the parameters, see [Scenario 1-b.](#)

Lastly, transmission rates are configurable by stage of disease. Here, the `Base_Infectivity` sets the transmission rates for the latent stage of HIV infection. A transmission rate can be applied for a configurable interval of time after infection, referred to here as the acute stage, and for a configurable interval of time before death, referred to here as the AIDS stage. The durations and transmission multipliers for these stages of disease are set in the config.json file:

```
"Acute_Duration_In_Months": 2.9,  
"Acute_Stage_Infectivity_Multiplier": 26,  
"AIDS_Duration_In_Months": 9,  
"AIDS_Stage_Infectivity_Multiplier": 10,
```

The Acute_Duration_In_Months determines time since infection, in months, over which the Acute_Stage_Infectivity_Multiplier is applied to coital acts occurring in that time period. Similarly, the AIDS_Duration_In_Months determines the time period prior to an AIDS-related death over which the AIDS_Stage_Infectivity_Multiplier is applied.

The duration of the latent stage of infection, during which neither of these multipliers is applied, is the overall survival time minus the duration of the acute and AIDS stages. Occasionally, an individual could receive an HIV survival time that is shorter than the sum of the acute and AIDS durations. In this case, the latent stage is eliminated, and the individual receives the acute multiplier for the full duration of the acute stage, followed by the AIDS multiplier for the remaining time. More rare still is the case in which survival is shorter than the acute stage duration. In this case, the acute multiplier is applied to the full survival duration. These situations are illustrated below for survival times of 15, 10, and 2 months:



You can explore the relationship between disease stages and survival time with the DiseaseStage.xlsx spreadsheet included in the figures folder for this scenario:

Scenarios\STIAndHIV\01_STI_Network\A_Welcome_to_STI_SIM\figs

3-b. Effect of Voluntary Male Medical Circumcision on Sexual Transmission

Voluntary male medical circumcision (VMMC) reduces a male's susceptibility to HIV by a configurable proportion. It is set in the config.json file through the parameter Circumcision_Reduced_Acquire:

```
"Circumcision_Reduced_Acquire": 0.6,
```

VMMC only impacts the probability of female to male transmission. It can be provided to males at any age. There is no built-in lag in the model between receiving VMMC and the effect of `Circumcision_Reduced_Acquire`, although a lag can be added by adding a delay prior to distributing the final intervention. Configuration of delays is described in [Scenario 4](#). The syntax for configuring VMMC interventions is described in [Scenario 4-2-1-b](#), and several examples are provided in [Scenario 5-1](#).

In campaign.json, VMMC is distributed through the intervention `MaleCircumcision`. The roll-out of VMMC can be linked to other HIV services such as different forms of testing outreach, which is demonstrated in [Scenario 5-1](#). In this demonstration, a simple campaign is used to bypass HIV testing and distribute VMMC directly to all males in the year 2025, as follows:

```
{
  "class": "CampaignEventByYear",
  "Event_Name": "Male circumcision for all (males) in 2025",
  "Start_Year": 2025,

  "Nodeset_Config": { "class": "NodeSetAll" },

  "Event_Coordinator_Config":
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Coverage": 1,
    "Target_Demographic": "ExplicitGender",
    "Target_Gender": "Male",

    "Intervention_Config":
    {
      "class": "MaleCircumcision"
    }
  }
},
```

This intervention applied VMMC to all males in the simulation in the year 2025. Rather than using the most basic [CampaignEvent](#) functionality, this example uses [CampaignEventByYear](#), which allows users to specify a calendar year for the intervention, rather than a day since simulation start. Similarly to [CampaignEvent](#), the [CampaignEventByYear](#) takes in a set of geographic nodes to be targeted. In this case, the model is not geographically distributed, so targeting all nodes applies the intervention to the single specified node. To target the intervention only to males, the [StandardInterventionDistributionEventCoordinator](#) is used with an explicit `Target_Gender`. Age targeting can also be performed by changing `ExplicitGender` to `ExplicitAgeRangesAndGender`, as demonstrated in [Scenario 5-1](#).

If birth is enabled, then individuals born after 2025 will not receive the VMMC intervention specified above. The example below shows how to distribute VMMC to infants born after 2025 using a birth-triggered intervention. It is also possible for males to receive VMMC at a specified age, or a random age

chosen from a specified distribution, using a delayed birth-triggered intervention. This is demonstrated in [Scenario 5-1-d](#).

```
{
  "class": "CampaignEventByYear",
  "Event_Name": "Male circumcision at birth starting in 2025",
  "Start_Year": 2025,

  "Nodeset_Config": { "class": "NodeSetAll" },

  "Event_Coordinator_Config":
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Coverage": 1,
    "Target_Demographic": "ExplicitGender",
    "Target_Gender": "Male",

    "Intervention_Config":
    {
      "class": "BirthTriggeredIV",

      "Actual_IndividualIntervention_Config":
      {
        "class": "MaleCircumcision"
      }
    }
  }
}
```

Note that the example above contains two nested interventions: first, a birth-triggered intervention called [BirthTriggeredIV](#), and nested within it, the actual intervention to be given out, [MaleCircumcision](#).

A simple way to observe the impact of VMMC in the model is to create discordant couples and observe the rate of transmission before and after distribution of VMMC. In this example, stable couples are formed and 100% of females are infected with HIV in the year 2021, using the [OutbreakIndividual](#) intervention targeted to females with a coverage of 1.0:

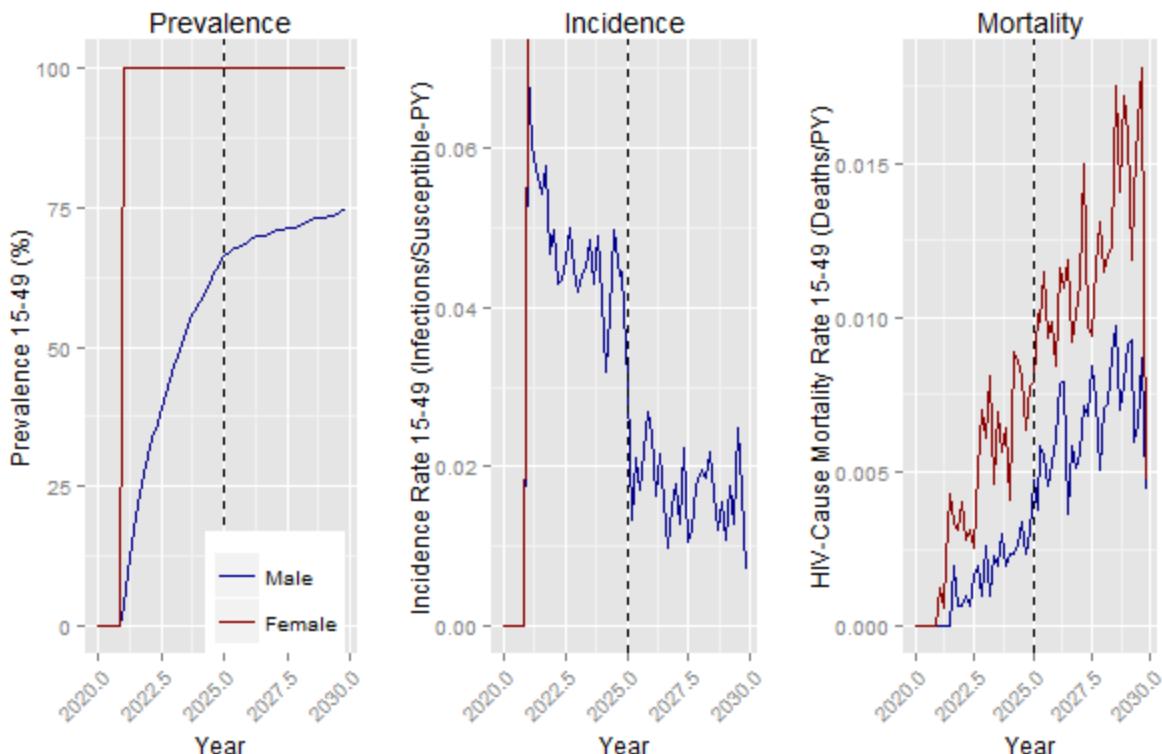
```
{
  "Description": "HIV Outbreak",
  "class": "CampaignEventByYear",
  "Start_Year": 2021,
  "Nodeset_Config": { "class": "NodeSetAll" },
  "Event_Coordinator_Config":
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Demographic_Coverage": 1.0,
    "Target_Demographic": "ExplicitGender",
```

```

    "Target_Gender": "Female",
    "Intervention_Config":
    {
        "class": "OutbreakIndividual",
        "Incubation_Period_Override": 1,
        "Outbreak_Source": "PrevalenceIncrease"
    }
}
}
}

```

The graph below shows the prevalence, incidence, and mortality in the 15 to 49 age group by gender, generated from the output file [ReportHIVByAgeAndGender.csv](#). As expected, female prevalence goes to 100% at the time of the outbreak. Incidence in males drops by 60% in 2025, when circumcision is provided. Prior to the circumcision campaign, the initial incidence in males is transiently elevated due to the simultaneous acute stages of infection in the females (an artifact of this simple demonstration).



3-c. Effect of Antiretroviral Therapy on Sexual Transmission

Successful antiretroviral therapy (ART) reduces the rate of probability of transmission by a configurable proportion. It is set in the config.json file through the parameter ART_Viral_Suppression_Multiplier:

```
"ART_Viral_Suppression_Multiplier": 0.08,
```

Whether this multiplier is applied depends on whether the quality of ART care or level of adherence associated with the ART intervention is sufficient to achieve viral suppression. This is configured using the `Viral_Suppression` parameter associated with the [ARTBasic](#) intervention. Other than the `Viral_Suppression` option, the syntax for applying ARTBasic is similar to the previous VMMC example.

```
{
  "class": "CampaignEventByYear",
  "Event_Name": "ART for all females in 2025",
  "Start_Year": 2025,

  "Nodeset_Config": { "class": "NodeSetAll" },

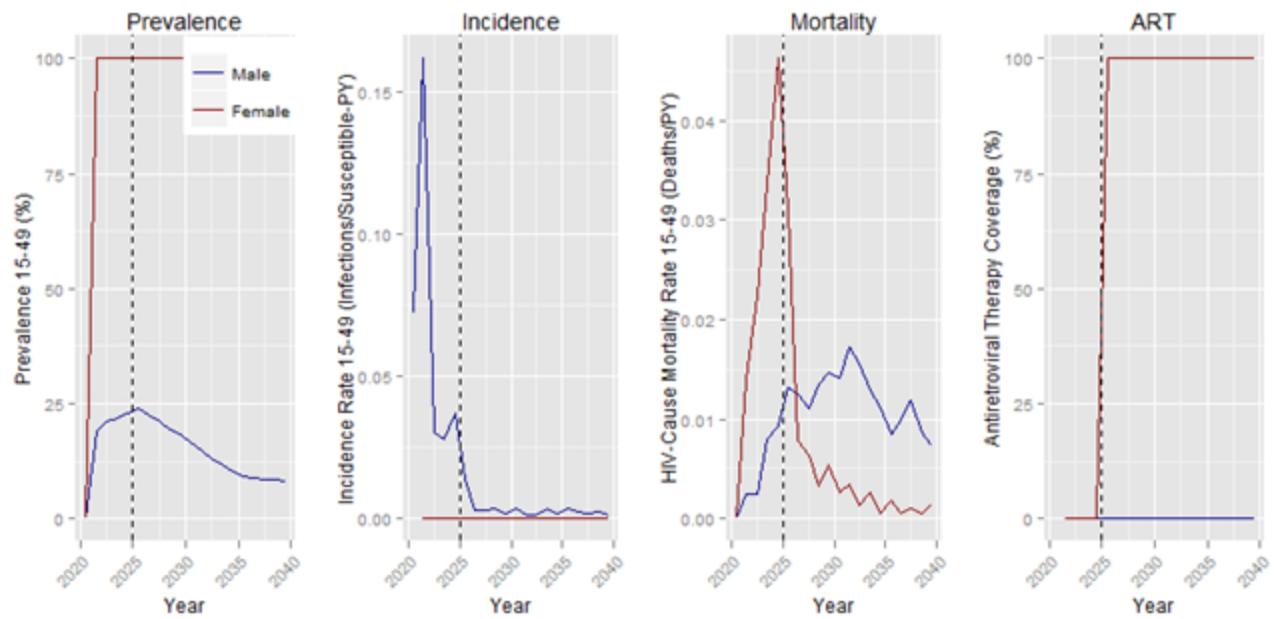
  "Event_Coordinator_Config":
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Coverage": 1,
    "Target_Demographic": "ExplicitGender",
    "Target_Gender": "Female",

    "Intervention_Config":
    {
      "class": "ARTBasic",
      "Viral_Suppression": 1
    }
  }
}
```

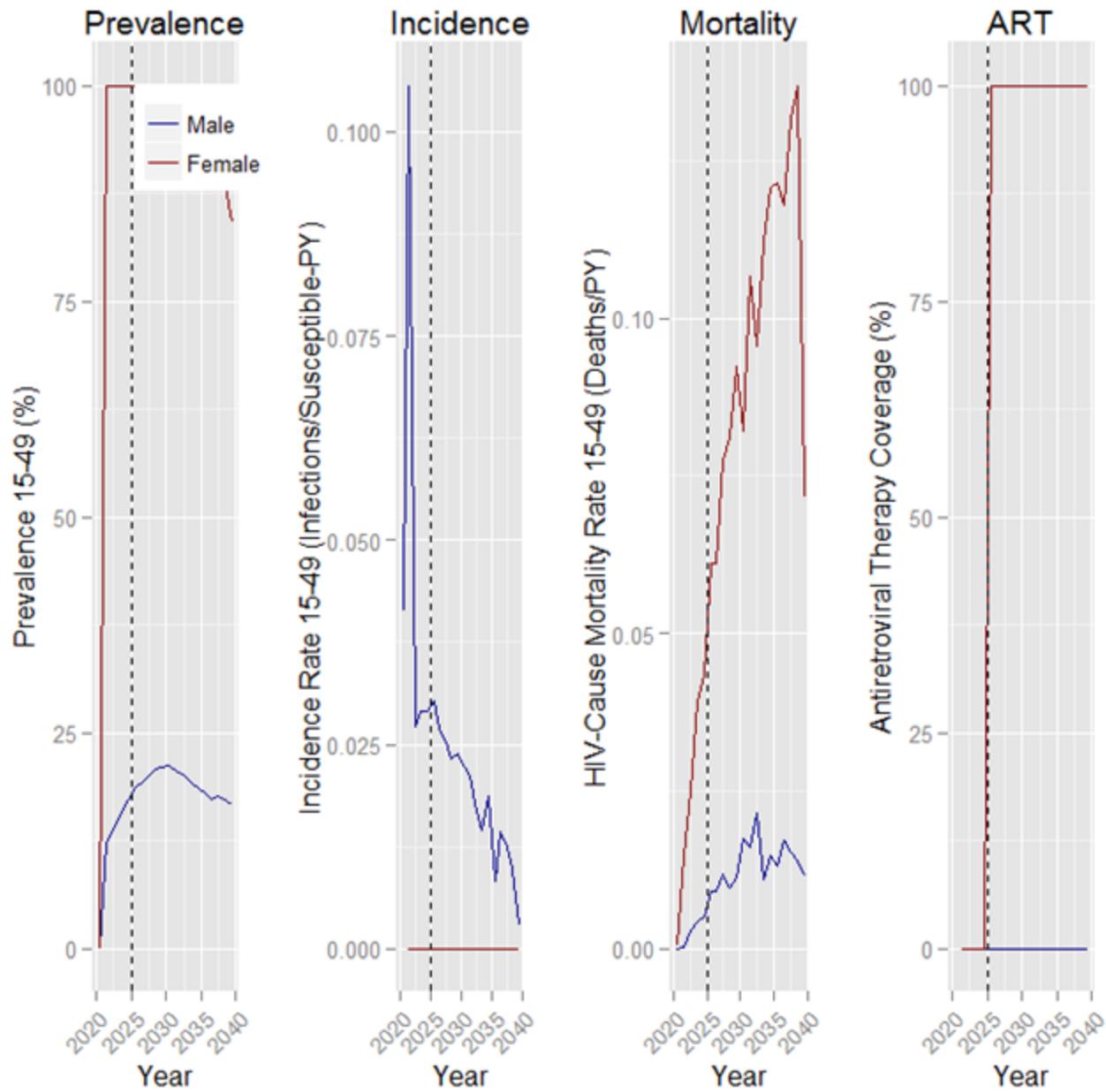
`Viral_Suppression` an optional parameter that is set to 1 by default.

If the `Viral_Suppression` parameter for ARTBasic is left out or set to 1, then the effect of the `ART_Viral_Suppression_Multiplier` is applied with the intervention, and the survival benefit of ART is also applied as described in [Scenario 2-f](#). If `Viral_Suppression` is set to 0, then the `ART_Viral_Suppression_Multiplier` is not applied, and the ARTBasic intervention does not affect the natural history of infection; i.e., the mortality ([Scenario 2-c](#)) and CD4 decline ([Scenario 2-d](#) and [Scenario 2-e](#)) continue as though ART had not been applied. Regardless of the `Viral_Suppression` parameter, the person-years of ART are counted in the output files. An economic analysis based on the output files would thus include the full cost of ART even for unsuccessful treatment.

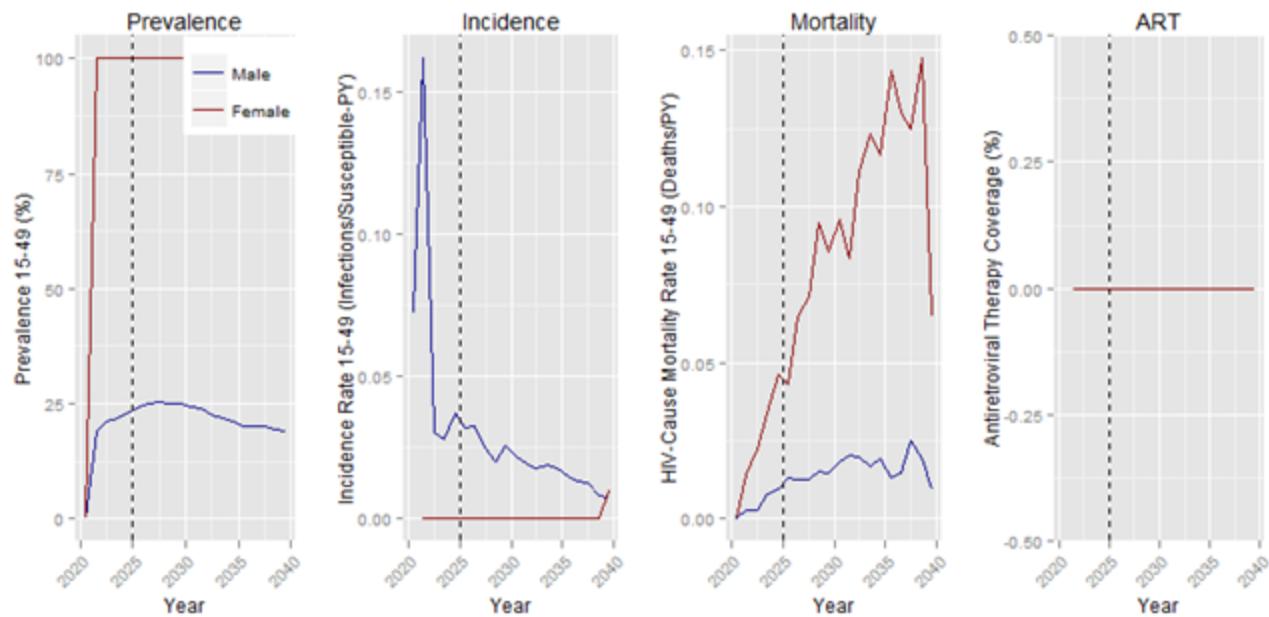
The graph below shows the prevalence, incidence, mortality, and ART coverage of infected individuals by gender for the 15-49 age group, generated from the output file [ReportHIVByAgeAndGender.csv](#). The demonstration incorporates both the survival and the transmission benefits of ART. As expected, female prevalence goes to 100% at the time of the outbreak. Mortality in females and incidence in males drops dramatically in 2025, when ART is provided to all females.



If the Viral_Suppression parameter were set to zero, then the graphs from ReportHIVByAgeAndGender.csv. would look like this:



Although ART is still distributed, with `Viral_Suppression` set to zero the mortality in females and incidence in males would continue as if ART were absent. In this example, incidence in males still declines due to the completion of the acute stage of infection and rising mortality in the female partners, but there is no dramatic drop in incidence in 2025. For comparison, below are the same graphs generated in a simulation with no ART intervention:



3-d. Effect of Condom Usage on Sexual Transmission

Condom usage reduces the rate of probability of transmission by a configurable proportion. It is set in the config.json file through the parameter `Condom_Transmission_Blocking_Probability`:

```
"Condom_Transmission_Blocking_Probability": 0.90,
```

Unlike the VMMC and ART parameters, this parameter represents the proportion reduction in transmission due to condoms. If set to 0, condoms would have no effect on transmission; if set to 1, condoms would always prevent transmission when used.

EMOD supports two ways to distribute the condom intervention: through the config.json file and through the campaign.json file. The config.json file can be used to configure a baseline rate of condom usage by relationship type.

Both methods use a sigmoid-shaped trend in condom usage, configured by setting the parameters of a logistic equation. The parameters set the right asymptote, the left asymptote, the time of the inflection point, and a rate parameter than is related to the slope at the inflection point. When the difference between the left and the right asymptote is 1, then the rate parameter can be divided by 4 to determine the slope at the inflection point. To explore this functional form, use the Excel sheet included with this scenario to set the parameters and view the curve and slope at the inflection point:

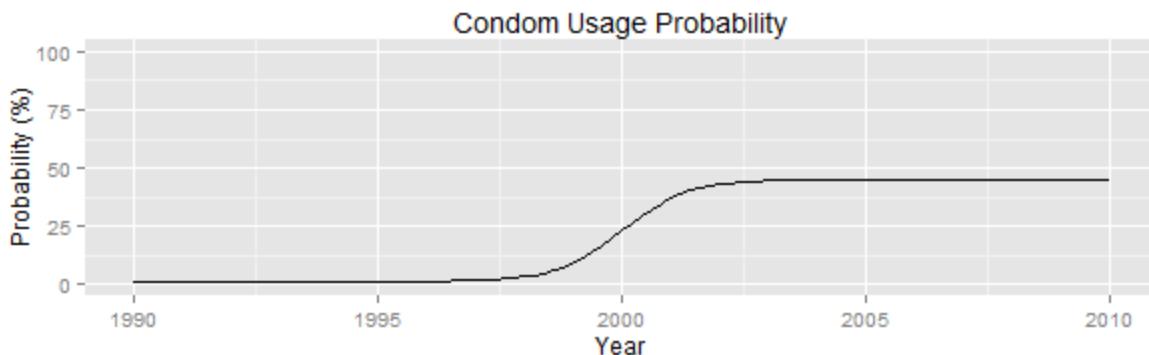
Scenarios\STIAndHIV\03_Transmission\03_Effect_of_Condoms\figs\Sigmoid.xlsx

Only sigmoid changes in condom usage over time are supported. For each relationship type, four parameters are used to define the sigmoid-shaped usage probability over time: the left asymptote for

probability (parameters ending with _Early), the right asymptote (ending with _Late), the time of the infection point (_Midyear), and the rate parameter proportional to the slope at the inflection point (_Rate).

```
"Condom_Usage_Probability_in_Transitory_Relationships_Early": 0.0125,
"Condom_Usage_Probability_in_Transitory_Relationships_Late": 0.45,
"Condom_Usage_Probability_in_Transitory_Relationships_Midyear": 2000,
"Condom_Usage_Probability_in_Transitory_Relationships_Rate": 1.5,
"Condom_Usage_Probability_in_Informal_Relationships_Early": 0.0125,
"Condom_Usage_Probability_in_Informal_Relationships_Late": 0.3,
"Condom_Usage_Probability_in_Informal_Relationships_Midyear": 2000,
"Condom_Usage_Probability_in_Informal_Relationships_Rate": 1.5,
"Condom_Usage_Probability_in_Marital_Relationships_Early": 0.000625,
"Condom_Usage_Probability_in_Marital_Relationships_Late": 0.2,
"Condom_Usage_Probability_in_Marital_Relationships_Midyear": 2003,
"Condom_Usage_Probability_in_Marital_Relationships_Rate": 1.5,
```

For example, the plot below shows the time-variable probability of condom usage in transitory relationships:



The campaign.json file provides an alternative way to distribute a condoms as an intervention. Again, the parameters of a sigmoid function over time must be specified, and the intervention must be targeted to one of three relationship types: TRANSITORY, INFORMAL, or MARITAL. It is not recommended to assign different condom usage probabilities according to gender, although this is permitted by the campaign framework. If the condom usage probability for a coital act is different between the two participants, then the probability assigned to the male participant is used.

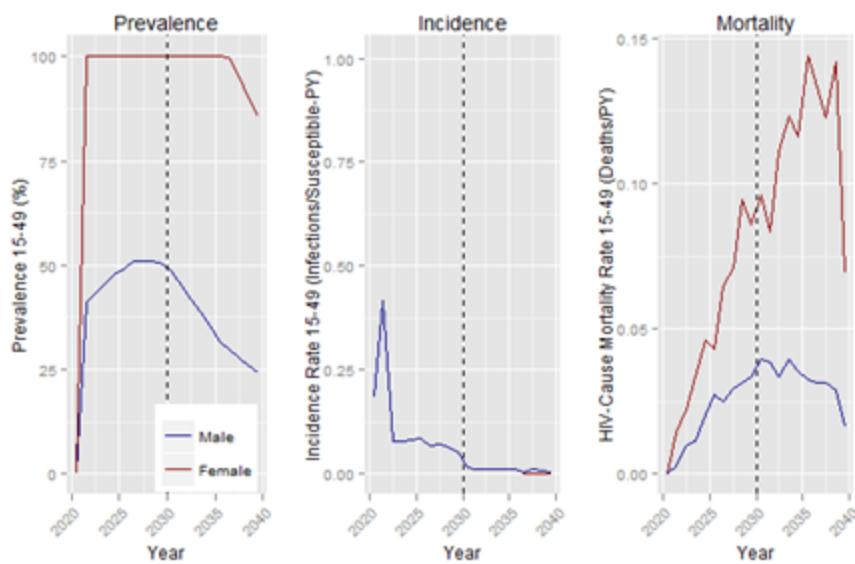
If a condom usage intervention is configured in campaign.json, it will override the probabilities configured in config.json only after the campaign's Start_Year. The example below shows an intervention targeted to 50% of transitory relationships, which provides a 50% probability of condom usage in the year 2025, ramping up to 100% with an inflection point in 2030. Prior to 2025, any condom usage configured in config.json will be applied.

```
{
  "class": "CampaignEventByYear",
  "Event_Name": "Condom usage in transitory relationships ramps up starting in 2025
with an inflection point in 2030",
  "Start_Year": 2025,

  "Nodeset_Config":
  {
    "class": "NodeSetAll"
  },

  "Event_Coordinator_Config":
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Coverage": 0.5,
    "Target_Demographic": "Everyone",
    "Intervention_Config":
    {
      "class": "STIBarrier",
      "Early": 0.5,
      "Late": 1,
      "MidYear": 2030,
      "Rate": 1,
      "Relationship_Type": "TRANSITORY"
    }
  }
}
```

The impact of the intervention can be seen in the rapid decline in incidence occurring near the inflection point in 2030:



3-e. Impact of Co-infections on Sexual Transmission

When running HIV_SIM, EMOD does not currently support simultaneous transmission of HIV and other sexually transmitted co-infections. Instead, the model supports non-transmitting co-infections that increase the infectiousness and susceptibility. A co-infection can be set or cleared for an individual using interventions, thereby allowing targeting of co-infections by [Individual Properties](#) (e.g., by sociodemographic category or HIV risk group). This scenario will demonstrate how to set or clear the effect of co-infection on HIV transmission, how to assign co-infection prevalence, and how modify co-infection status (e.g., to represent a change in prevalence of co-infections, or as part of an STI treatment intervention).

Individuals who are co-infected receive a multiplier on the probability of both acquisition and transmission of HIV by a factor configured through the `STI_Coinfection_Multiplier`:

```
"STI_Coinfection_Multiplier": 10,
```

The co-infection status can be modified using the intervention [ModifyStiCoInfectionStatus](#), which is described in more detail in [4-2-1. Standard Interventions](#).

In this example, all individuals get a co-infection in year 2021 using the following campaign event:

```
{
  "class": "CampaignEvent",
  "Event_Name": "Set STI Co-Infections on day 1",
  "Start_Day": 1,
  "Nodeset_Config": { "class": "NodeSetAll" },
  "Event_Coordinator_Config":
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Demographic_Coverage": 1,

    "Intervention_Config":
    {
      "class": "ModifyStiCoInfectionStatus",
      "New_STI_CoInfection_Status": 1
    }
  }
},
```

Then in year 2025, all co-infections are cured by setting `New_STI_CoInfection_Status` to zero:

```
{
  "class": "CampaignEventByYear",
  "Event_Name": "Cure all STI Co-Infections in 2025",
```

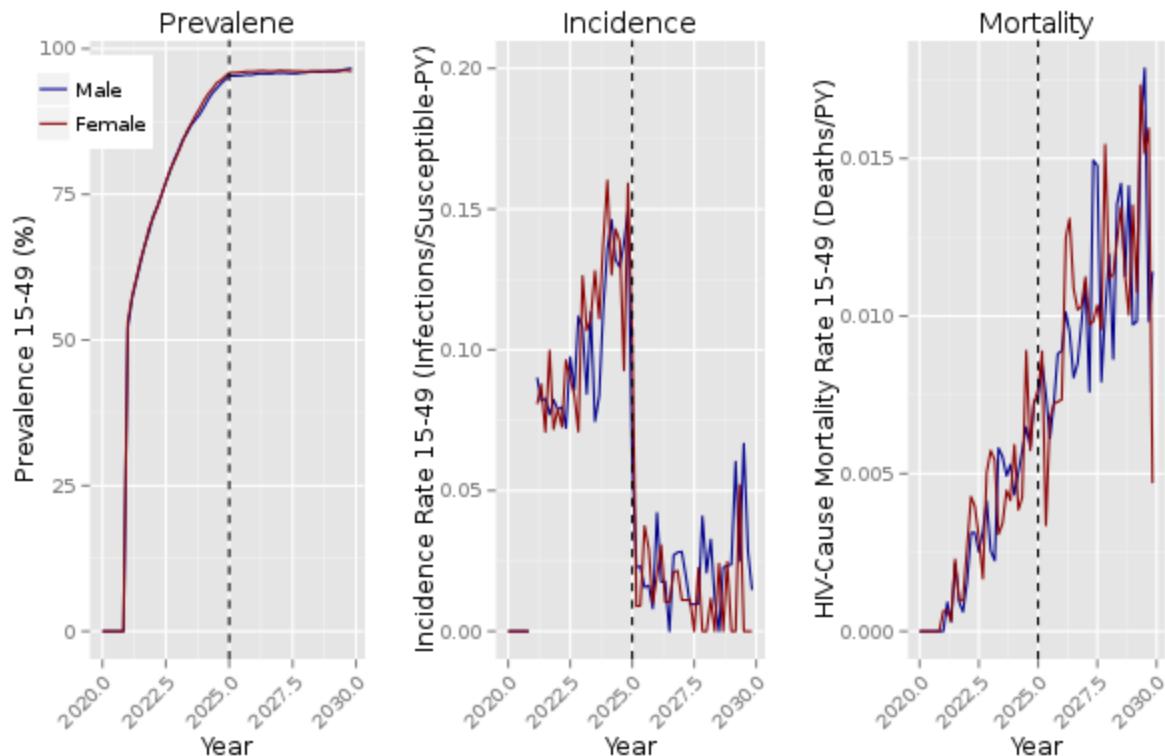
```

"Start_Year": 2025,
"Nodeset_Config": { "class": "NodeSetAll" },
"Event_Coordinator_Config":
{
    "class": "StandardInterventionDistributionEventCoordinator",
    "Demographic_Coverage": 1,

    "Intervention_Config":
    {
        "class": "ModifyStiCoInfectionStatus",
        "New_STI_CoInfection_Status": 0
    }
}
}

```

The plot below shows the HIV prevalence, incidence, and mortality after the 2025 co-infection treatment intervention:



3-f. PrEP and Vaccines

Using the generic intervention [SimpleVaccine](#), EMOD supports roll-out of Pre-Exposure Prophylaxis (PrEP) through per-act reduction of HIV acquisition. In our example, we allow only for transitory relationship formation. The relationship duration is Weibull distributed with heterogeneity and scale parameters set in the config.json file such that the mean duration is particularly long:

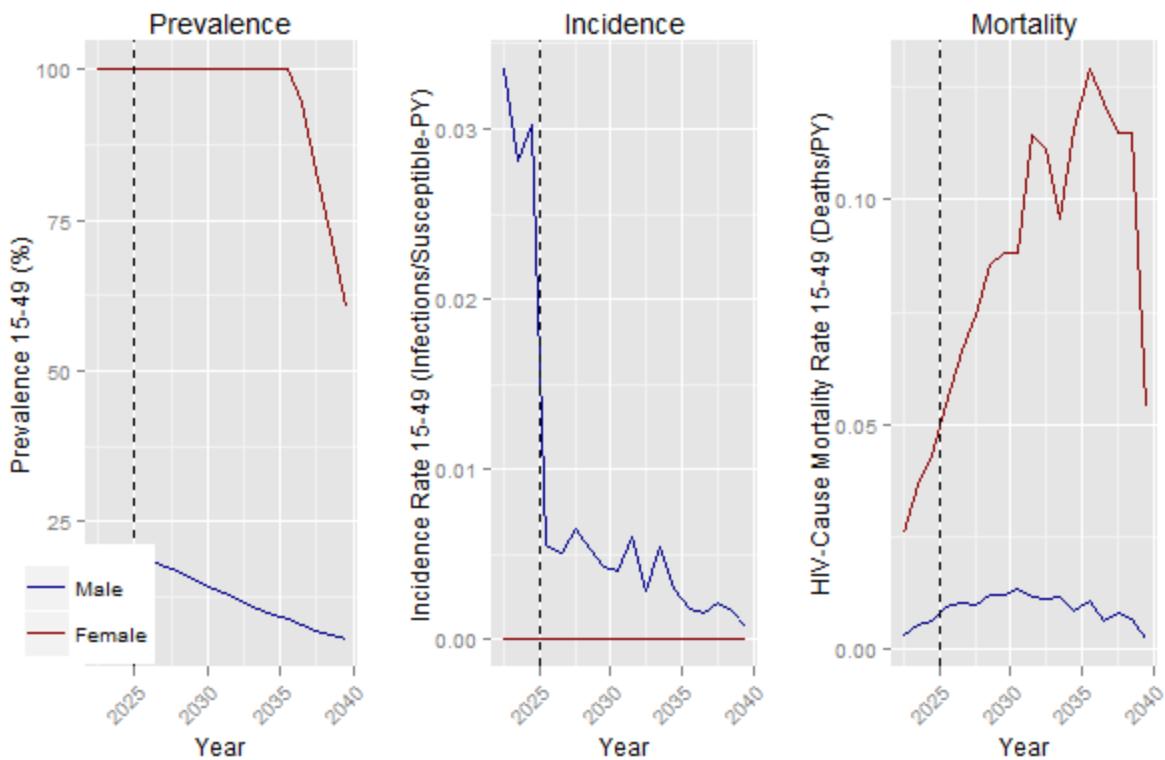
```
"Transitory_Formation_Rate_Heterosexual": 1,
"Informal_Formation_Rate_Heterosexual": 0,
"Marriage_Formation_Rate_Heterosexual": 0,
"Relationships_Transitory_Weibull_Heterogeneity" : 0.1,
"Relationships_Transitory_Weibull_Scale" : 1051025.709,
```

We seed a general epidemic, and ten years later we hand out PrEP to all individuals. We assume a 0.8 fraction of per act acquisition blocking homogeneously across the population, as given in the campaign.json:

```
{
  "class": "CampaignEventByYear",
  "Event_Name": "Give a vaccine to all in 2030",
  "Start_Year": 2030,
  "Nodeset_Config": { "class": "NodeSetAll" },
  "Event_Coordinator_Config":
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Demographic_Coverage": 1,

    "Intervention_Config":
    {
      "class": "SimpleVaccine",
      "Durability_Time_Profile": "BOXDURABILITY",
      "Primary_Decay_Time_Constant": 9000,
      "Vaccine_Type" : "AcquisitionBlocking",
      "Reduced_Acquire" : 0.8
    }
  }
}
```

The plot below shows the HIV prevalence, incidence, and mortality after the 2030 SimpleVaccine intervention:



3-g. Vertical Transmission

EMOD supports vertical transmission of HIV via mother-to-child transmission (MTCT). This feature is enabled by setting the config.json parameter `Enable_Maternal_Transmission` to 1.

```
"Enable_Maternal_Transmission": 1,
```

Because the model must link the HIV status of specific mother with the exposure of a specific child, this feature will only work when the model is simulating individual pregnancies, as configured by the following parameter:

```
"Birth_Rate_Dependence": "INDIVIDUAL_PREGNANCIES_BY_AGE_AND_YEAR"
```

When a child is born to an HIV-infected mother who is not receiving any interventions, the probability that the child will be born with an HIV infection is set by the config.json parameter `Maternal_Transmission_Probability`.

```
"Maternal_Transmission_Probability": 0.3,
```

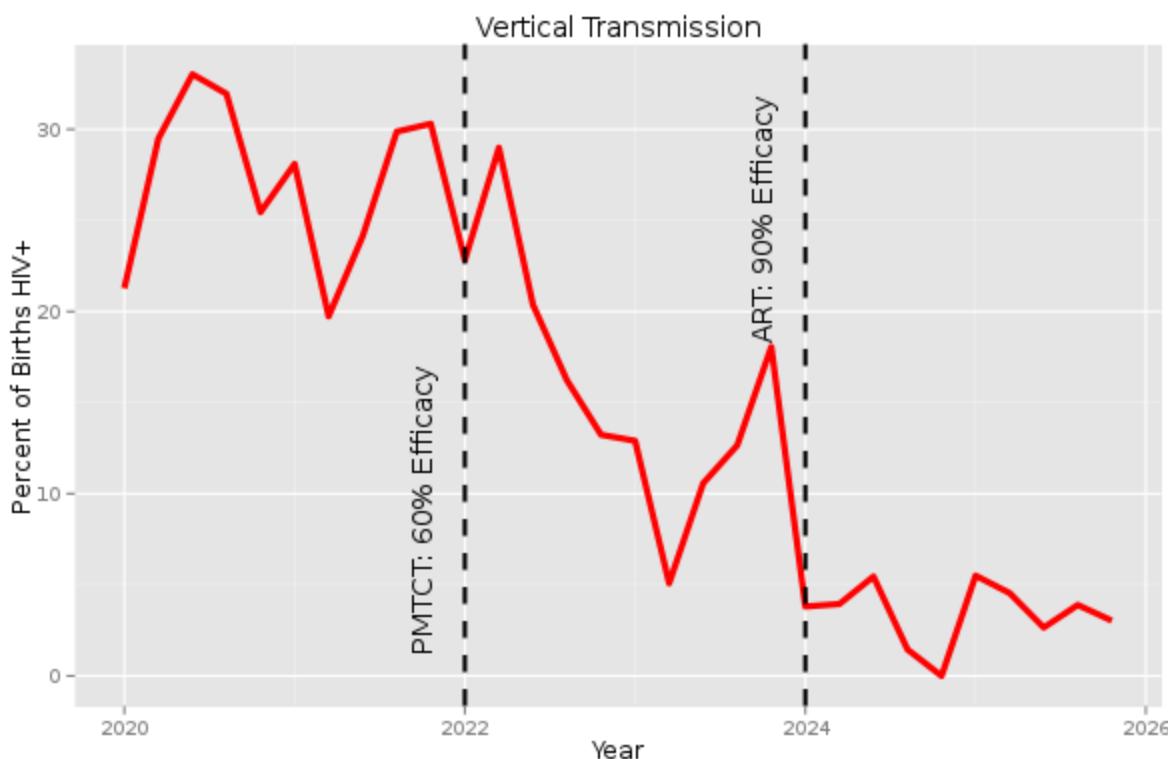
If the mother is on antiretroviral therapy at the time of childbirth, then the `Maternal_Transmission_Probability` is multiplied by a factor, `Maternal_Transmission_ART_Multiplier`.

```
"Maternal_Transmission_ART_Multiplier": 0.1
```

For example, setting `Maternal_Transmission_ART_Multiplier` to 0.1 reduces the rate of MTCT ten-fold, from 30% to 3%.

In addition, the `campaign.json` file can distribute interventions for prevention of mother-to-child transmission (PMTCT). Each intervention can be configured with its own target population, time scale of roll-out, and efficacy (expressed as a rate ratio of MTCT between women receiving the intervention and women not receiving the intervention). If a woman is receiving ART at the time that a [PMTCT](#) intervention is applied, then the preventative efficacy of ART is used to calculate the MTCT probability for that pregnancy, and the efficacy of the PMTCT intervention is ignored.

The example below shows the effect of a PMTCT intervention with 60% efficacy distributed to all females attending a 14-week antenatal care visit after 2022, followed by ART for all females after 2024. The rate of MTCT declines from 30% to 18% after 2022. The effect does not take place immediately in 2022, because women are enrolled in PMTCT in their 14th week of pregnancy (LMP), so there is a delay between enrollment and childbirth at week 40. In contrast, ART enrollment in this example does not need to be triggered by a 14-week antenatal visit, so it takes effect immediately for all childbirths after 2024. After 2024, the average MTCT probability is 3%.



HIV Tutorial 4: Health Care

In tutorials 1 through 3, you learned how to use a campaign.json file to initialize epidemics and distribute interventions such as antiretroviral therapy, voluntary male medical circumcision (VMMC), treatment and of co-infections. This tutorial will explain how to use the campaign.json file to build up a health care system.

The model will execute the healthcare process you have specified in the campaign.json file, without the need to change or recompile the EMOD source code. This allows you to systematically change aspects of the health care system using the same core model.

This tutorial has three parts.

- [4-1. Structure and Syntax of Health Care Interventions](#) provides a text description of the syntax, components, and methods for designing healthcare systems.
- [4-2. Building Blocks of a Health Care System](#) describes the available HIV interventions, delays, and decision-making tools such as diagnostics.
- [4-3. Sub-Saharan Africa Epidemic Model with Transmission and Health Care](#) shows how these interventions have been combined to represent HIV services in a generalized HIV epidemic.

Sample model input and output files have been provided to demonstrate some of the more complex components of the health care model, and for the full configuration of the sub-Saharan Africa epidemic. Additional examples demonstrating different health care model components have been provided with many of the scientifically-driven scenarios, especially [HIV Tutorial 5: Intervention Examples](#).

4-1. Structure and Syntax of Health Care Interventions

The health care specification in campaign.json is built up of JSON structures that, like blocks, can be "snapped together" by linking the outcome of one block to the trigger condition of another. The purpose of a block could include distributing an intervention, discontinuing an intervention, creating a delay, recording the current state of a biomarker, or making a choice according to time, a current biomarker, a recorded biomarker, and/or a sociodemographic category. Collectively, these building blocks define how individuals move through the healthcare process.

Each individual building block contains information about when it goes into effect, who can receive it, and what it does. These properties are defined using a nested structure, as shown in the diagram below. This scenario will introduce you to the structure syntax of the health care building blocks.



Many of the features used for HIV modeling are shared by the different disease types supported in EMOD, and are described in the [general EMOD documentation](#). This tutorial focuses on interventions that were added to EMOD to support HIV modeling.

The health care system used by an HIV simulation is configured in the campaign.json file. This file need not have to be called campaign.json: you can change the name by altering the Campaign_Filename parameter in config.json.

```
"Campaign_Filename": "campaign.json"
```

Within campaign.json are three elements: Campaign_Name (which can be any string), Use_Defaults (which is set to 1 to allow some parameters to be left out of the file, as long as those parameters have pre-configured default values), and Events, which is a JSON array containing the healthcare system building blocks. Note the square brackets following "Events", which are used to create a JSON array.

```
{
  "Use_Defaults": 1,
  "Campaign_Name": "",
  "Events": [
    {
      "Brick": "Red"
    },
    {
      "Brick": "Yellow"
    }
  ]
}
```

```

    },
    {
      
    },
  ]

```

Each of the event blocks has a nested structure that is described in the following three sections. Section A describes the outer layer, which specifies its Event_Name, when and where the event can be applied, and whether the time of the event is specified in simulation days or in calendar years. Section B describes the middle layer, which specifies the sociodemographic group being targeted. Section C describes the inner layer, which specifies what is to be distributed to those individuals and, optionally, what triggers the intervention to take effect.

4-1-a. Campaign Events: Controlling "When" and "Where"

The outer layer of the intervention blocks determines when and where the intervention takes place. For HIV modeling, the "where" functionality is used by setting the intervention class to CampaignEventByYear. This class builds on the class [CampaignEvent](#) by allowing a calendar year to be specified, as follows in this example of an outbreak occurring in 1985:

```

"class":
  "CampaignEventByYear",
  "Event_Name": "Epidemic seeding",
  "Start_Year": 1985,
  ...
  "Event_Coordinator_Config":
  {
    ...
  }

```

The Start_Year of an intervention determines when the intervention is applied. It does not need to be an integer value. For example, 1985.5 would apply an intervention midway through the year 1985. The year of each timestep in the simulation is calculated by starting the simulation at the Base_Year, which is specified in config.json, and moving forward in time by the number of days associated with each simulation timestep by the parameter Simulation_Timestep. All years have 365 days; leap years are not included.

In other EMOD diseases it is also possible to use CampaignEvent to specify the geographic nodes where the intervention is applied. Geographic nodes are not yet supported for STI and HIV simulations,

although individuals can be targeted based on [IndividualProperty](#) (e.g., by sociodemographic category or HIV risk group).

The above configuration would do something starting in simulation year 1985. Some interventions act immediately, such as the HIV outbreak example above. Others begin to listen for a trigger event that can occur any time after Start_Year. (Triggered interventions are discussed below.) Thus, the start year may or may not determine the time at which the effect of the intervention is delivered; it simply guarantees that the intervention cannot happen before Start_Year.

4-1-b. Event Coordinator: Controlling "Who"

The files for this scenario are located in the directory Scenarios\STIAndHIV\04_Health_Care\4_1_b_and_c_Property_Restriction\RestrictAtEventCoordinator

The next configuration layer is called the Event Coordinator, and is responsible for filtering individuals by age/gender, [IndividualProperty](#) (e.g., by sociodemographic category or HIV risk group). The HIV scenarios make use of the [StandardInterventionDistributionEventCoordinator](#) class of Event Coordinator. Here is an example that would apply some intervention to 75% of males between 15 and 25 years of age who have an individual property named Accessibility with value Yes:

```
"class": "StandardInterventionDistributionEventCoordinator",
"Demographic_Coverage": 0.75,
"Target_Demographic": "ExplicitAgeRangesAndGender",
"Target_Age_Min": 15,
"Target_Age_Max": 25,
"Target_Gender": "Male",
"Property_Restrictions": [ "Accessibility:Yes" ],
"Intervention_Config": {
    ...
}
```

When Target_Demographic is set to ExplicitAgeRangesAndGender as in the above example, the variables Target_Age_Min, Target_Age_Max, and Target_Gender filter potential recipients by age and gender. Other possible Target_Demographic choices include Everyone, ExplicitAgeRanges, and ExplicitGender.

The campaign.json file provided with this scenario gives another example in which VMMC is only provided to those with the property "Accessibility:Yes".

4-1-c. Intervention: Controlling "What" and "Why"

The files for this scenario are located in the directory Scenarios\STIAndHIV\04_Health_Care\4_1_b_and_c_Property_Restriction\RestrictAtNodeLevelHealthTriggeredIV

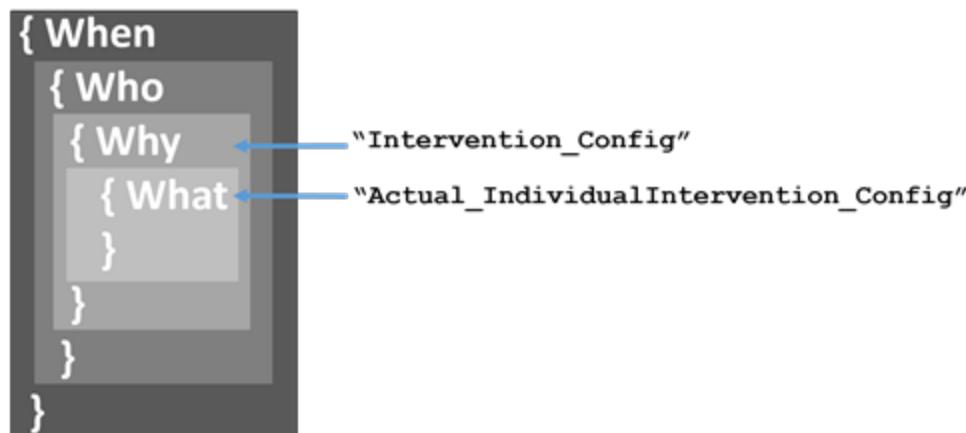
The innermost layer determines what the intervention does. As with the other layers, the inputs depend on the "class" parameter. For example, the "OutbreakIndividual" class requires a value for "Outbreak_Source."

```
"class": "OutbreakIndividual",
"Outbreak_Source": "PrevalenceIncrease"
```

In this way, each intervention can be configured as needed. If you have set Use_Defaults to 1, then some parameters can be omitted from the configuration, as long as they have default values. You can see each parameter's description, data type, ranges, and defaults in the [schema file](#). The next section of this tutorial will describe the available interventions for HIV modeling.

In addition to configuring "what" the intervention delivers, it is also possible to configure "why" the intervention is delivered by adding a trigger condition for the intervention. For example, interventions can be triggered by notifications broadcast by an individual upon some life event, such as Births (the individual's own birth), GaveBirth, NewInfectionEvent, TwelveWeeksPregnant, STIDebut, HIVSymptomatic, and EveryUpdate. It is also possible to have one intervention trigger another intervention by asking the first intervention to broadcast a unique string, and having the second intervention be triggered upon receipt of that string.

The "why" component of the intervention is optional. If it is not specified, then the intervention is applied at the time of the Start_Year or Start_Day specified in the outermost Campaign Event layer. To add a "why" component, or trigger, change the class of the "what" layer to NodeLevelHealthTriggeredIV, and add an additional layer to the intervention as follows:



The Intervention_Config layer contains information about what triggers the intervention, while the innermost Actual_IndividualIntervention_Config layer contains information about that the intervention does when it is triggered. The example below shows how to configure an intervention that is triggered by Births, an event that is broadcast by an individual on the day that he/she is born.

```
"class": "NodeLevelHealthTriggeredIV",
"Trigger_Condition": "Births",
"Property_Restrictions_Within_Node":
[
    {
        "Accessibility": "Yes"
    },
],
"Actual_IndividualIntervention_Config":
{
    ...
}
```

In the next section, you will learn about another way to achieve birth-triggered interventions using the intervention class [BirthTriggeredIV](#).

In the example above, the intervention is only distributed to those who have access to healthcare by using the property restriction "Accessibility": "Yes". Property restrictions can be placed either in the outermost CampaignEvent layer, as in the previous example, or, if used, the [NodeLevelHealthTriggeredIV](#) layer. The campaign.json file provided with this tutorial gives another example of property restriction through NodeLevelHealthTriggeredIV.

In addition to the built-in triggers such as Births, you can add your own trigger conditions by setting the Trigger_Condition field to "TriggerString", and adding a new field with any string of your choice, as follows:

```
"Trigger_Condition": "TriggerString",
"Trigger_Condition_String": "String_of_Your_Choice",
```

The String_of_Your_Choice must be added to the Listed_Events array in the config.json file. Any intervention can broadcast the event String_of_Your_Choice, and any other intervention become triggered by it using the syntax above. This enables you to "snap" together the "lego blocks" into a cascade of health care events. You will see many examples of this in the fully configured health care system in [Scenario 4-3: Sub-Saharan Africa Epidemic Model with Transmission](#) and in [Tutorial 5: Intervention Examples](#).

For convenience, some strings have been pre-configured as acceptable without having to be added to the Listed_Events array. These "whitelisted" strings contain the names of each of the Cascade_States (described in the following section), followed by the number 0 through 9. You will see many examples of these strings being used in [Tutorial 5: Intervention Examples](#).

When adding a new event, you can either use one of the unused numbers for a Cascade_State, or create your own custom string and add it to the Listed_Events array. In some of the tutorial example files, these strings have also been added to the Listed_Events list in config.json, even though this is not necessary for the specific strings that are "whitelisted."

It is also possible to have more than one possible trigger condition, including combinations of custom and built-in triggers. To do this, set the `Trigger_Condition` to "TriggerList" and list the trigger conditions as follows:

```
"Trigger_Condition": "TriggerList",
"Trigger_Condition_List": [ "HIVSymptomatic", "TwelveWeeksPregnant", ... ]
```

4-1-d. Categorizing Stages of Health Care with Cascade State

The innermost layer of each intervention has a field called `Cascade_State`, which is used to set the category of healthcare associated with the intervention. Examples of categories include repeat testing, linking to ART, or being on ART. The config.json parameter `Valid_Cascade_States` lists all possible Cascade States in a simulation. To add a new category of health care, choose a name and add it to the `Valid_Cascade_States`.

As soon as an intervention has been applied to an individual, the individual's Cascade State is set to the one listed under `Cascade_State` for that intervention block. The individual is considered to be in this state until another intervention with a different Cascade State is applied.

It is possible to change an individual's Cascade State without applying any other interventions. To do so, use the intervention class [HIVSetCascadeState](#), as demonstrated below.

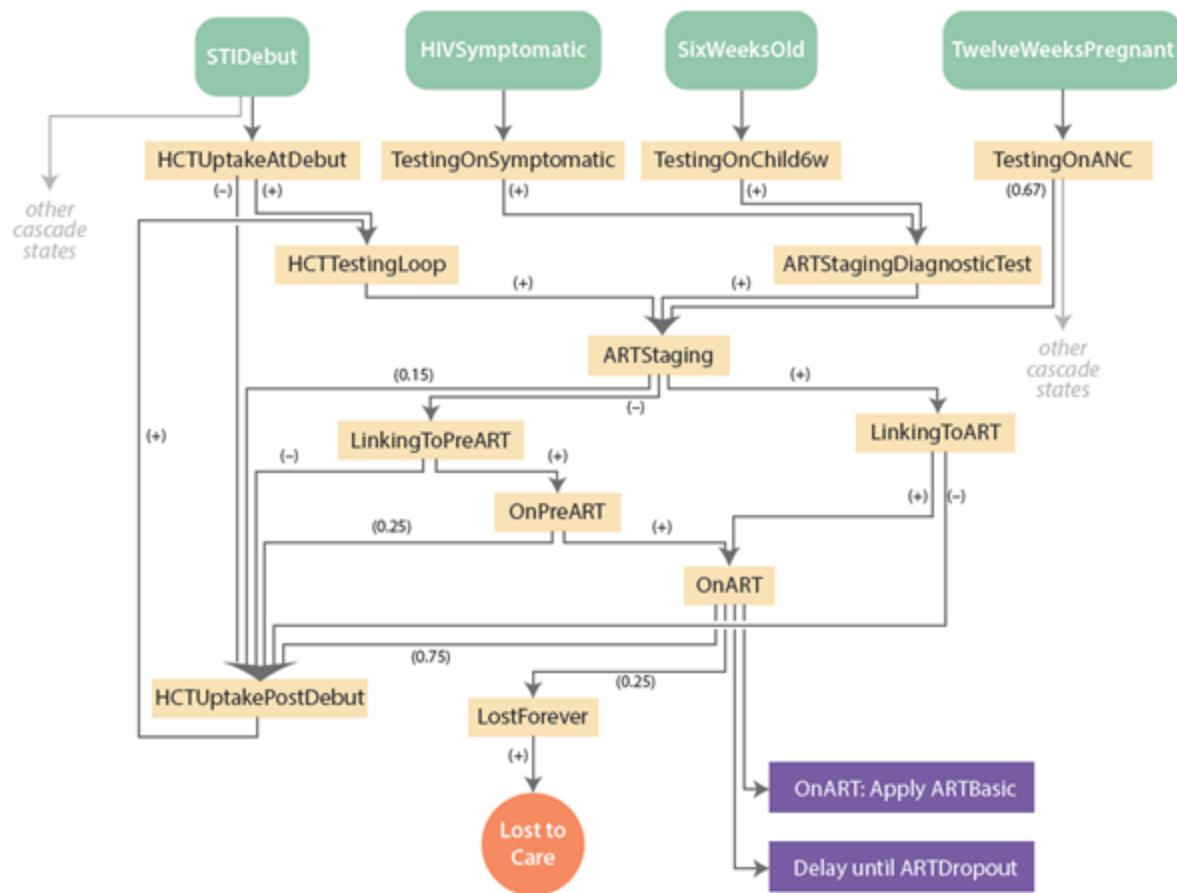
```
{
  ...
  {
    "class": "HIVSetCascadeState",
    "Abort_States": [],
    "Cascade_State": "LostForever",
    "Event_Or_Config": "Event",
    "Positive_Diagnosis_Event": "Cascade_State_Has_Been_Set"
  }
  ...
}
```

Multiple health care building blocks can be assigned the same `Cascade_State`. For example, ART staging includes a number of steps, including a potential delay, a potential probability of loss to care, and a choice between ART initiation and pre-ART monitoring based on multiple factors (the year, the individual's CD4 count, clinical presentation, and demographic factors).

Grouping these steps into a Cascade State enables easier tracking of individuals and visualization of the health care system. At the end of this scenario, a sub-Saharan Africa model configuration will be demonstrated, and the detailed health care system will be visualized by grouping the steps by `Cascade_State`.

In the diagram, provides a preview of visualizing a health care system grouped by cascade state. Triggers for entry into care are represented by green rectangles, interventions that belong to cascade states

are grouped into yellow rectangles, and the actual intervention being applied to the individual is represented with a purple rectangle -- e.g., STI infection, PMTCT, ART initiation, or ART discontinuation. The red circle indicates that a block does not link to any specific intervention or outcome.



Another use of `Cascade_State` is to determine which categories of care can be accessed by other categories of care. This capability is explained and demonstrated in the following section.

4-1-e. Using cascade state to control future health seeking

The files for this scenario are located in the directory `Scenarios\STIAndHIV\04_Health_Care\4_1_e_CascadeState_and_AbortState`

In some cases, access to one form of health care may prevent individuals from re-accessing another form of health care. For example, it may be desirable to prevent individuals from re-testing for HIV while currently enrolled in ART. To control this, the model allows each intervention to have a list of `Cascade_States` that are incompatible with the intervention. This list is called `Abort_States`.

Located in the innermost intervention layer alongside `Cascade_State`, the `Abort_States` array is a list of `Cascade_States` that must be a subset of the config.json array `Valid_Cascade_States`. At the

time that the intervention is supposed to be applied, the individual's current `Cascade_State` is compared to the new intervention's `Abort_States`. If the `Cascade_State` matches any of the `Abort_States`, then the intervention will not be applied.

To demonstrate this usage of `Cascade_State` and `Abort_States`, this scenario provides a simple example with only two `Valid_Cascade_States`, called "Infinite_Loop" and "Abort_Infinite_Loop".

The campaign.json file contains three intervention blocks. The first block causes all individuals to broadcast "Loop_Entry_InitialPopulation" on the first day of the simulation.

```
{
  "Description": "Drive initial population into a loop",
  "class": "CampaignEvent",
  "Start_Day": 1,
  "Nodeset_Config": { "class": "NodeSetAll" },
  "Event_Coordinator_Config": {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Intervention_Config": {
      "class": "BroadcastEvent",
      "Broadcast_Event": "Loop_Entry_InitialPopulation"
    }
  }
},
```

The second intervention block causes individuals to wait one year before broadcasting "Done_Waiting", and also sets the `Cascade_State` to "Infinite_Loop". Both "Loop_Entry_InitialPopulation" and "Done_Waiting" are triggers for the second intervention, and the intervention also has one `Abort_State` called "Abort_Infinite_Loop".

```
{
  "Description": "Wait one year",
  "class": "CampaignEvent",
  "Start_Day": 1,
  "Nodeset_Config": { "class": "NodeSetAll" },
  "Event_Coordinator_Config": {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Demographic_Coverage": 1,
    "Intervention_Config": {
      "class": "NodeLevelHealthTriggeredIV",
      "Trigger_Condition": "TriggerList",
      "Trigger_Condition_List": [
        "Loop_Entry_InitialPopulation",
        "Loop_Entry_Birth",
        "Done_Waiting"
      ],
      "Actual_IndividualIntervention_Config":
```

```

        {
            "class": "HIVDelayedIntervention",
            "Abort_States": [ "Abort_Infinite_Loop" ],
            "Cascade_State": "Infinite_Loop",
            "Delay_Distribution": "FIXED_DURATION",
            "Delay_Period": 365,
            "Broadcast_Event": "Done_Waiting"
        }
    }
},

```

The third intervention is also triggered by "Done_Waiting" and assigns the Cascade_State "Abort_Infinite_Loop". This intervention has a Start_Day of 1095, so it can only go into effect three years after the start of the simulation.

```

{
    "Description": "Abort the infinite loop, starting 3 years into the simulation",
    "class": "CampaignEvent",
    "Start_Day": 1095,
    "Nodeset_Config": { "class": "NodeSetAll" },
    "Event_Coordinator_Config":
    {
        "class": "StandardInterventionDistributionEventCoordinator",
        "Demographic_Coverage": 1,
        "Intervention_Config":
        {
            "class": "NodeLevelHealthTriggeredIV",
            "Trigger_Condition": "TriggerString",
            "Trigger_Condition_String": "Done_Waiting",
            "Actual_IndividualIntervention_Config":
            {
                "class": "HIVSetCascadeState",
                "Abort_States": [ ],
                "Cascade_State": "Abort_Infinite_Loop"
            }
        }
    }
}

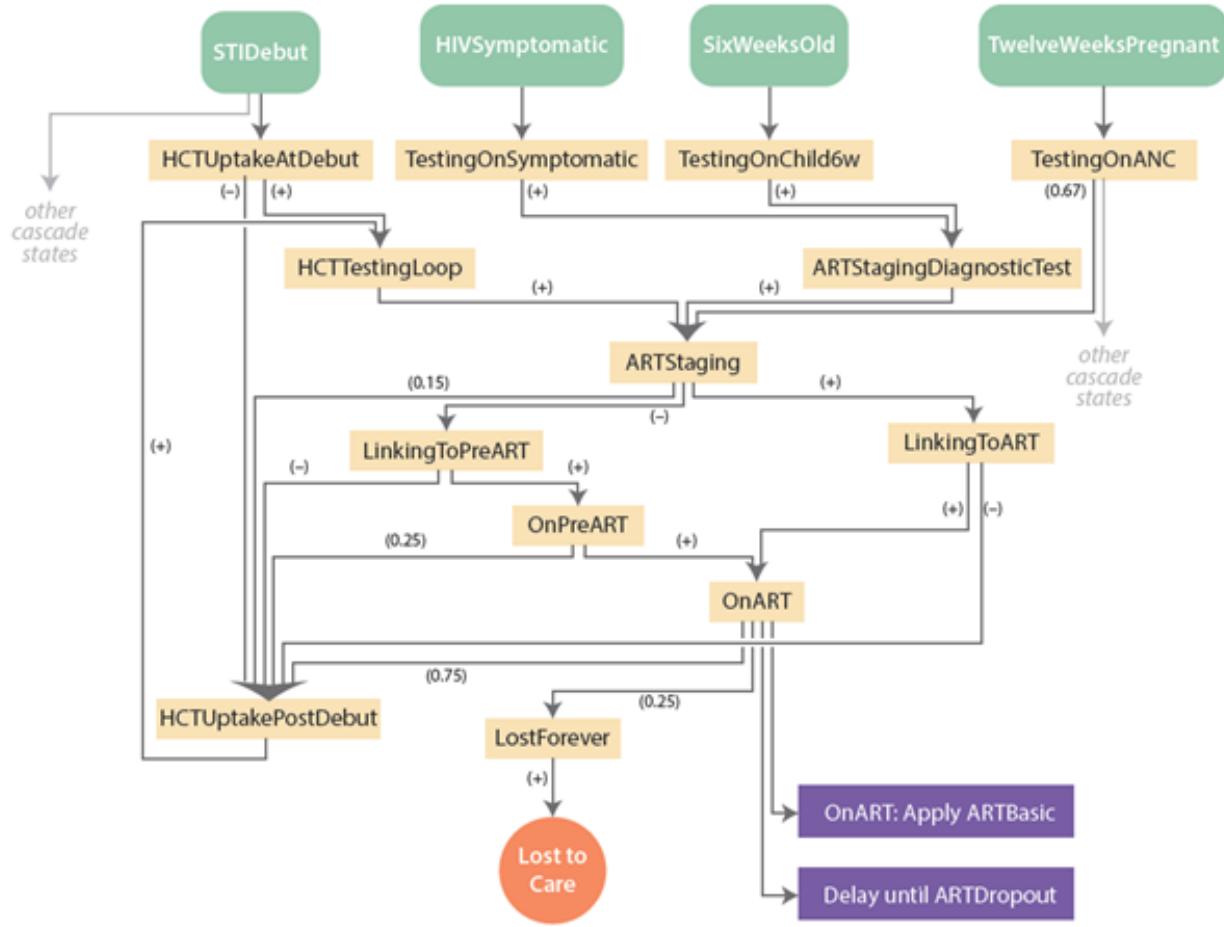
```

The Cascade_State "Abort_Infinite_Loop" is broadcast by the third intervention, and is in the Abort_States list of the second intervention. When the third intervention reaches its Start_Day of 1095, it is able to set the Cascade_State to one that prevents the second intervention from being applied.

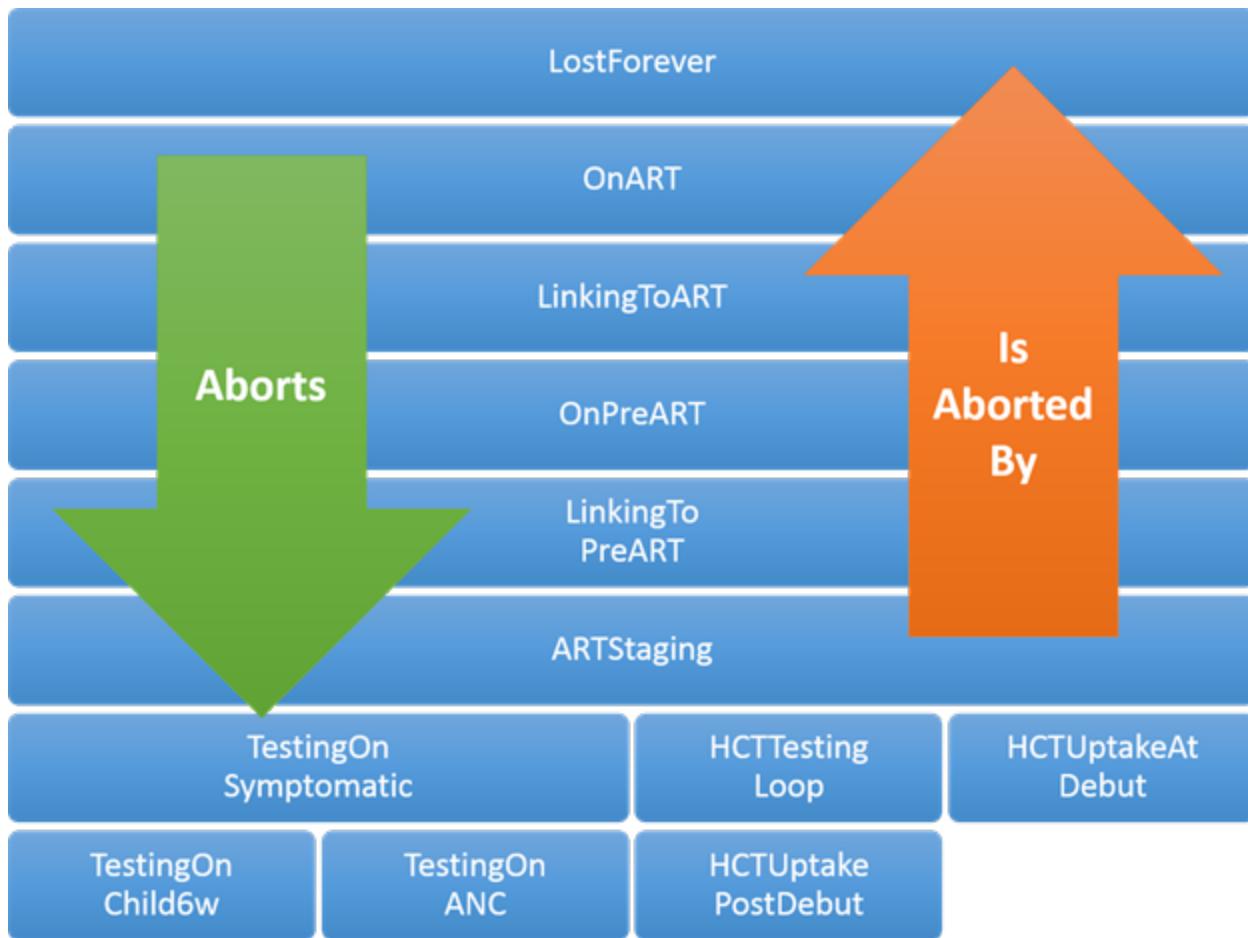
There is no way to control the order in which interventions fire. Both the second and the third interventions will fire in response to "Done_Waiting." If the second intervention fires first, then individuals will wait a fourth year of delay time before exiting the infinite loop due to the incompatibility of the Cascade_

States. If the third intervention fires first, then the incompatibility will be detected on Day 1095 and the second intervention will not be applied for a fourth year. These events can be logged using the event recorder described in [Appendix A](#), and visualized using the event recorder plotting scripts in R or Python, described in [Appendix B-4](#). (For additional details on configuring this report, see [EventRecorder Report File](#) in the File Format Layout Descriptions section of the online documentation.)

In the previous section, you received a preview of the ART-related portion of the configured health care system:



In this configuration, Abort_States are used in a hierarchical pattern. For example, LostForever is a terminal state that is listed in the Abort_States of every other intervention. OnART is listed by all interventions other than LostForever to prevent redundant access to care while already receiving ART. Linking to ART aborts all interventions except LostForever and OnART, and so forth. The hierarchy is depicted below.



Congratulations! You have learned the structure and syntax and health care building blocks. Now you are ready to learn the specific interventions available for HIV modeling.

4-2. Building Blocks of a Health Care System

A number of interventions have been built for the purpose of modeling HIV health care systems and interventions. The aim of this section is to describe each of the HIV interventions in four categories: standard interventions, diagnostics, decisions, and delays.

Some of the features used by HIV are shared with other diseases, and are not documented in detail here. You may find the following EMOD documentation topics to be helpful.

Intervention Class	Purpose
OutbreakIndividual	Start an HIV epidemic by seeding the first infections.
NodeLevelHealthTriggeredIV	Link interventions together by allowing an intervention to be triggered by an event.. Events can be broadcast from individuals within the model, or can be broadcast by other interventions.

Intervention Class	Purpose
BirthTriggeredIV	Allows an intervention to be triggered when an individual is born. Another way to achieve this functionality is to use NodeLevelHealthTriggeredIV with Trigger_Condition set to Births.
PropertyValueChanger	Change an IndividualProperty (from one value to another).
SimpleVaccine	Apply a transmission or acquisition blocking vaccine. Can be used to model HIV pre-exposure prophylaxis (PrEP).

4-2-1. Standard Interventions

Standard interventions can be thought of as acting directly on an individual, as opposed to diagnostics/decisions/delays, which mainly govern the process by which individuals access standard interventions.

4-2-1-a. Antiretroviral Therapy (ART)

Antiretroviral therapy (ART) is provided to the individual using the [ARTBasic](#) intervention. This ART implementation takes only one parameter that governs whether or not the recipient will achieve "Viral_Suppression."

```
"Viral_Suppression": 1,
```

The default value for Viral_Suppression is 1. The effect of ART and Viral_Suppression on mortality, CD4 count, and transmission are described in [Scenario3-c](#). [Scenario 2-f](#) illustrates the effect of applying and discontinuing ART.

Note that if the ARTBasic intervention is distributed to a HIV-negative individual, the intervention has no effect on the individual. Preventative benefits of antiretroviral medications must be configured through [SimpleVaccine](#) instead of ARTBasic.

4-2-1-b. Voluntary Male Medical Circumcision (VMMC)

Voluntary medical male circumcision (VMMC) is achieved using the [MaleCircumcision](#) class. The class has no configurable parameters, and will not be distributed to females even if the Target_Demographic includes females. Distribution of MaleCircumcision to males results in a multiplicative reduction in the per-act transmission probability. The multiplicative factor is configured by the following config.json parameter.

```
"Circumcision_Reduced_Acquire": 0.6,
```

Additional details about this intervention are provided in [Scenario 3](#) and examples of configuring trends in VMMC by age and over time are provided in [Scenario 5-1](#).

4-2-1-c. Prevention of Mother to Child Transmission

Mother-to-child transmission (MTCT) can be included in EMOD simulations, but will only work when the model is simulating individual pregnancies, as configured by the following parameter.

```
"Birth_Rate_Dependence": "INDIVIDUAL_PREGNANCIES_BY_AGE_AND_YEAR",
```

The probability of MTCT for each live birth depends on the ART status of the mother. The configuration of these probabilities is described in [Scenario 3-g](#) and is configured with the following parameters in config.json:

```
"Enable_Maternal_Transmission": 1,
"Maternal_Transmission_Probability": 0.30,
"Maternal_Transmission_ART_Multiplier": 0.10,
```

The [PMTCT](#) intervention modifies the probability of mother to child transmission from an HIV-infected mother who is not on suppressive ART. This class takes a single parameter that determines the efficacy of vertical transmission blocking.

```
{
  ...
  {
    "class": "PMTCT",
    "Efficacy": 0.9
  }
}
```

An efficacy of 0.9, as in the above example, will multiply the maternal transmission probability without suppressive ART by 0.1. When Maternal_Transmission_Probability is configured to 0.3, as above, this results in an MTCT probability of $0.30 \times 0.1 = 3\%$.

The PMTCT intervention is intended to be used in combination with a [NodeLevelHealthTriggeredIV](#) that triggers on Pregnant, TwelveWeeksPregnant or FourteenWeeksPregnant. The Decisions section of this tutorial describes how one of these triggers could feed into a piecewise constant, piecewise linear, or sigmoidal probability that determines if an individual should receive PMTCT.

The MTCT rate is independently calculated for each pregnancy because the PMTCT intervention automatically expires 40 weeks after it is distributed. At this time, the efficacy is reset to 0.

Using the capabilities of health care Decisions, it is possible to configure multiple PMTCT options with different levels of efficacy, without allowing the same pregnancy to receive PMTCT multiple times.

However, if PMTCT is accidentally applied multiple times during the same pregnancy, only the higher efficacy is retained.

4-2-1-d. STI Co-Infection and STI Treatment

[Scenario 3-e](#) describes how a fraction of the population is given a quasi-static co-infection flag that simply modifies the transmission probability of a STI or HIV infection. There are two ways to distribute the co-infection flag.

First, you can set the following config.json parameter to distribute the flag to a fixed fraction of the population.

```
"STI_Coinfection_Probability": 0.05,
```

The above parameter setting would result in 5% of the population receiving the co-infection flag. Note that this distribution applies both to the initial population and to individuals born during the simulation.

The second method of distributing the STI co-infection flag is via the campaign.json file through the intervention class [ModifyStiCoInfectionStatus](#). This feature allows for demographic targeting of STI co-infections, and allows for treatment of STI co-infections.

The ModifyStiCoInfectionStatus class takes a single parameter that determines if the co-infection flag should be set (creating STI co-infections) or cleared (treating co-infections). If an individual already has the New_STI_CoInfection_Status, then the intervention has no effect.

```
{
  ...
  {
    "class": "ModifyStiCoInfectionStatus",
    "New_STI_CoInfection_Status": 1
  }
}
```

For episodic co-infections such as HSV-2 or bacterial vaginosis, it is possible to use the delay loop pattern described later in this tutorial to configure episodic increases in susceptibility. EMOD offers many choices for delay distributions and heterogeneities.

4-2-1-e. Condom Usage

Similarly to STI co-infection, condom usage can be configured through the config.json file and also modified through interventions in the campaign.json file. As described in [Scenario 3-d](#), the probability of condom usage can be different for each relationship type and varies sigmoidally over time.

The [STIBarrier](#) intervention overrides the config.json probabilities with different parameters to govern the sigmoid time-varying probability of condom usage:

```
{
  ...
  {
    "class": "STIBarrier",
    "Relationship_Type": "Transitory",
    "Early": 0.1,
    "Late": 0.7,
    "MidYear": 2020,
    "Rate": 0.5
  }
}
```

For individuals receiving the STIBarrier intervention, the "Early," "Late," "MidYear," and "Rate" parameters replace the config.json condom sigmoid parameters for the specified relationship type. Reversion to default parameters can only be accomplished by a subsequent STIBarrier intervention that replaces the parameters with the config.json values.

Within a relationship, the probability of using a condom for each coital act is determined by evaluating the sigmoid for the corresponding year and relationship type. Because STIBarrier allows you to modify the sigmoid parameters, it is possible that the two individuals in the relationship will have differing condom usage probabilities. In this case, the condom usage probability of the male partner is used.

4-2-2. Diagnostics

Diagnostics are used to route individuals to the interventions described above.

4-2-2-a. Testing for HIV

There are three varieties of diagnostics to determine HIV status.

[SimpleDiagnostic](#) is available for all diseases supported by EMOD. When running STI_SIM or HIV_SIM, it diagnoses with a desired sensitivity and specificity whether the individual is infected. A limitation of SimpleDiagnostic is that an action can only be taken upon positive diagnosis. For example, in order to use SimpleDiagnosis to provide VMMC to HIV-negative men, you would have to set the sensitivity and specificity of the test to zero, which would invert the outcome of every test (providing a "positive" result for HIV-negative individuals). There is no way to link two different outcomes, one for positive and one for negative diagnosis.

```
{
  ...
  {
    "class": "SimpleDiagnostic",
    ...
    "Event_Or_Config": "Event",
    "Positive_Diagnosis_Event": "SomeEventOfYourChoice"
  }
}
```

```
    }
}
```

[HIVSimpleDiagnostic](#) extends the generic SimpleDiagnostic to allow for different actions to be taken upon positive and negative diagnosis. In [Scenario 5-1](#), you will see how this functionality can be used to provide HIV testing that leads to either treatment or prevention services, depending on the outcome of the test. HIVSimpleDiagnostic also differs from SimpleDiagnostic in its ability to associate with a Cascade_State and to include Abort_States to prevent multiple entries into care, as described earlier in this tutorial.

The following template illustrates the features added by HIVSimpleDiagnostic:

```
{
  ...
  {
    "class": "HIVSimpleDiagnostic",

    "Cascade_State": "Example",
    "Abort_States": [
      "AbortExample",
      ...
    ],
    "Event_Or_Config": "Event",
    "Positive_Diagnosis_Event": "BroadcastThisIfPositive",
    "Negative_Diagnosis_Event": "BroadcastThisIfNegative",
  }
}
```

[HVRapidHIVDiagnostic](#) has the features of HIVSimpleDiagnostic, and also updates the individual's knowledge of HIV status. This could potentially change the individual's future access to ART, sero-sorting behavior, and future testing behavior. This diagnostic should be chosen only if you wish to include the effects of knowledge of status as part of the impact of the intervention.

4-2-2-b. Measuring CD4 count

The [HIVDrawBlood](#) intervention is analogous to performing phlebotomy. It logs an HIV-infected individual's current CD4 count to their medical chart for later use by the CD4-dependent ART eligibility diagnostic and for model output reporting. The outcome of an HIVDrawBlood is always considered a "positive" diagnosis, so there is no sense in including a Negative_Diagnosis_Config or Negative_Diagnosis_Event.

```
{
  ...
  {
```

```
    "class": "HIVDrawBlood",
    "Abort_States": [ ],
    "Cascade_State": "ARTStaging",

    "Event_Or_Config": "Event",
    "Positive_Diagnosis_Event": "ARTStaging1"
}
...
}
```

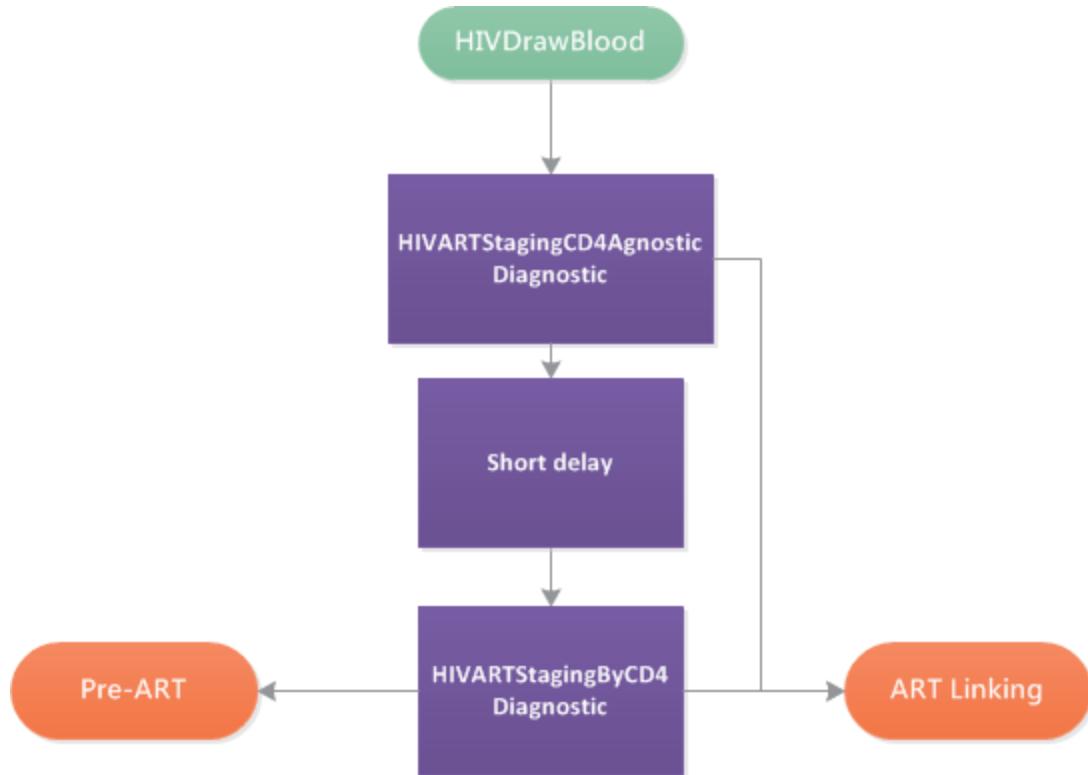
It is important to include an HIVDrawBlood intervention ahead of CD4-dependent ART staging, to ensure that a CD4 count has been performed prior to determination of eligibility.

4-2-2-c. Determining ART Eligibility

The files for this scenario are located in the directory Scenarios\STIAndHIV\04_Health_Care\4_2_2_c_ART_Eligibility

Eligibility to receive antiretroviral therapy is determined by two related interventions, [HIVARTStagingCD4AgnosticDiagnostic](#) and [HIVARTStagingCD4Diagnostic](#). The CD4-agnostic variant evaluates ART eligibility using factors that do not depend on CD4 count such as age, WHO clinical stage, TB, and pregnancy. The by-CD4 intervention determines eligibility using the lowest-ever CD4 result recorded using HIVDrawBlood.

The diagram below illustrates how the two ART staging diagnostics can be integrated into ART staging. Loss to follow-up is not illustrated below, but can be added using blocks covered later in this tutorial, such as [HIVRandomChoice](#).



If a program does not routinely perform CD4 counts for those eligible by non-CD4 criteria, then the order of the blood draw and the CD4-agnostic eligibility can be reversed so that a blood draw is recorded to the medical chart only when needed. The effect on model output would include reduced numbers of CD4 tests performed and an altered distribution of CD4 counts at ART initiation.

A typical HIVARTStagingCD4AgnosticDiagnostic is shown in the following campaign.json snippet. The years and values should be set according to the history and projected future of treatment guidelines in the setting being modeled.

```
{
  ...
  {
    "class": "HIVARTStagingCD4AgnosticDiagnostic",
    "Adult_Treatment_Age": 5,
    "Adult_By_WHO_Stage": {
      "Times": [2004, 2011.8],
      "Values": [4, 3]
    },
    "Adult_By_TB": {
      "Times": [2013.2],
      "Values": [1]
    }
  }
}
```

```

"Adult_By_Pregnant": {
    "Times": [2013.2],
    "Values": [1]
},

"Child_Treat_Under_Age_In_Years_Threshold": {
    "Times": [2010.34, 2013.2],
    "Values": [1, 5]
},

"Child_By_WHO_Stage": {
    "Times": [2010, 2011.8],
    "Values": [3, 2]
},

"Child_By_TB": {
    "Times": [2004],
    "Values": [0]
},

"Abort_States": [ ],
"Cascade_State": "ARTStaging",

"Event_Or_Config": "Event",
"Negative_Diagnosis_Event": "Not_ART_Eligible_by_CD4AgnosticDiagnostic"
}
...
}

```

The age cutoff for "adults" is determined by `Adult_Treatment_Age`, which is in years. Eligibility for individuals younger than this age is determined with the variables preceded by "Child_", whereas eligibility for individuals older than this age is determined with the variables preceded by "Adult_".

Other than `Adult_Treatment_Age`, each of the criteria contains a pair of `Times` and `Values`. `Times` indicates the years when guidelines change, and do not have to be integer values. `Values` are held constant between `Times` so that guidelines change only at the points in time indicated by `Times`.

The CD4-agnostic criteria by which adults can be deemed eligible for ART are WHO stage, tuberculosis, and pregnancy. Each of these criteria can vary in time. Eligibility by TB and pregnancy is either 0, for not eligible, or 1, for eligible. The value before the left-most year in `Times` being assumed as 0 (not eligible). Eligibility by WHO stage similarly varies in time, but here the default value used before the first year in the `Times` array is 6, meaning that no individuals will be eligible by WHO stage (since the maximum is 4).

For pediatric ART, the CD4-agnostic eligibility criteria include age, WHO stage, and TB. WHO stage and TB operate as above. Children under the age specified in the values of the `Child_Treat_Under_Age_In_Years_Threshold` are always considered eligible.

Once eligibility has been determined, you can choose to broadcast an event on positive or negative diagnosis, or nest an intervention in the `Positive_Diagnosis_Config`.

Configuration for [HIVARTStagingByCD4Diagnostic](#) is based on the simulation year CD4 and count, and can be configured differently for individuals with active TB or pregnancy. Similarly to the CD4-agnostic eligibility, each of these thresholds can vary in time in a piecewise-constant manner. Before the first value in the `Times` array, a default value of zero is assumed.

```
{
  ...
  {
    "class": "HIVARTStagingByCD4Diagnostic",

    "Threshold": {
      "Times": [2004, 2011.8, 2015],
      "Values": [200, 350, 500]
    },

    "If_Active_TB": {
      "Times": [2010.34],
      "Values": [350]
    },

    "If_Pregnant": {
      "Times": [2010.34],
      "Values": [350]
    },

    "Abort_States": [ ],
    "Cascade_State": "ARTStaging",

    "Event_Or_Config": "Event",
    "Positive_Diagnosis_Event": "ART_Eligible_by_CD4DependentDiagnostic",
    "Negative_Diagnosis_Event": "Not_ART_Eligible"
  }
  ...
}
```

Remember that unlike the `CD4Diagnostic`, the `HIVARTStagingByCD4Diagnostic` uses the lowest-ever recorded CD4 count based on the medical history created with `HIVDrawBlood`. Universal ART eligibility can be achieved by setting the value of `Adult_By_WHO_Stage` to 0 in the `HIVARTStagingCD4AgnosticDiagnostic`, or by setting the CD4 threshold to a large value in the `HIVARTStagingByCD4Diagnostic`.

gingByCD4Diagnostic. The former method assumes that universal eligibility will eliminate the prerequisite for a CD4 count prior to ART initiation.

[Scenario 5-2](#) explores this difference and describes other ways to configure the potential impact of universal ART eligibility.

4-2-3. Decisions

In addition to diagnostics, EMOD has other building blocks that result in a decision being made based on a time, an individual's current state, or just a random coin flip. The decision blocks use similar syntax to the diagnostic blocks, with different outcomes resulting from positive or negative "diagnosis." Some even have 'diagnostic' in their names -- such as AgeDiagnostic -- even though they are do not represent a diagnostic laboratory test in the literal sense.

4-2-3-a. Random Choice

Individuals can make a choice based on a random coin flip (or dice roll, for >2 choices) using the [HIVRandomChoice](#) intervention class. HIVRandomChoice supports Cascade_State and Abort_States. It adds a Choices array with configurable probabilities of choosing each outcome. In the example below, ARTStaging2 will be broadcast 25% of the time, whereas HCTTestingLoop3 will be broadcast the remaining 75% of the time. You can list more than two choices. If the sum of the probabilities is not equal to 1, then the model will automatically normalize their sum to 1, keeping their proportions the same.

```
{  
  ...  
  {  
    "class": "HIVRandomChoice",  
    "Abort_States": [ "LostForever", "OnART", ... ],  
    "Cascade_State": "HCTTestingLoop",  
    "Choices":  
    {  
      "ARTStaging2": 0.25,  
      "HCTTestingLoop3": 0.75,  
    }  
    ...  
  }  
  ...  
}
```

4-2-3-b. Making Decisions According to Most Recent CD4 Count

The [CD4Diagnostic](#) makes a decision according to an individual's current CD4 count. Note the difference between CD4Diagnostic and [HIVARTStagingCD4Diagnostic](#) -- the former uses the current CD4 count at the time of the diagnostic, while the latter uses the lowest-ever recorded CD4 count based on the medical history created with [HIVDrawBlood](#).

Note that the Low and High age ranges need not be exclusive. The EMOD model compares the age of the individual to each entry of the array, and broadcasts each compatible event. Thus, overlapping ranges could result in multiple Event outcomes.

```
{
  ...
  {
    "class": "CD4Diagnostic",
    "CD4_Thresholds": [
      {
        "Low": 0,
        "High": 200,
        "Event": "CD4_Under_200"
      },
      {
        "Low": 200,
        "High": 350,
        "Event": "CD4_200_to_350"
      },
      {
        "Low": 500,
        "High": 10000,
        "Event": "CD4_Above_500"
      }
    ]
  }
  ...
}
```

4-2-3-c. Making Decisions According to Calendar Time

Time-varying probability blocks allow you to configure a probability that varies with simulation year. Because they build off the EMOD diagnostics capabilities, these blocks have two possible outcomes: a "positive" diagnosis event and a "negative" diagnosis event. The probability of "positive" versus "negative" diagnosis over time can take on any functional form you wish.

If the desired functional form over time is sigmoid (logistic), then you can use the [HIVSigmoidByYearAndSexDiagnostic](#). This block enables you to configure a "positive diagnosis" probability that varies sigmoidally in time while also supporting the Abort_States and Cascade_State. Four parameters define the sigmoid trend: the left asymptote of probability is Ramp_Min, the right asymptote is Ramp_Max, the time of the infection point is Ramp_Midyear, and the rate parameter related to the slope at the inflection point is Ramp_Rate. For more information about these parameters, see the Excel sheet provided in [Scenario 3d](#).

```
{
  ...
  {
    "class": "HIVSigmoidByYearAndSexDiagnostic",
    "Cascade_State": "",
    "Abort_States": [],
    "Ramp_Min": 0.0,
    "Ramp_Max": 0.3,
    "Ramp_MidYear": 2002.0,
    "Ramp_Rate": 0.5,
    "Positive_Diagnosis_Event": "HIVNeedsMaleCircumcision"
  }
  ...
}
```

For any other functional form over time, use HIVPiecewiseByYearAndSexDiagnostic

[HIVPiecewiseByYearAndSexDiagnostic](#). This class supports piecewise constant (stairs) and piecewise-linear probability functions of time.

The Time_Value_Map pairs an array of Times with an array of Values, which allows for a time-variable probability that can take on any shape over time. The Times and Values must be of equal length, and can be as short as a single value each. Times must be monotonically increasing.

When queried at a simulation year corresponding to one of the listed Times, the probability will match the corresponding Value. When queried in between listed Times, it either returns the value for the most recent past time (when Interpolation_Order is 0) or linearly interpolates Values between Times (when Interpolation_Order is 1).

When queried earlier than the first listed Time, it returns the Default value. Values before the first time receive Default_Value. If Default_Value is not specified, it is assumed to be zero. When queried after the last Time in the list, it returns the last Value.

The Female_Multiplier provides you with a simple way to make the probability vary by gender. A value of 2 for this parameter would result in females having double the probability of receiving the positive result. You may find this easier than creating two separate blocks by gender.

```
{
  ...
  {
    "class": "HIVPiecewiseByYearAndSexDiagnostic",
    "Abort_States": [ "LostForever", "OnART", "LinkingToART", ... ],
    "Cascade_State": "TestingOnChild6w",

    "Default_Value": 0,
    "Interpolation_Order": 1,
```

```

    "Time_Value_Map" :
    {
        "Times": [2004, 2005, 2006, ...],
        "Values": [0, 0.03, 0.1, ...]
    },
    "Female_Multiplier": 2,
    "Event_Or_Config": "Event",
    "Positive_Diagnosis_Event": "ARTStaging0"
}
...
}

```

It is also possible to apply the intervention to only one gender using the [Event Coordinator functionality](#) described previously.

4-2-3-d. Making Decisions According to Current Age

The [AgeDiagnostic](#) contains an Age_Thresholds array. Each entry in the array contains a "Low," "High," and "Event." If the age of the individual is greater than or equal to the Low value and less than the High value, the corresponding Event will be broadcast. This pattern is also used in the CD4Diagnostic.

Note that the Low and High age ranges need not be exclusive. The EMOD model compares the age of the individual to each entry of the array, and broadcasts each compatible event. Thus, overlapping ranges can result in multiple "Event" outcomes.

```

{
...
{
    "class": "AgeDiagnostic",
    "Age_Thresholds":
    [
        {
            "Low": 0,
            "High": 15,
            "Event": "Age_0_to_15"
        },
        {
            "Low": 15,
            "High": 25,
            "Event": "Age_15_to_25"
        },
        {
            "Low": 15,
            "High": 50,
            "Event": "Age_15_to_50"
        }
    ]
}

```

```

    {
        "Low": 50,
        "High": 100,
        "Event": "Age_50_to_100"
    }
]
}
...
}

```

4-2-3-e. Making Decisions According to Individual's Sexual Debut Status

[STIIIsPostDebut](#) enables you to stratify individuals by their sexual debut status. If Post_Debut is set to True, as in the example below, and then the Positive_Diagnosis_Event will be called for individuals that are past the age of sexual debut. A Negative_Diagnosis_Event can be included as well, to apply to individuals before the age of sexual debut.

```

{
...
{
    "class": "STIIIsPostDebut",
    "Post_Debut": "True",
    "Abort_States": [ "LostForever", "OnART" ],
    "Cascade_State": "HCTUptakePostDebut",
    "Event_Or_Config": "Event",
    "Positive_Diagnosis_Event": "Individual_Is_Post_Debut"
}
...
}

```

4-2-4. Delays

4-2-4-a. Distributions of delay time

A cross-disease feature of EMOD is the [DelayedIntervention](#). This feature allows you to set the delay time until the outcome of an event is broadcast. It can be a fixed delay time, with the same duration assigned every time, or it can be random, drawn from a variety of available probability distributions. Some additional options for delay distributions were added as part of EMOD-HIV v2.0. Below is a table of available distributions. Note that the actual delay period will be an integer multiple of the Simulation_Timestep: the delay will end on the first timestep that occurs after the end of the delay time.

Distribution Name	Description	Input Parameters
FIXED_DURATION	Exact length of time specified, in days. Event will occur on the first timestep to occur on or after the initial time plus the Delay_Period.	Delay_Period
UNIFORM_DURATION	Duration chosen randomly between a minimum and a maximum, with every time in the interval having equal probability of being chosen.	Delay_Period_Min, Delay_Period_Max
EXPONENTIAL_DURATION	Duration chosen from an exponential distribution with rate parameter equal to 1/Delay_Period, in days.	Delay_Period
GAUSSIAN_DURATION	Duration chosen from a Gaussian distribution with the specified mean and standard deviation, in units of days.	Delay_Period_Mean, Delay_Period_Std_Dev

See the parameter reference guide for details on how to configure each of these distributions.

4-2-4-b. Delay with expiration and Cascade State

The [HIVDelayedIntervention](#) builds upon DelayedIntervention by adding Cascade_State, Abort_States, and Expiration_Period.

Because a delay state is occupied by an individual for multiple timesteps, it is possible for the individual to enter one of the Abort_States while waiting in the delay. If this happens, the delay will be aborted at that time. As with other interventions, the delay will not be distributed at all if the individual is already in one of the Abort_States when the delay begins.

Expiration_Period allows a delay to be applied for no longer than a fixed period of time, and for a different outcome to occur if the individual is still in the delay at the time of the Expiration_Period.

In the example below, a delay is configured with a uniform distribution between 1 and 365 days. This gives the delay a 1 in 365 probability of ending on any day of the first year. If this occurs prior to the 183rd day, then the result is to broadcast "DoneWaiting." However, the delay has an Expiration_Period of 183 days. If the event has not occurred before the 183rd day (which in this example will happen approximately 50% of the time), then the delay will expire. Instead of broadcasting "DoneWaiting", it will broadcast "DelayExpired".

```
{
  {
    "class": "HIVDelayedIntervention",
```

```
"Delay_Distribution": "UNIFORM_DURATION",
"Delay_Period_Min": 1,
"Delay_Period_Max": 365,

"Expiration_Period": 183,

"Abort_States": [],
"Cascade_State": "",

"Broadcast_Event": "DoneWaiting",
"Broadcast_On_Expiration_Event": "DelayExpired"
}
...
}
```

4-2-4-c. Restricting multiple entries with a muxer

The files for this scenario are located in the directory Scenarios\STIAndHIV\04_Health_Care\4_2_4_c_HIVMuxer

Health care in EMOD is bi-directional: can be applied to individuals, or can sought by individuals in response to various triggering events including birth, sexual debut, pregnancy, or AIDS symptoms. A potential problem created by this structure is that an individual could end up in care multiple times. For example, an individual might have an antenatal care (ANC) visit and, in the same timestep, seek health care for AIDS symptoms, both leading to HIV testing and staging.

These situations can often be handled by the `Cascade_State` and `Abort_States` features described earlier in this tutorial. For example, the stages of HIV care could each have a cascade state that is listed in the `Abort_States` of the ANC and HIVSymptomatic diagnostic tests.

The [HIVMuxer](#) provides a second mechanism that can be used to prevent multiple entries into care. The purpose of an HIVMuxer is to count the number of times an individual is simultaneously waiting in the same delay state or group of delay states, and to restrict the maximum number of entries for that individual. The name Muxer derives from a term in signal processing that refers to joining together multiple data signals.

HIVMuxer builds upon HIVDelayedIntervention, but adds the parameters `Muxer_Name` and `"MaxEntries"`. The `Muxer_Name` is used to label a group of muxers. Multiple blocks can be assigned the same `Muxer_Name`. If two HIVMuxer interventions have the same `Muxer_Name`, they share a counter on the number of current entries.

The total number of entries is not allowed to exceed `MaxEntries`. `MaxEntries` must be a positive integer. All the examples provided for configuring health care set the number of `MaxEntries` to 1,

ensuring that an individual can only be waiting in the delay one time. A second entry to the muxer will be denied until the first entry completes the delay period or expires.

In the included example, individuals are placed into a delay loop that triggers itself annually. After three years, the individuals attempt to re-enter the delay loop, but are denied entry because the Max_Entries is set to 1, as follows:

```
{  
    ...  
    {  
        "class": "HIVMuxer",  
        "Abort_States": [ "Abort_Infinite_Loop" ],  
        "Cascade_State": "Infinite_Loop",  
  
        "Delay_Distribution": "FIXED_DURATION",  
        "Delay_Period": 365,  
  
        "Muxer_Name": "Delay_Loop_Muxer",  
        "Max_Entries": 1,  
  
        "Broadcast_Event": "DoneWaiting"  
    }  
    ...  
}
```

4-3. Sub-Saharan Africa epidemic model with transmission and health care

The files for this scenario are located in the directory Scenarios\STIAndHIV\04_Health_Care\4_3_Health_Care_Model_Baseline

This scenario provides a set of input files that integrate the components for modeling HIV transmission and health care in sub-Saharan Africa. The included age-mixing patterns are those demonstrated in [Scenario 1-g](#) based on a demographic surveillance study in Kwazulu-Natal, South Africa. The disease progression assumptions are those described in [Tutorial 2](#), based mostly upon clinical cohort studies from sub-Saharan Africa. The historical guidelines and numbers on treatment are matched to the national antiretroviral treatment program in South Africa. This tutorial will walk you through the structure and components of this example health care system, composed of the building blocks described earlier in this tutorial.

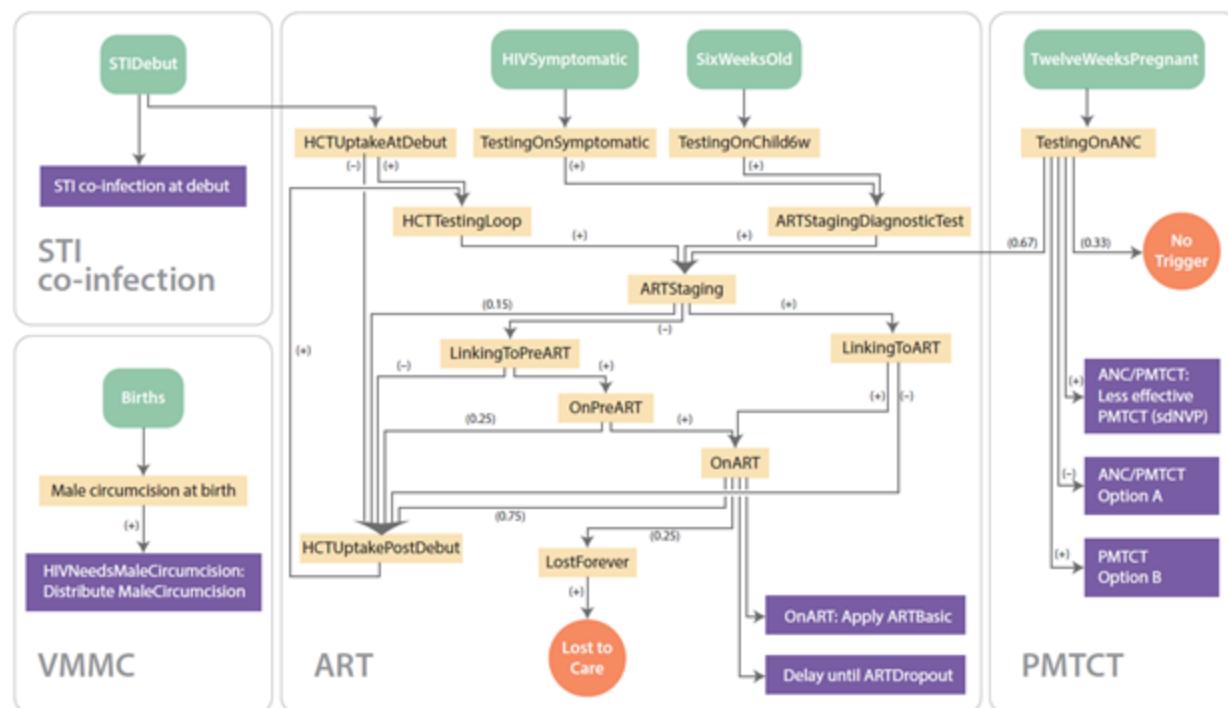
The baseline health care campaign.json file provided with this scenario contains voluntary male medical circumcision (VMMC) for HIV prevention in men, prevention of mother-to-child transmission (PMTCT), and antiretroviral therapy (ART) for treatment in children and adults. [Tutorial 5](#) demonstrates many possible extensions of this baseline health care system, such as expansion of ART eligibility, increased

efficiency and retention in care, and expanded prevention services such as VMMC and PrEP. In addition to healthcare, the campaign.json file also includes initialization of HIV infections to begin the simulated epidemic, and creation of STI co-infections.

This scenario adds a campaign override file (campaign_override.json) to the scenario directory. For the Quick Start tutorials, campaign override files only highlight the interventions that are of interest in a scenario and do not override the interventions in the campaign.json file. However, for the regression test scenarios in the EMOD source, campaign override files will override interventions when used with the regression_test.py script. See [Verifying the EMOD Executable](#) if you would like more information on regression tests.

There are no interventions in the campaign_override.json for this scenario as the campaign.json file is the baseline health care campaign file. [Tutorial 5](#) uses campaign override files to highlight the interventions that extend the baseline health care system.

The diagram below shows the interventions provided in the campaign.json file for this scenario. Triggers for entry into care are represented by green rectangles (note that the size of the rectangle does not mean anything; they are simply scaled to the length of the trigger name). The intervention blocks grouped into yellow rectangles by Cascade_State. Purple rectangles indicate an actual intervention being applied to the individual, such as STI infection, PMTCT, ART initiation, or ART discontinuation. The red circles indicates that a block does not link to any specific intervention or outcome. After receiving such an event, individuals can still uptake other pathways to HIV care, provided the [Cascade_State/Abort_States](#) mechanism allows it.

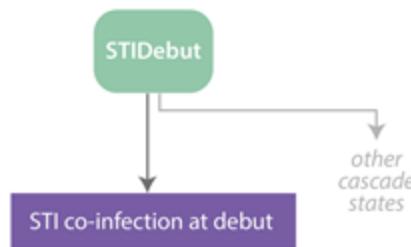


4-3-1. Initializing HIV and Co-Infections

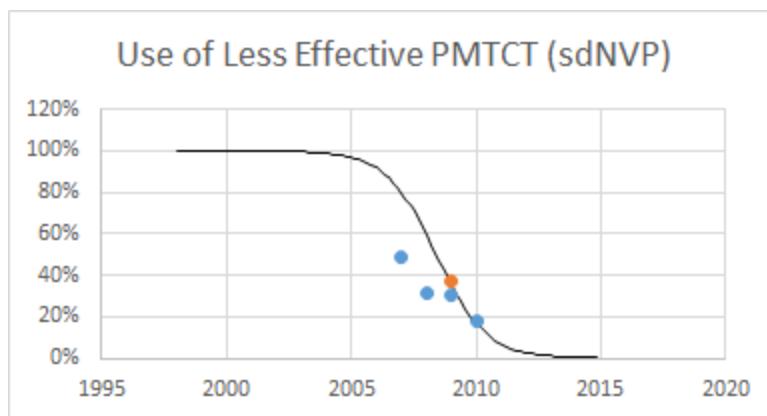
In addition to specifying health care, the campaign.json file is also responsible for initializing HIV infections and STI co-infections in the model.

Initializing HIV infections is not shown in the overview diagram because it consists of only a single intervention block, targeting HIV infection to a specified age/gender using the [OutbreakIndividual](#) intervention. See [Scenario 2a](#) for an example of using OutbreakIndividual.

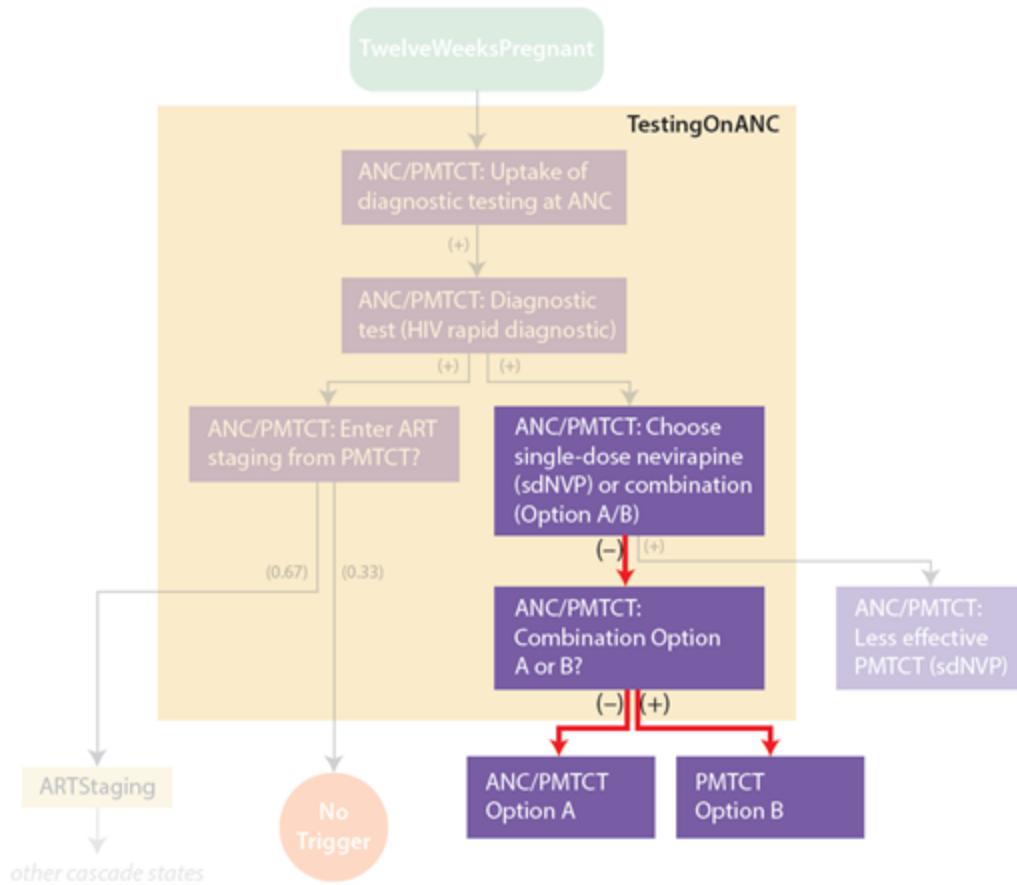
The simple configuration provided in this tutorial applies STI co-infection to a proportion of individuals upon sexual debut, and does not treat the co-infections. The simple structure of the intervention is shown in the diagram below:



There are many possible ways to configure more complex STI co-infection. As described in [Scenario 4-2-1d](#), both creation and treatment of co-infections is possible through campaign.json. Episodic co-infections can be configured using a delay loop, building on the pattern demonstrated in [Scenario 4-3-4c](#). Co-infections can also be made to resolve over time with complex and complex heterogeneities, using the delay functions described in [Scenario 4-2-4a](#), and differences across sociodemographic categories can be created as described in [Scenario 4-1](#).



If the less effective regimen is not used, then an additional choice is made between Option A and Option B, as illustrated below:



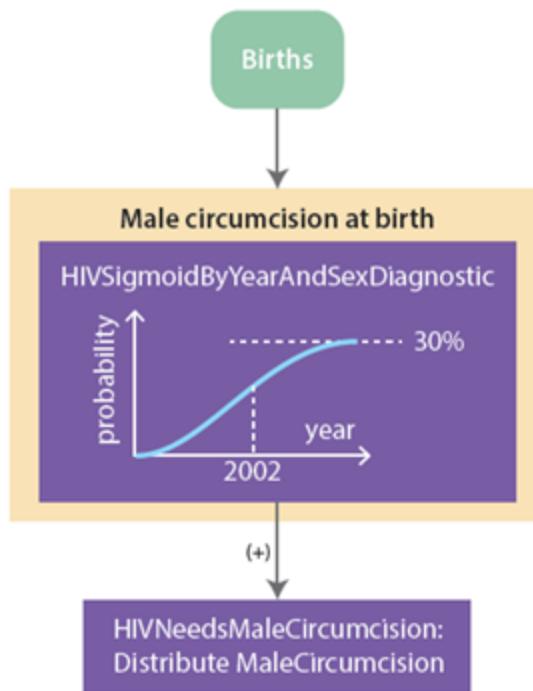
These are configured to reduce transmission by 10-fold and 30-fold, respectively, with an overall MTCT rate of 3% and 1%. The switch from Option A to Option B is made on April 1, 2013, per national guidelines.

4-3-2. Voluntary male medical circumcision (VMMC)

As with STI co-infection, there are many complex ways to configure voluntary male medical circumcision (VMMC). Several are demonstrated in [Scenario 5-1](#).

The campaign.json file in this tutorial uses a birth trigger for VMMC, with a time-variable sigmoidal uptake rate rising from 0% to 30% and an inflection point at 15% in the year 2002. Even though the intervention is applied at birth, the transmission effect of VMMC does not take place until the males have their first exposure to HIV, sometime after sexual debut. Thus, the true effect of the intervention is lagged by 15 to 20 or more years.

The diagram below illustrates the structure of the VMMC intervention. The first block is triggered by the Births event and creates a time-varying sigmoid probability of reaching the second block. The second block provides the actual VMMC intervention.

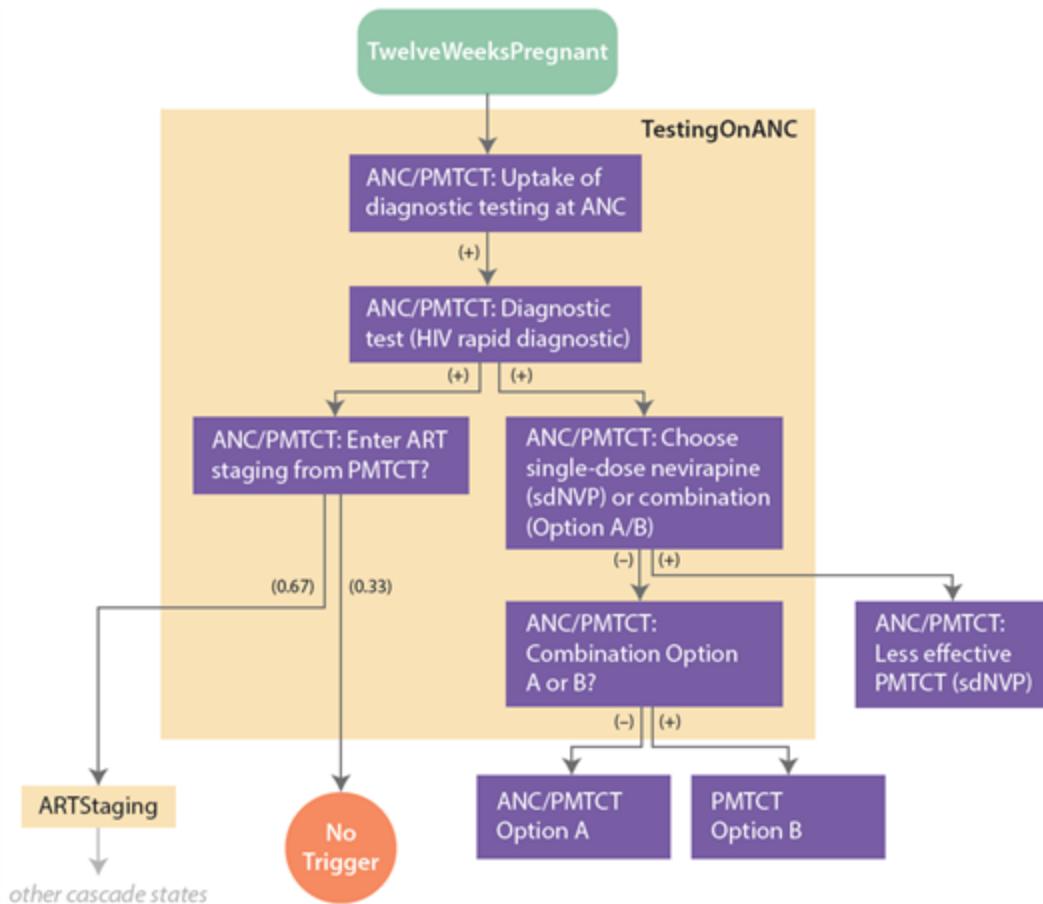


4-3-3. Prevention of Mother-to-Child Transmission (PMTCT)

The ANC/PMTCT component of the campaign.json file includes time-variable coverage of ANC and of the different PMTCT regimens configured based on program information from South Africa. These data sources and their fits to the model's uptake assumptions are summarized in an Excel spreadsheet provided with this scenario: PMTCT_data_sources_and_curve_fits.xlsx. The scripts used to fit sigmoid time-variable uptake, and resulting charts, are also provided. These can be found in the PMTCT directory:

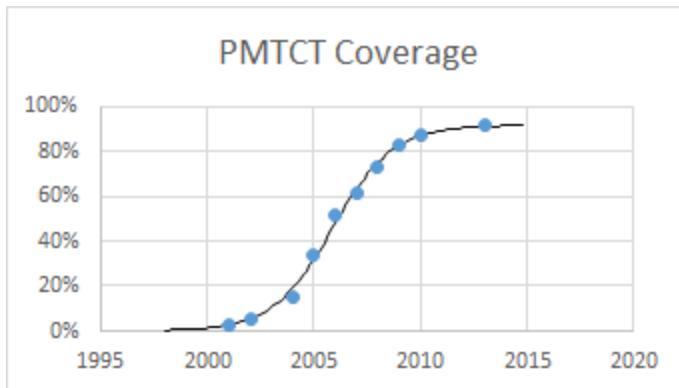
Scenarios\STIAndHIV\04_Health_Care\4_3_Health_Care_Model_Baseline\PMTCT

HIV testing through care (ANC) can lead to both antiretroviral therapy for a pregnant woman's own health, and prevention of mother-to-child transmission (PMTCT). The diagram below provides an overview of the possible outcomes of ANC testing:



The first block is triggered when women reach the 12th week of pregnancy. It represents a time-variable sigmoid probability of receiving antenatal HIV testing for that pregnancy. ANC testing coverage ranges

from 0% to 91.5% with an inflection point near the end of 2005, as shown in the following chart, fit to data trends referenced here^{1,2,3,4,5,6} and in the Excel sheet.



Women diagnosed HIV-negative receive no interventions, and may re-test at a later time, including a future pregnancy or one of the other testing modalities. Women diagnosed HIV-positive simultaneously receive a 67% probability of linking to ARTStaging, and an opportunity to receive one of three PMTCT options: less effective nevirapine-based PMTCT, Option A, or Option B.

The scenario is configured so that ART has the same efficacy for PMTCT as configured for Option B: a 30-fold reduction in transmission with an overall 1% rate of MTCT. Because the ANC HIV test links to both ARTStaging and PMTCT, a women may receive ART and a PMTCT intervention during the same pregnancy. If this happens, the efficacy of ART is used, and that of the PMTCT regimen is ignored.

After testing positive, the choice of PMTCT regimen is made based on the time that ANC was accessed. The first decision is whether a less effective (nevirapine-based) regimen is used, as shown in the following diagram:

¹An evaluation of the prevention of mother-to-child transmission (PMTCT) of HIV Initiative in South Africa. (http://www.hst.org.za/uploads/files/pmtct_national.pdf)

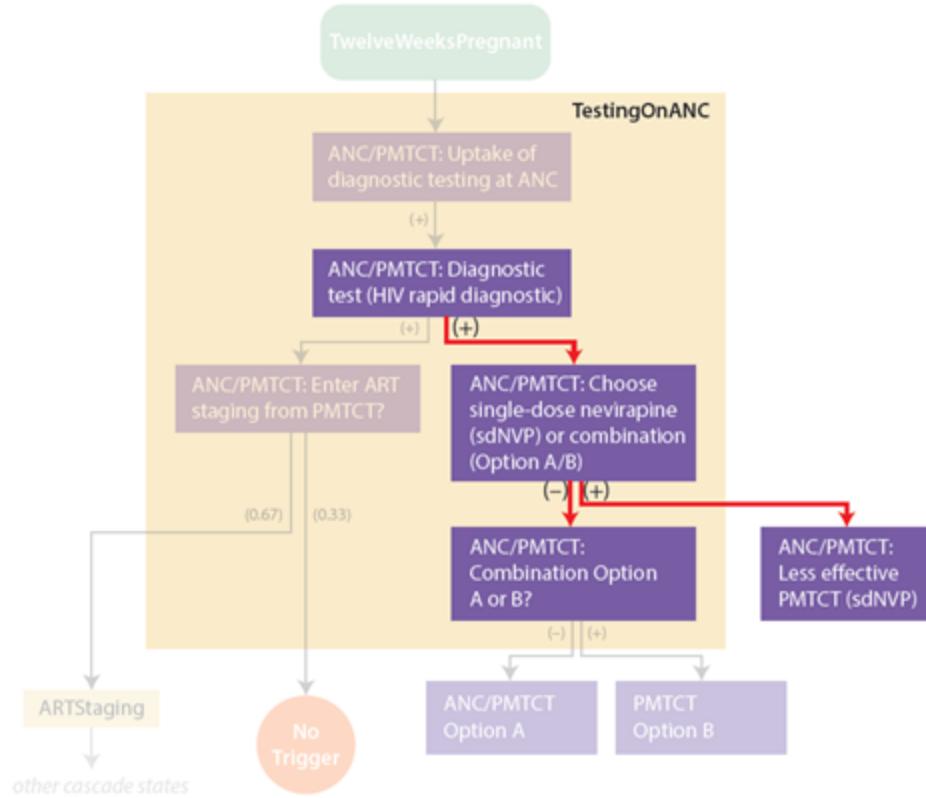
²Countdown to 2015: Maternal, newborn, & child survival. Tracking progress in maternal, newborn, & child survival: The 2008 report. (<http://www.childinfo.org/files/Countdown2015Publication.pdf>)

³UNICEF South Africa PMTCT Fact Sheet 2010 (http://www.unicef.org/aids/files/SAfrica_PMTCTFactsheet_2010.pdf)

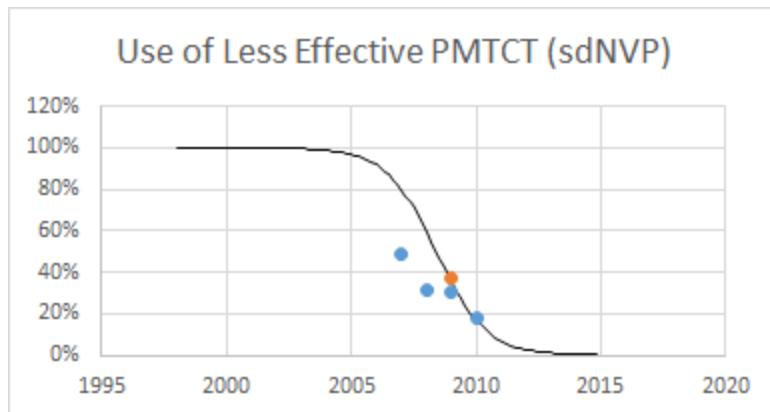
⁴Evaluation of the effectiveness of the national prevention of mother-to-child transmission (PMTCT) programme on infant HIV measured at six weeks postpartum in South Africa(<http://www.doh.gov.za/docs/reports/2012/pmtceffectiveness.pdf>)

⁵Global HIV/AIDS response: Epidemic update and health sector progress towards universal access, progress report 2011 (<http://www.afro.who.int/en/clusters-a-programmes/dpc/acquired-immune-deficiency-syndrome/features/3439-global-hivaids-response-progress-report-2011.html>)

⁶Joint Review of HIV, TB and PMTCT Programmes in South Africa October 2013 Main Report. <http://www.hst.org.za/publications/joint-review-hiv-tb-and-pmtct-programmes-south-africa-april-2014>



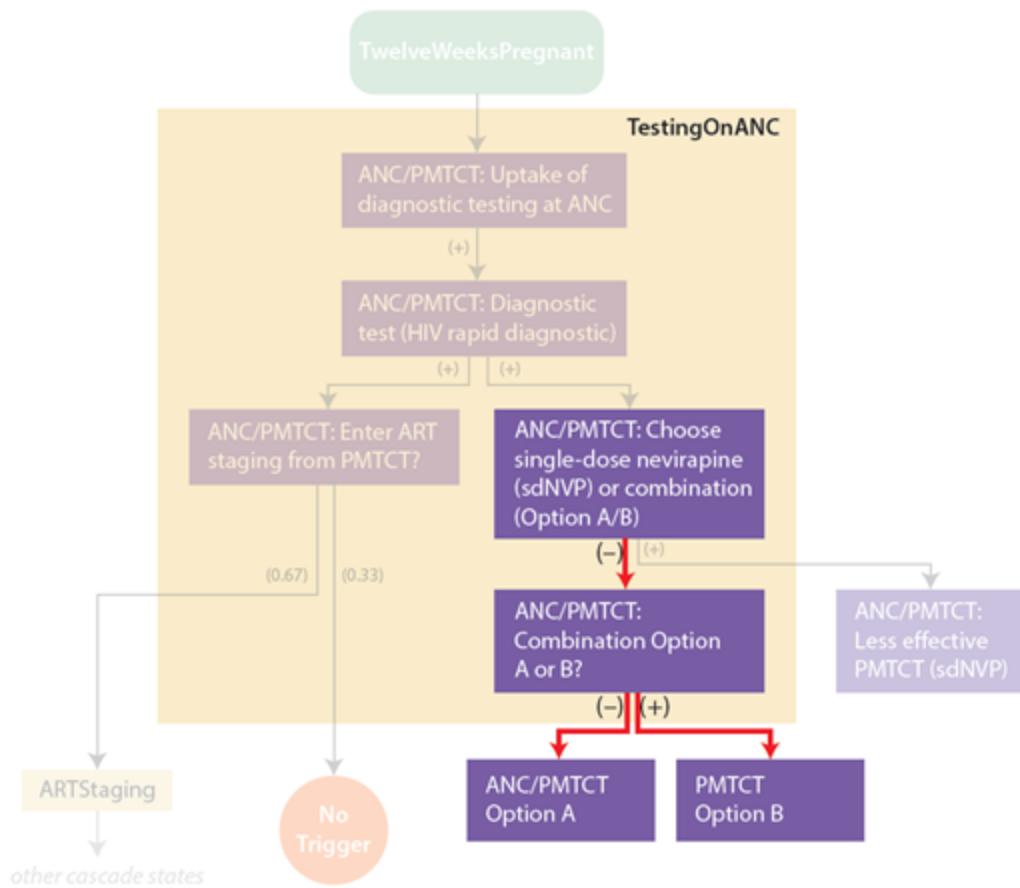
The graph below shows the sigmoid probability of using the less effective regimen over time, fit to data trends listed in the Excel sheet^{1,2}.



If the less effective regimen is not used, then an additional choice is made between Option A and Option B, as illustrated below:

¹Fig. 7.8 in the WHO Progress Report 2011: Global HIV/AIDS Response (http://whqlibdoc.who.int/publications/2011/9789241502986_eng.pdf)

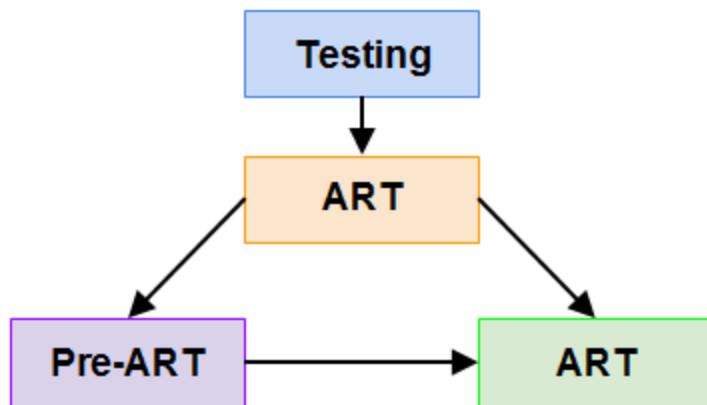
²Fig. 5.11 in the WHO Progress Report 2009: Global HIV/AIDS Response (http://www.who.int/hiv/pub/tuapr_2009_en.pdf)



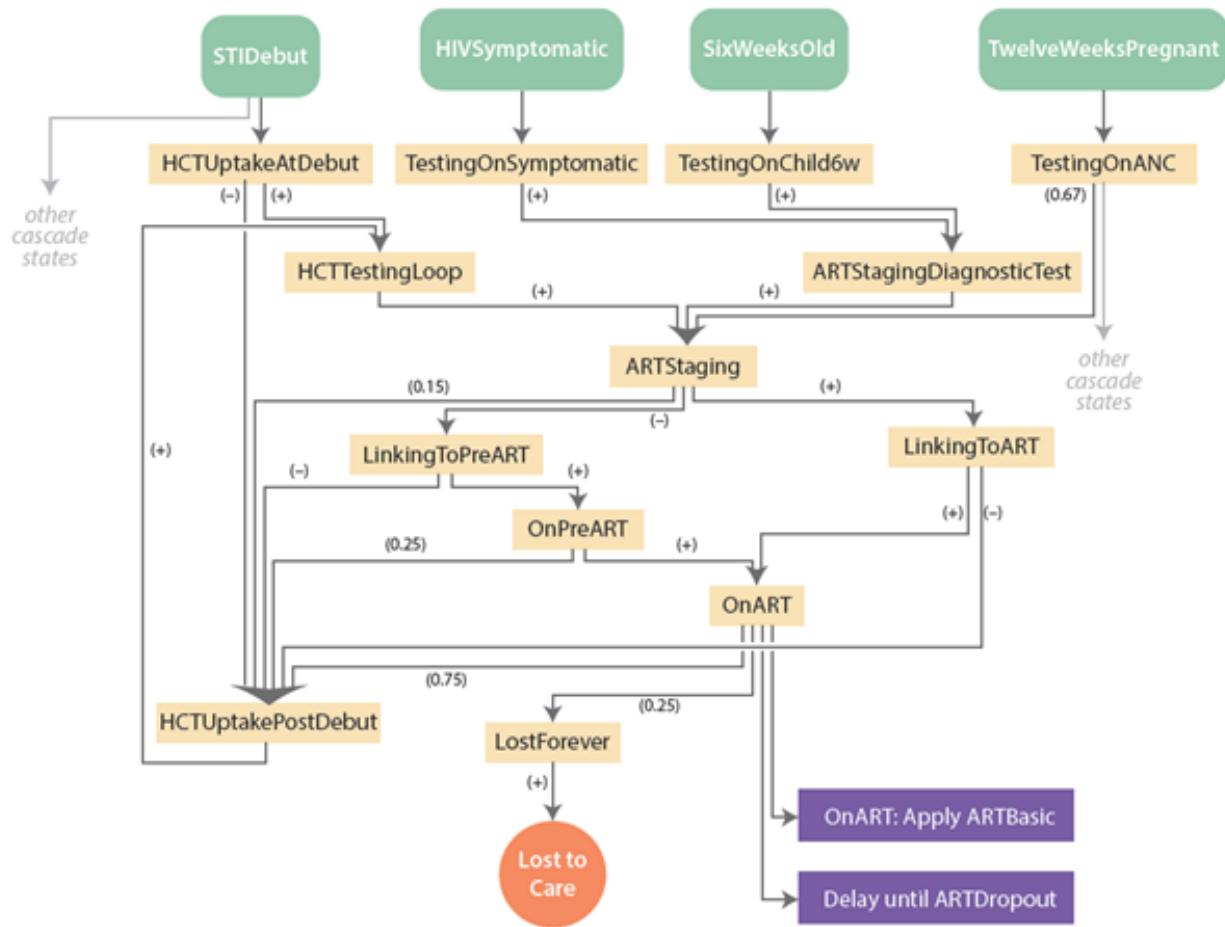
These are configured to reduce transmission by 10-fold and 30-fold, respectively, with an overall MTCT rate of 3% and 1%. The switch from Option A to Option B is made on April 1, 2013, per national guidelines.

4-3-4. Overview of Antiretroviral Treatment (ART)

The most complex aspect of the healthcare configuration is the antiretroviral treatment process. This can be subdivided into four broad categories: testing, staging, pre-ART, and ART. A schematic of these stages (not including discontinuation and re-initiation) is provided below.



The Cascade_States for ART are more numerous than these broad categories:



The reason there are more Cascade_States than broad categories of care is that Cascade_States are used for more than just categorization: they also interact with the Abort_States hierarchy discussed in [Scenario 4-1-e](#).

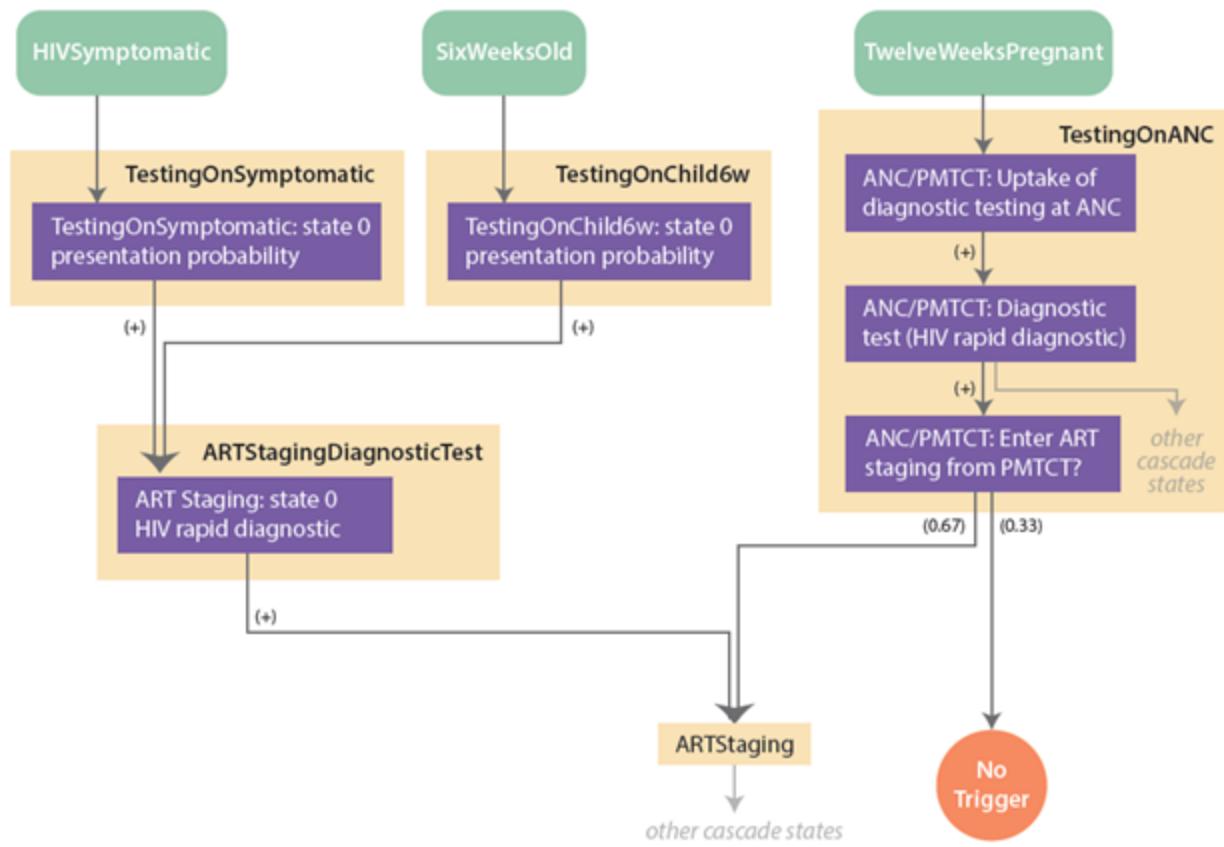
For example, ARTStagingDiagnosticTest is a separate cascade state than ARTStaging itself in order to allow HIV-negative individuals to re-test at a later date. ARTStaging assumes that all individuals have already been diagnosed HIV-positive, and therefore aborts simultaneous re-testing for HIV. On the other hand, ARTStagingDiagnosticTest can be applied to either HIV-positive or HIV-negative individuals. If ARTStagingDiagnosticTest were part of ARTStaging, then HIV-negative individuals would be blocked from re-testing later, as long as their last contact with health care were an ARTStagingDiagnosticTest.

The rest of this tutorial will look inside each of the yellow rectangles in the ART diagram, examining the building blocks of each ART Cascade_State.

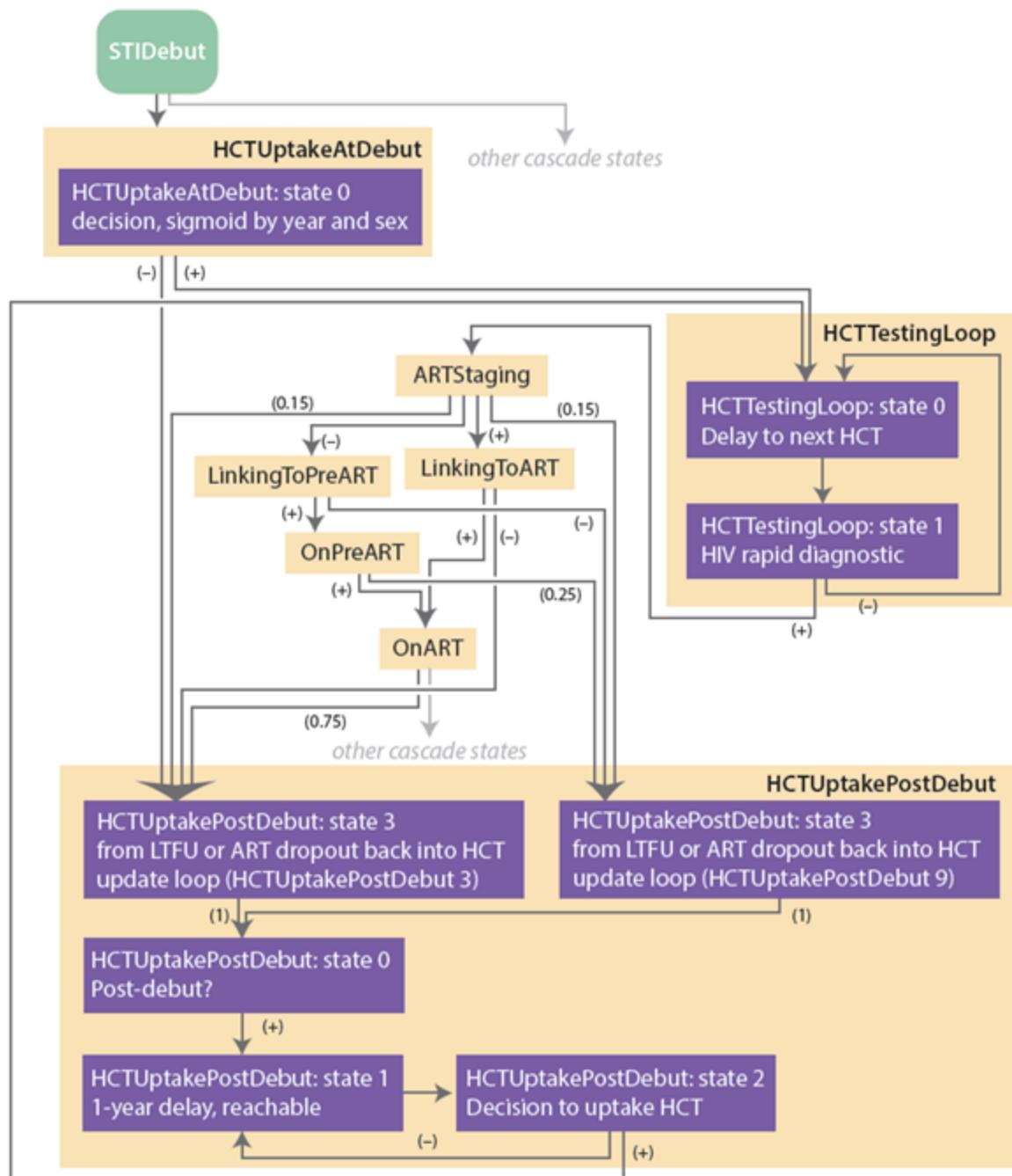
4-3-5. Testing

People take diagnostic HIV tests for a variety of reasons. The campaign.json file in 04_Health_Care/E_Health_Care_Model_Baseline contains four separate modes of testing: health seeking due to AIDS-related symptoms, testing as part of antenatal care (ANC), pediatric testing at six weeks of age, and routine/voluntary testing via HIV counselling and testing (HCT).

The first three of these ([symptomatic](#), [pediatric](#), and [antenatal](#)) are composed of relatively simple pathways to testing, illustrated below. Each mode of testing is described in detail in parts a through c of this section.



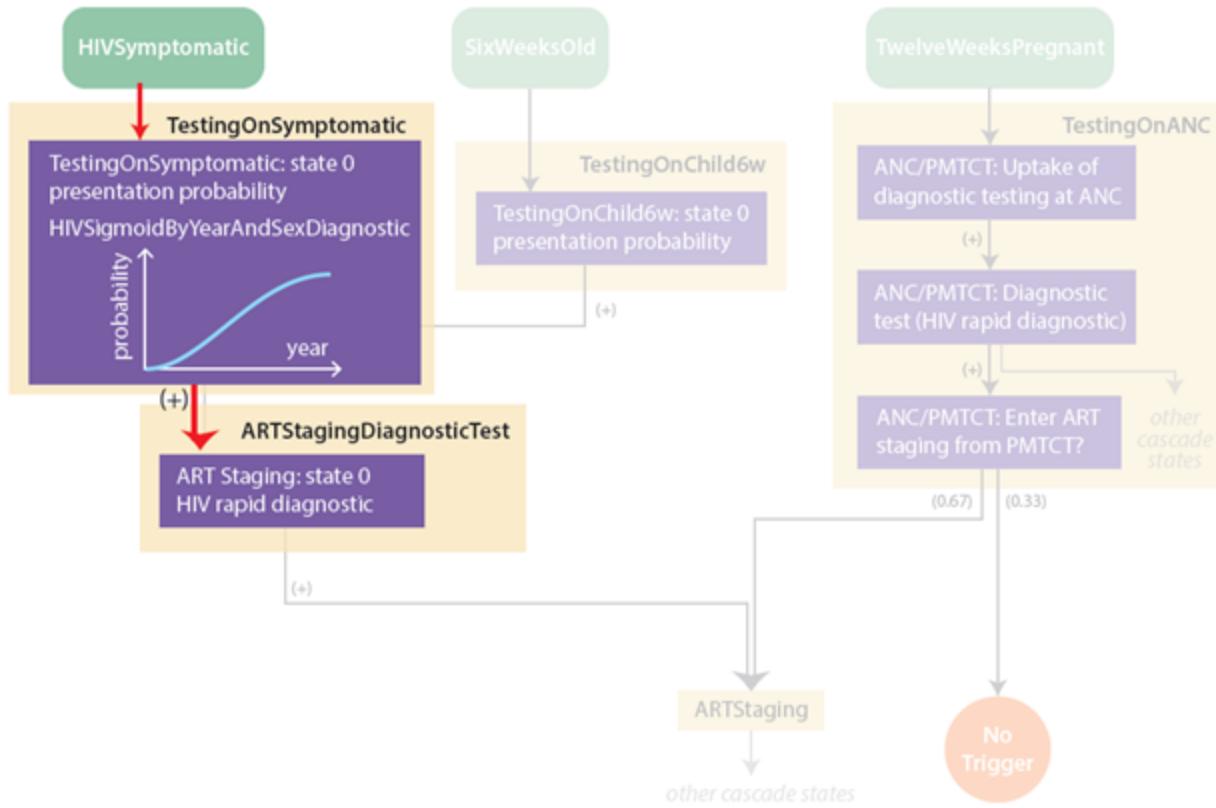
The fourth mode of testing, [routine/voluntary testing via HCT](#), is more complex. It is illustrated below, and described in detail in [part d](#).



[Scenario 5-3](#) contains campaign.json files with additional testing modalities such as community-based testing and self-testing.

4-3-5-a. Symptom-Driven Testing

The diagram below illustrates the pathway for symptom-driven HIV testing.



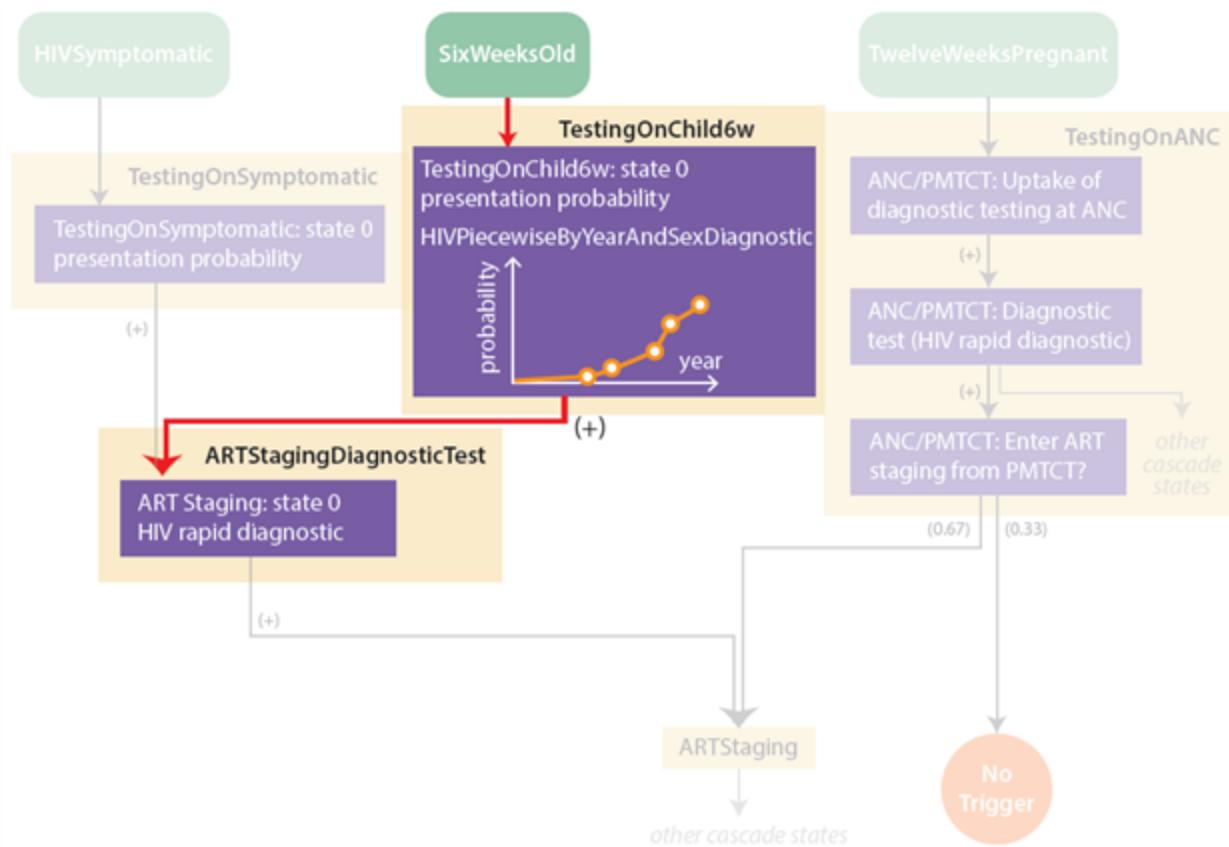
The testing is triggered by an individual's health-seeking behavior due to AIDS-related symptoms. The timing of symptomatic presentation is described in [Scenario 2-d](#). Briefly, the time between symptomatic presentation and (untreated) AIDS-related death is drawn from a Weibull distribution with configurable parameters located in config.json:

```
"Days_Between_Symptomatic_And_Death_Weibull_Heterogeneity": 0.5,
"Days_Between_Symptomatic_And_Death_Weibull_Scale": 618.341625,
```

The trigger leads to a time-variable probability of undergoing HIV testing, ranging from 0% to 55% with an inflection point in the year 2000. This reflects increasing knowledge about HIV/AIDS and availability of HIV testing. If the individual receives a positive outcome of the time-variable probability, then an HIV diagnostic test is performed and the individual is linked to ARTStaging.

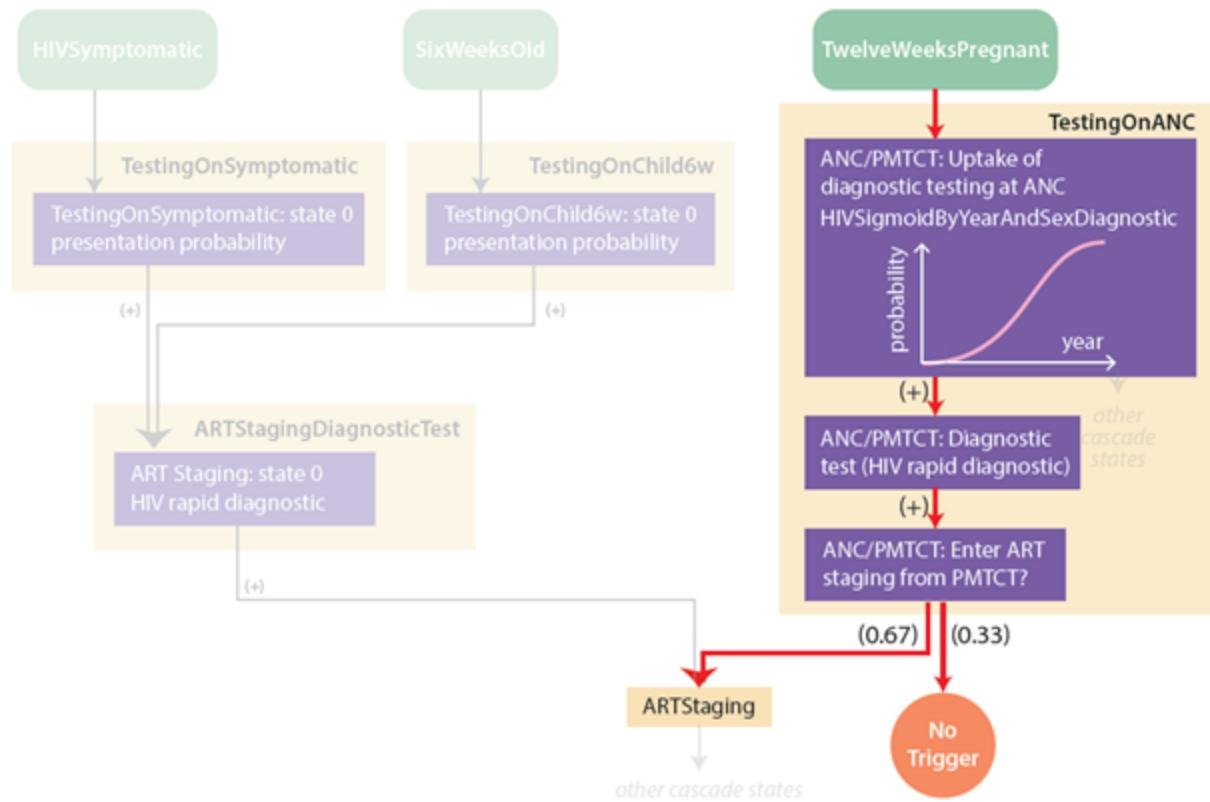
4-3-5-b. Pediatric Testing

When an infant becomes six weeks old, the SixWeeksOld event is broadcast by the model, triggering an HIV test with a time-variable probability. Unlike symptomatic and antenatal testing, which use sigmoid-shaped probabilities, this [NodeLevelHealthTriggeredIV](#) uses a piecewise-linear probability over time, configured with a [HIVPiecewiseByYearAndSexDiagnostic](#), raising the coverage of testing from 0% to 34% over the time period between 2004 and 2009. If receiving pediatric testing, the child is linked to the same diagnostic testing block that is used in the AIDS-symptomatic testing pathway, as illustrated below.



4-3-5-c. Antenatal Testing

The [PMTCT section](#) of this tutorial describes how women have a sigmoidally-increasing probability of undergoing HIV testing at 12 weeks of pregnancy. The probability of receiving an HIV test during pregnancy grows from 0% to 91.5% with an inflection point in late 2005. If receiving HIV testing as part of ANC, women take a diagnostic test and, if positive, have a 67% probability of linking to HIV services, beginning with staging for ART. This occurs in addition to the PMTCT interventions described [earlier](#). The diagram below illustrates the steps of antenatal HIV testing:

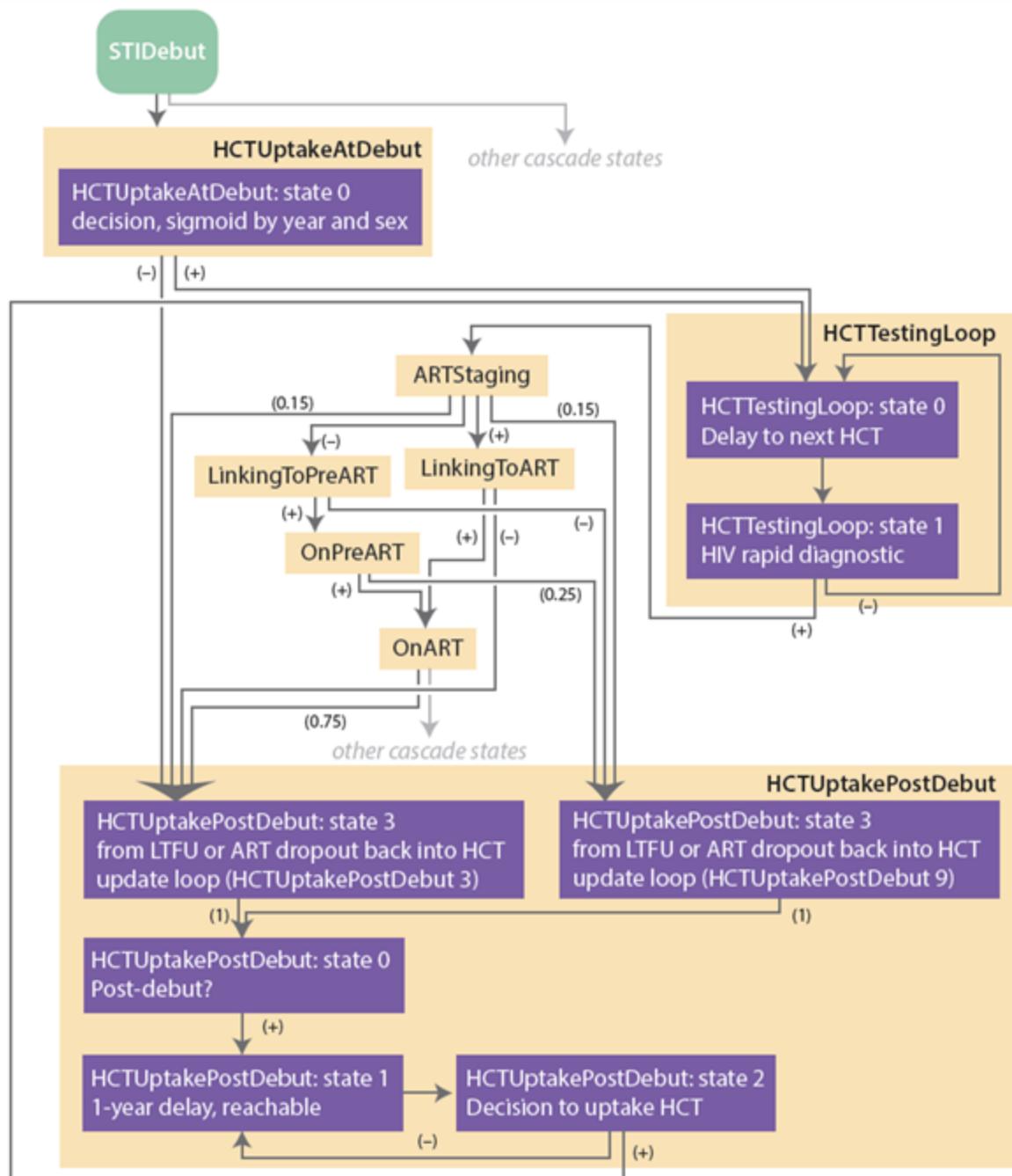


4-3-5-d. Routine/Voluntary HIV Testing and Counseling

Repeat testing via HIV testing and counseling (HTC, also abbreviated HTC) facilities is triggered for some individuals either at the time of sexual debut, and for others at a later time beyond the age of sexual debut.

In the included campaign.json file, this form of “voluntary” testing is restricted to individuals who are assigned the [Individual Property](#) "Accessibility" : "Yes". The proportion of individuals assigned this property is configured in the demographics file. In this example, the proportion is fixed 80%. Just because 80% of individuals have the potential to undergo HTC, does not mean that all individuals will do so; the delay times until HTC uptake will, for some, exceed the HIV survival time without ART. Still others end up accessing ART via a different testing modality.

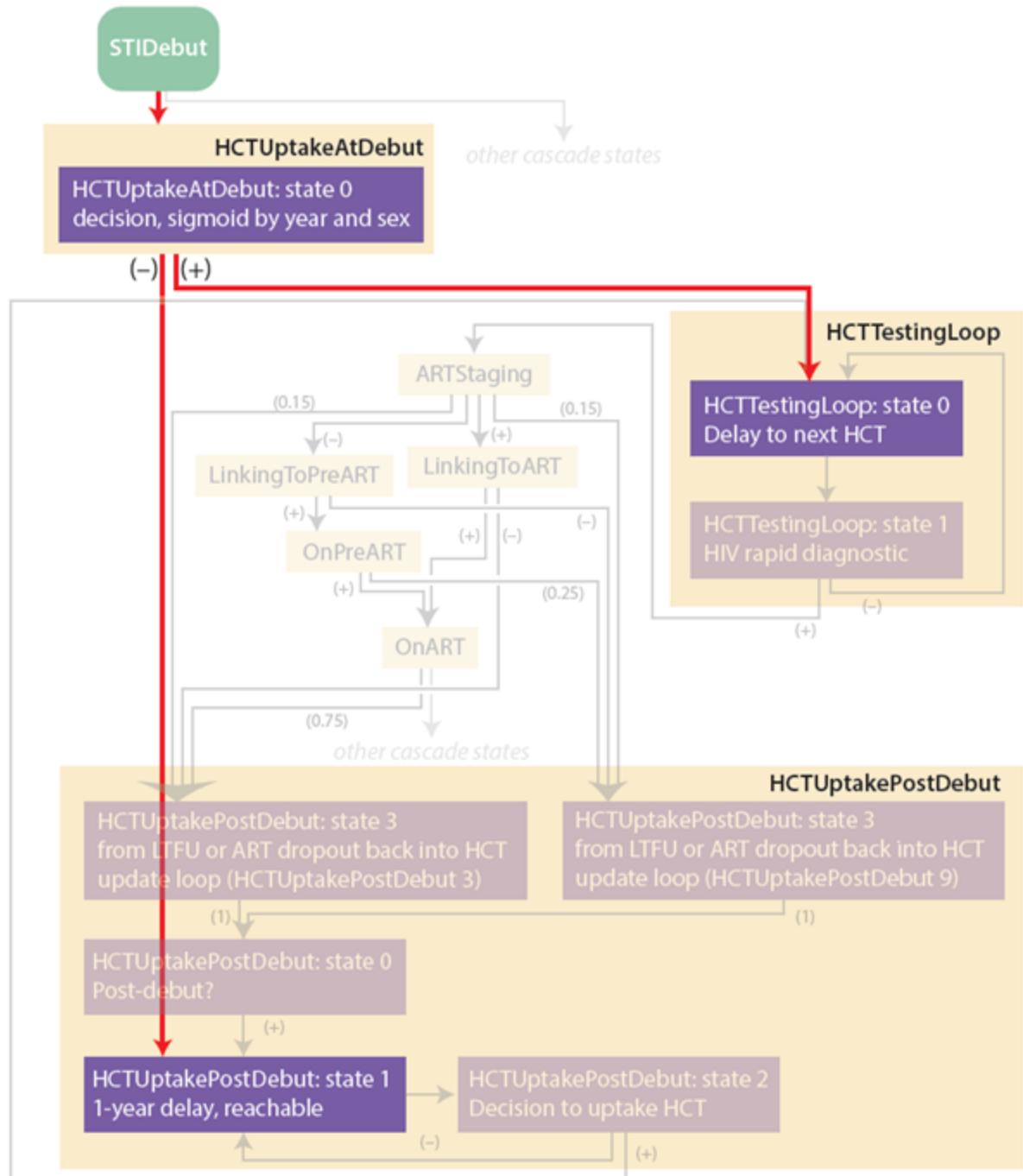
The diagram below shows the overall process of routine/voluntary testing.



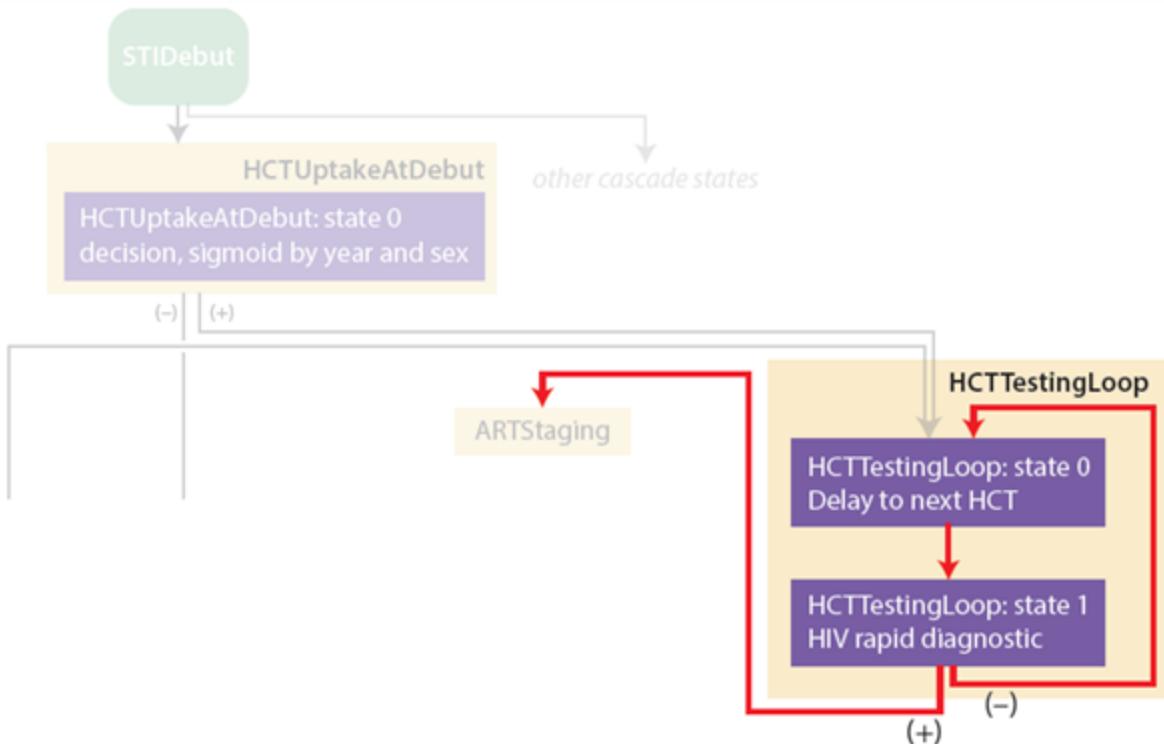
HTC uptake is one of the most complex parts of the config.json file, so the rest of this section will highlight sub-parts of the diagram to describe the flow step by step.

The process for HTC uptake begins with an individual's sexual debut. The probability that an individual will uptake HTC upon reaching sexual debut is configured as a sigmoid probability that varies by calendar year, ramping from 0% to 5% with an inflection point in 2005. Individuals who do uptake HTC at sexual debut enter a 1-year delay loop, whereas individuals who do not uptake HTC at debut have an opportunity to uptake HTC later by entering a separate delay pathway. The diagram below shows the decision pathway for individuals who have just reached sexual debut. The (+) and (-) signs indicate the

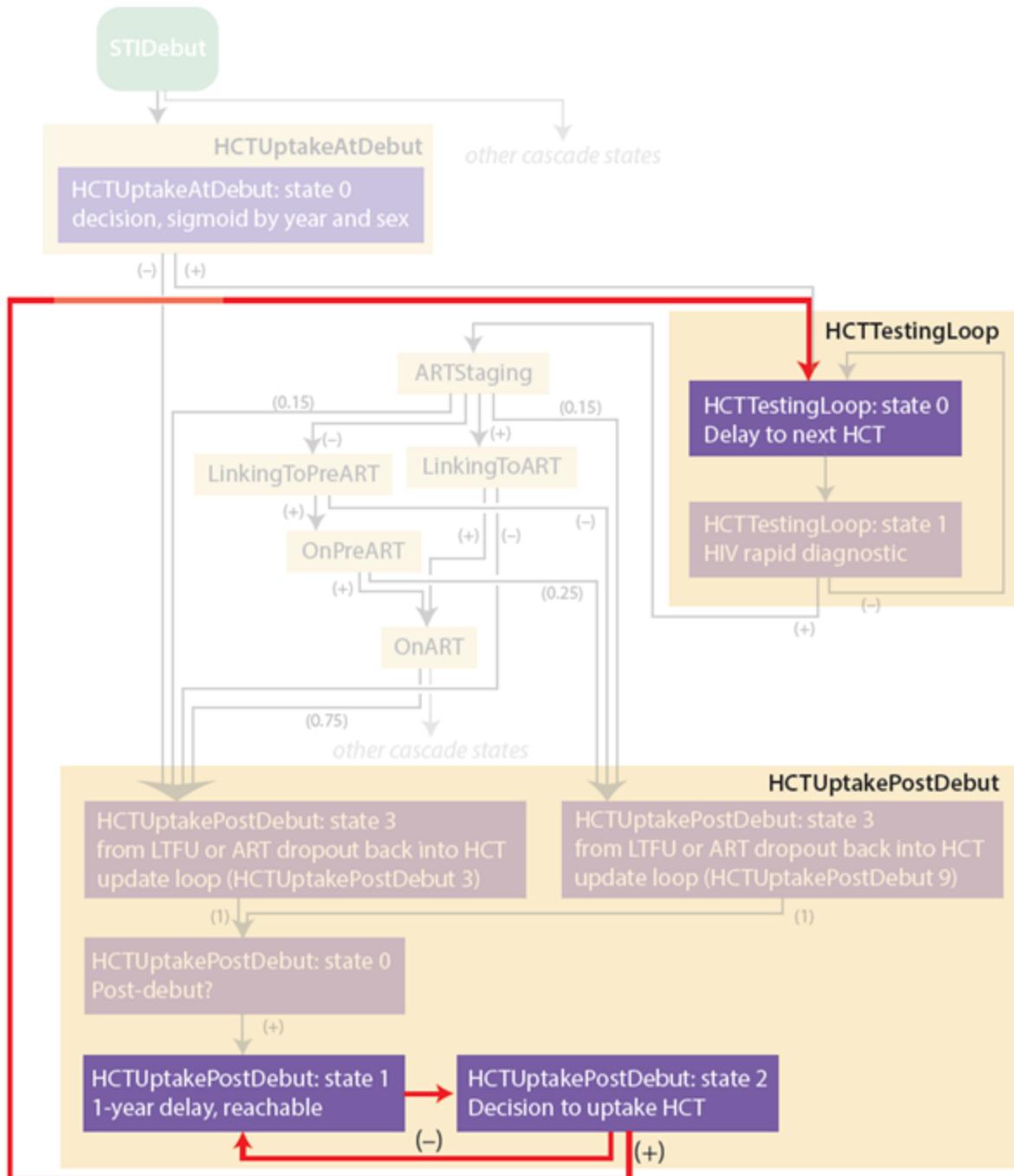
flow of individuals who receive a positive versus a negative outcome of the probability of HTC uptake at debut.



If an individual does uptake HTC at sexual debut, they enter a pattern of repeat testing. The frequency of testing is continued to be annual with a random, exponentially distributed time between repeat tests. If tested positive, the individual links to ART staging. If tested negative, they re-enter the delay loop.



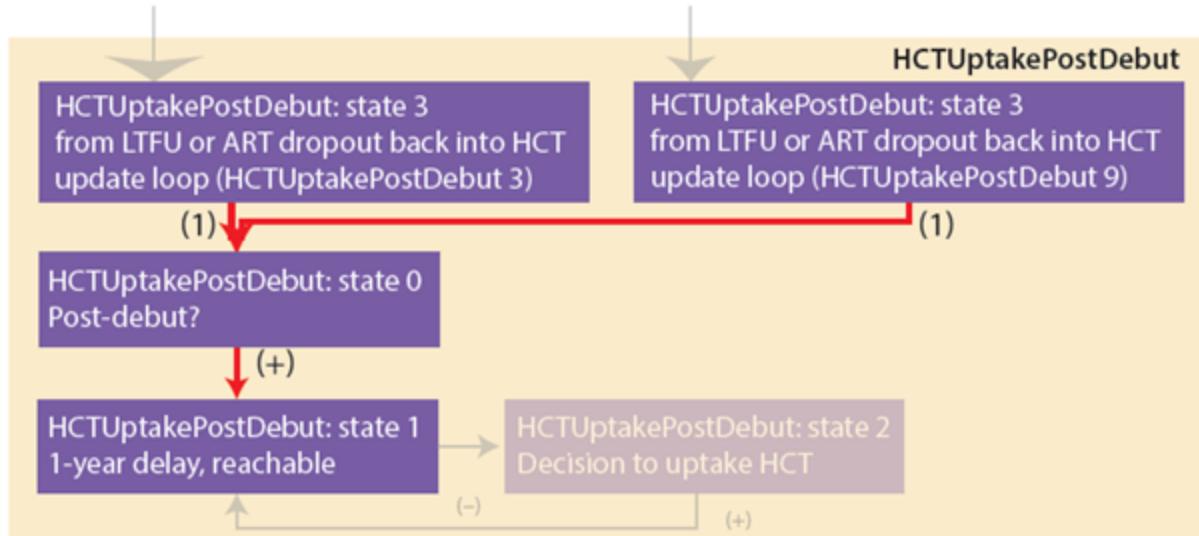
Individuals who do not uptake HTC at the time of sexual debut have an opportunity to uptake HTC later. At a rate of once per year, these individuals query an [HIVSigmoidByYearAndSexDiagnostic](#) block, which dictates their probability of uptaking HTC during that annual attempt. The probability of successfully uptaking HTC ramps from 0% to 60% with an inflection point in 2007. If these individuals do not uptake HTC, they return to the 1-year delay block until the next attempt. This flow is highlighted in the diagram below. At the bottom of the diagram, individuals cycle between a 1-year delay and a year-dependent sigmoid function. If they pass the sigmoid probability of HTC uptake, then they move to the same state that would have followed at-debut uptake: a 1-year delay until HTC.



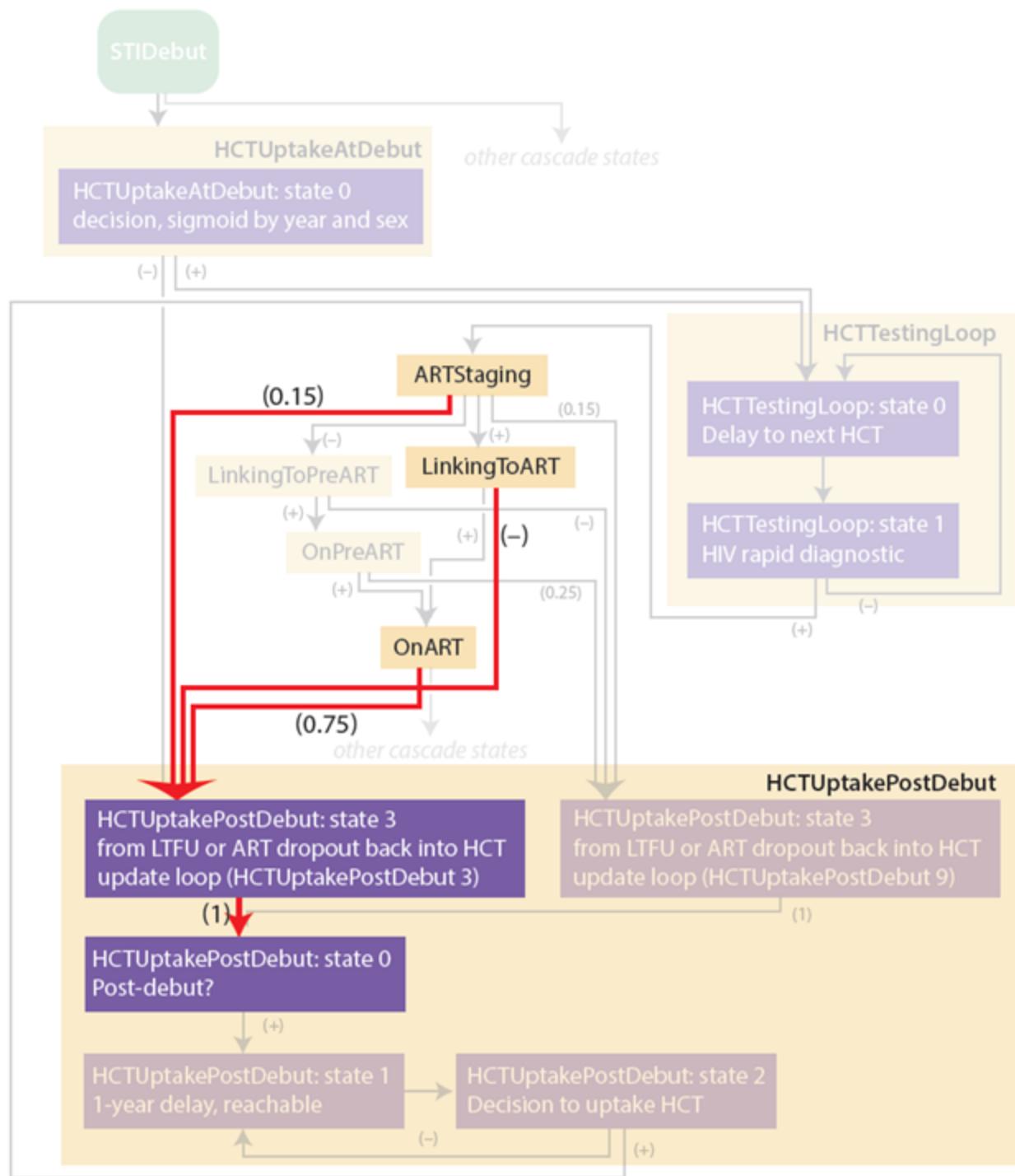
The previous diagram shows additional states within the `Cascade_State` `HCTUptakePostDebut`, which are bypassed by individuals who enter the post-debut uptake loop after failing to uptake testing at debut. Those states are only used by individuals who discontinued ART and have a configurable probability of re-initiating ART. By sharing these structures, it is assumed that the delay times and probability over time of re-initiating ART is the same as that of HTC uptake post-debut.

The diagram below highlights the states that are bypassed by ART-naive individuals, but used by individuals who have discontinued ART and are entering a delay until possible re-initiation of ART. The top

two boxes are triggered by the events HCTUptakePostDebut3 and HCTUptakePostDebut9, which originate from multiple points of failure to link or be retained in care. Note that the two events actually share the same JSON block using a TriggerList, but for clarity, separate boxes are drawn for each trigger so that you can see which events led to which of the triggers.



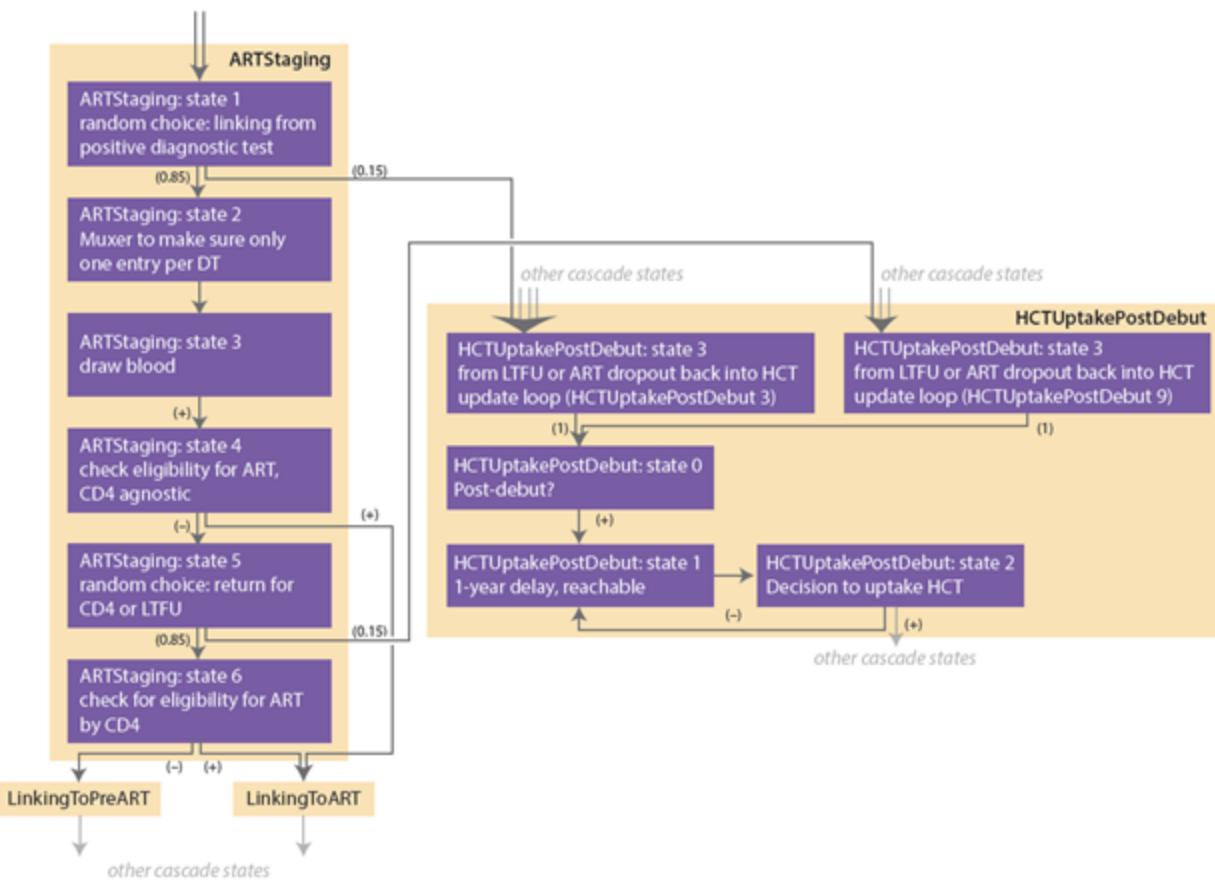
The diagram below emphasizes the different input pathways into the two re-initiation blocks of HCTUptakePostDebut. In general, HCTUptakePostDebut3 is used by individuals who were lost to follow-up while eligible for ART, whereas HCTUptakePostDebut9 used by for individuals who were ineligible, or not known to be eligible.



The reason ARTStaging contributes to both pathways of loss to follow-up is that ARTStaging contains multiple sub-components, some of which occur before determination of eligibility, and some after. The following section will explain the individual building blocks of ARTStaging.

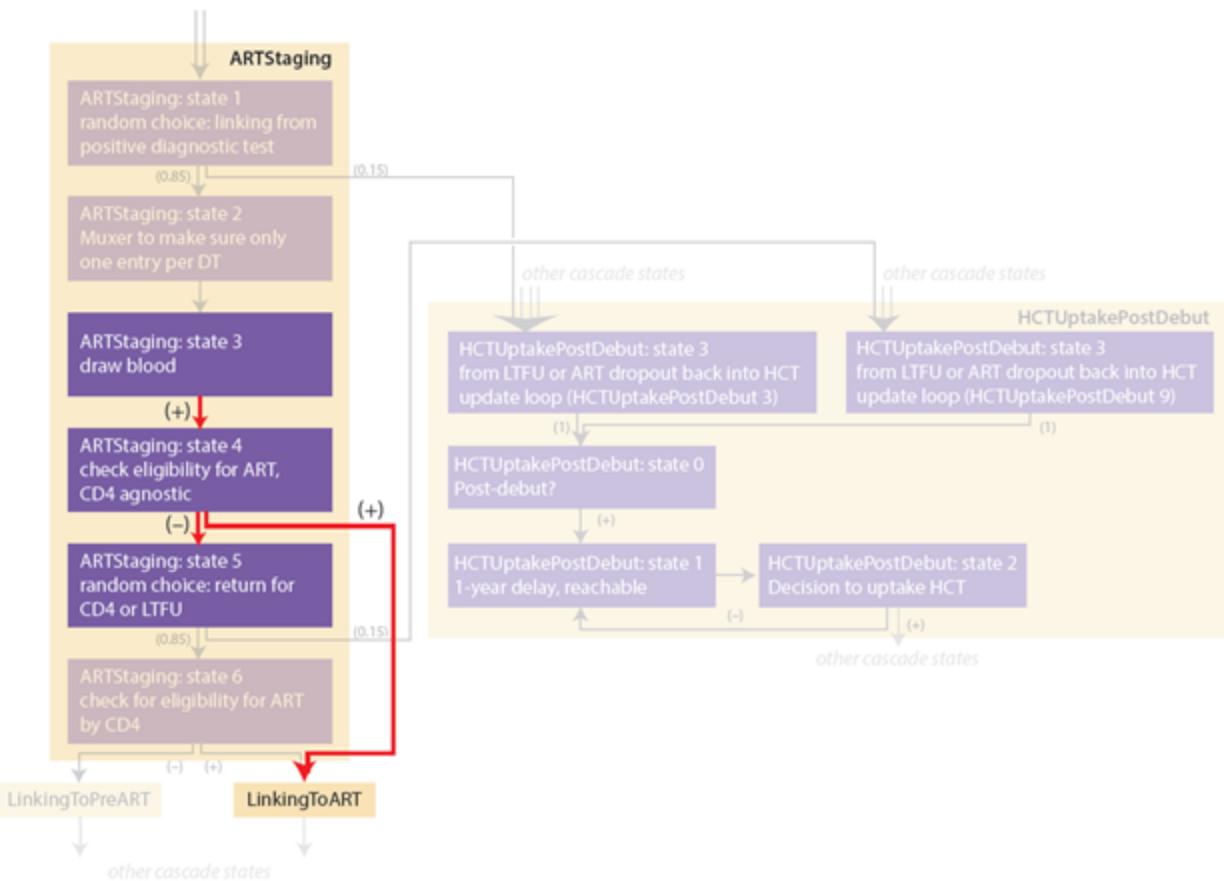
4-3-6. Staging

ART staging contains a linear flow of building blocks, without loops. The left part of the diagram below shows the steps of ART staging, from top to bottom:



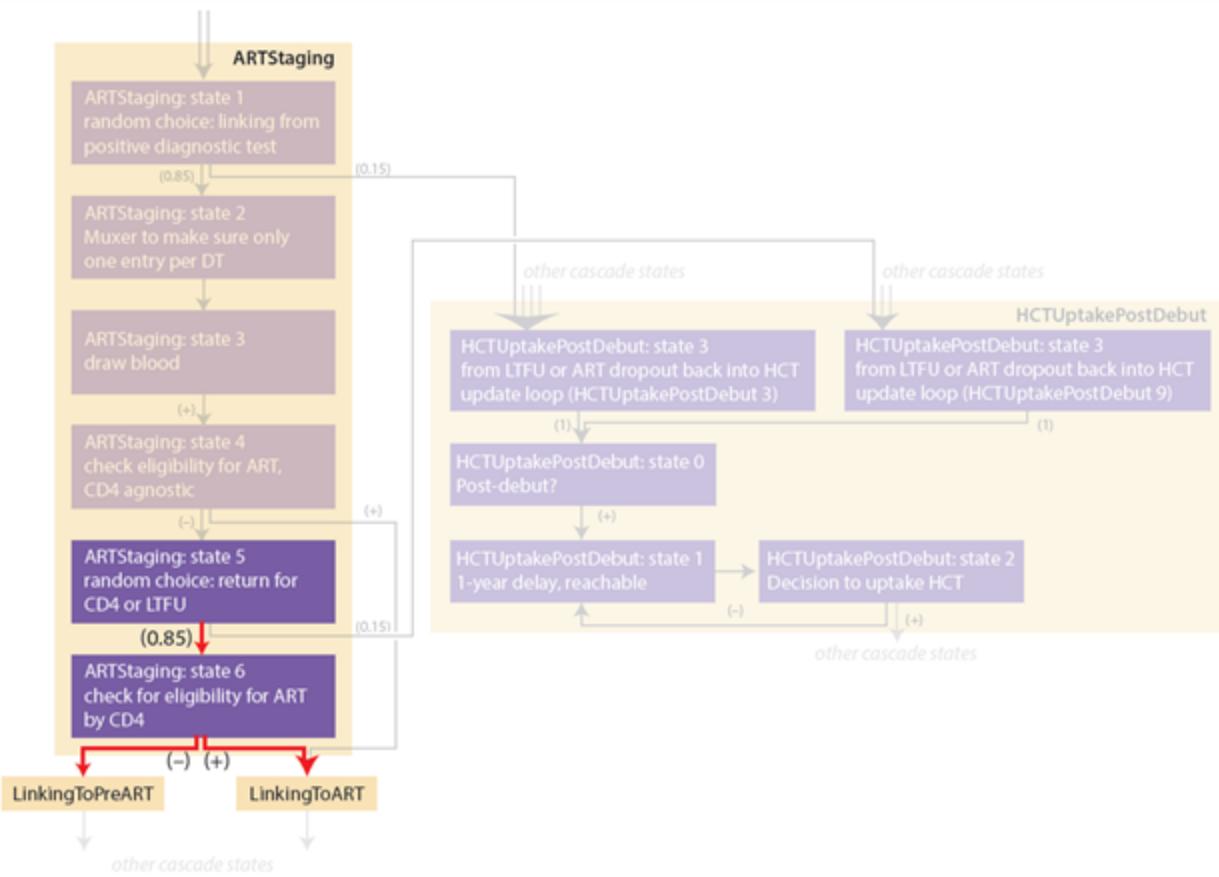
As you saw in the previous scenario, there are two different points in ART staging where individuals can be lost to follow-up. The first step of ART staging is a RandomChoice with a 15% probability of loss to follow-up, linking to the lefthand HCTUptakePostDebut block for potential re-initiation. The penultimate step is where individuals who are not eligible based on CD4-agnostic criteria must wait for a CD4 result. This is also a RandomChoice with 15% probability of loss to follow-up, and this one links to the righthand HCTUptakePostDebut block.

After the first loss to follow-up block, individuals pass through a [muxer](#) with a one-timestep delay (to avoid multiple entries into ART staging), receive phlebotomy with an HIVDrawBlood block, and are then tested for CD4-agnostic eligibility. Eligible individuals proceed to ART, whereas ineligible individuals go to the next step of ARTStaging. This pathway is highlighted below.



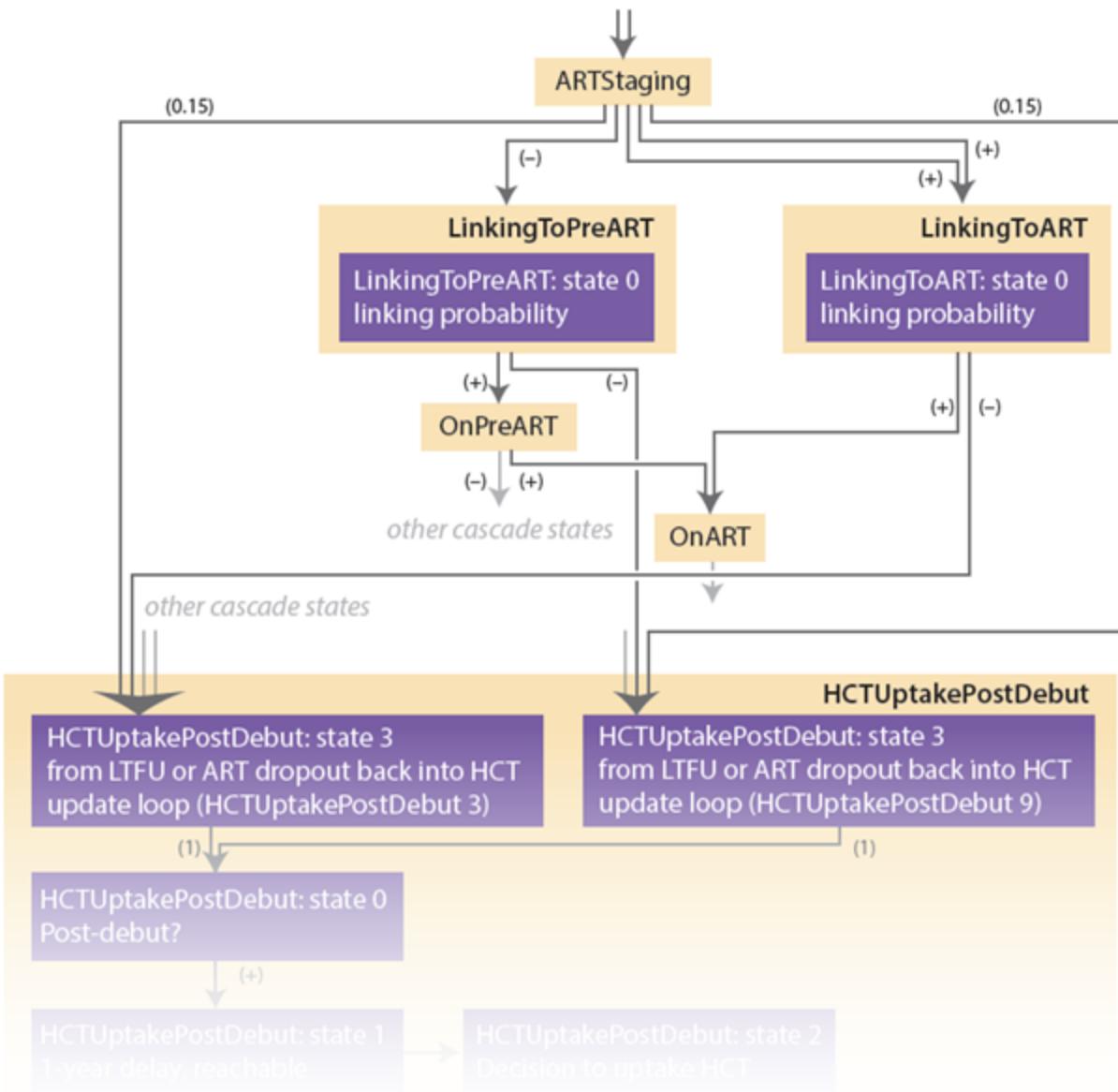
The next step of ART staging is another 15% loss to follow-up probability, which is applied only to individuals who are ineligible based on CD4-independent criteria. This represents an increased loss to follow-up associated with a CD4 count as a prerequisite for ART.

For those who are retained in ART staging at the penultimate step, the final step of ART staging is determining CD4-based eligibility. Those who are eligible go to LinkingToART, and those who are ineligible go to LinkingToPreART.



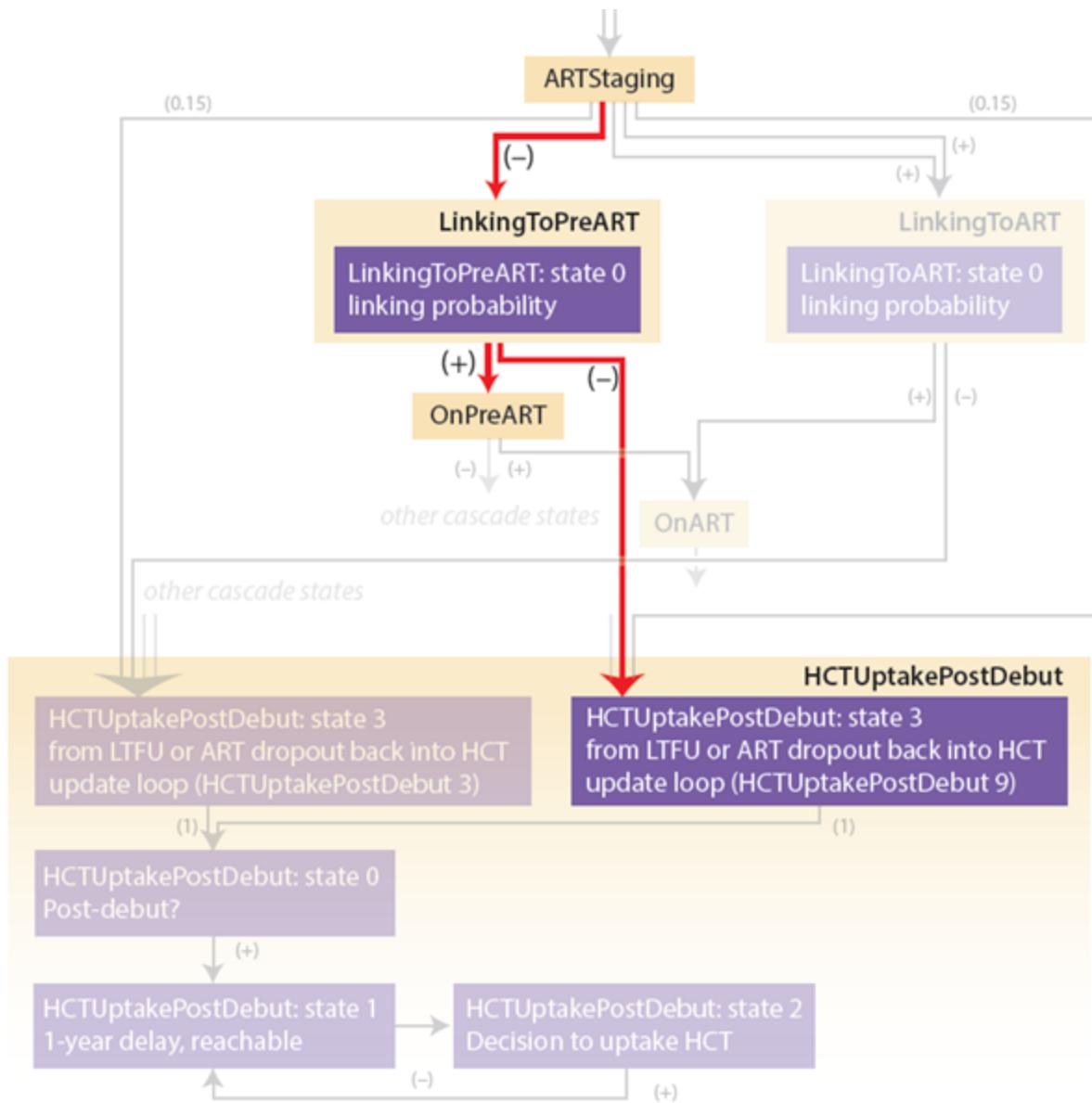
4-3-7. Linking to Care

The cascade states **LinkingToPreART** and **LinkingToART** each contain only one block, which is an **HIVSigmoidByYearAndSex**. It is also possible to include a gender bias in linkage probability using the parameter **Female_Multiplier**. The two blocks can link to pre-ART or ART, respectively, or can lead to loss to follow-up. The diagram below show how the two blocks fit into the healthcare process.



4-3-7-a. Linking to pre-ART

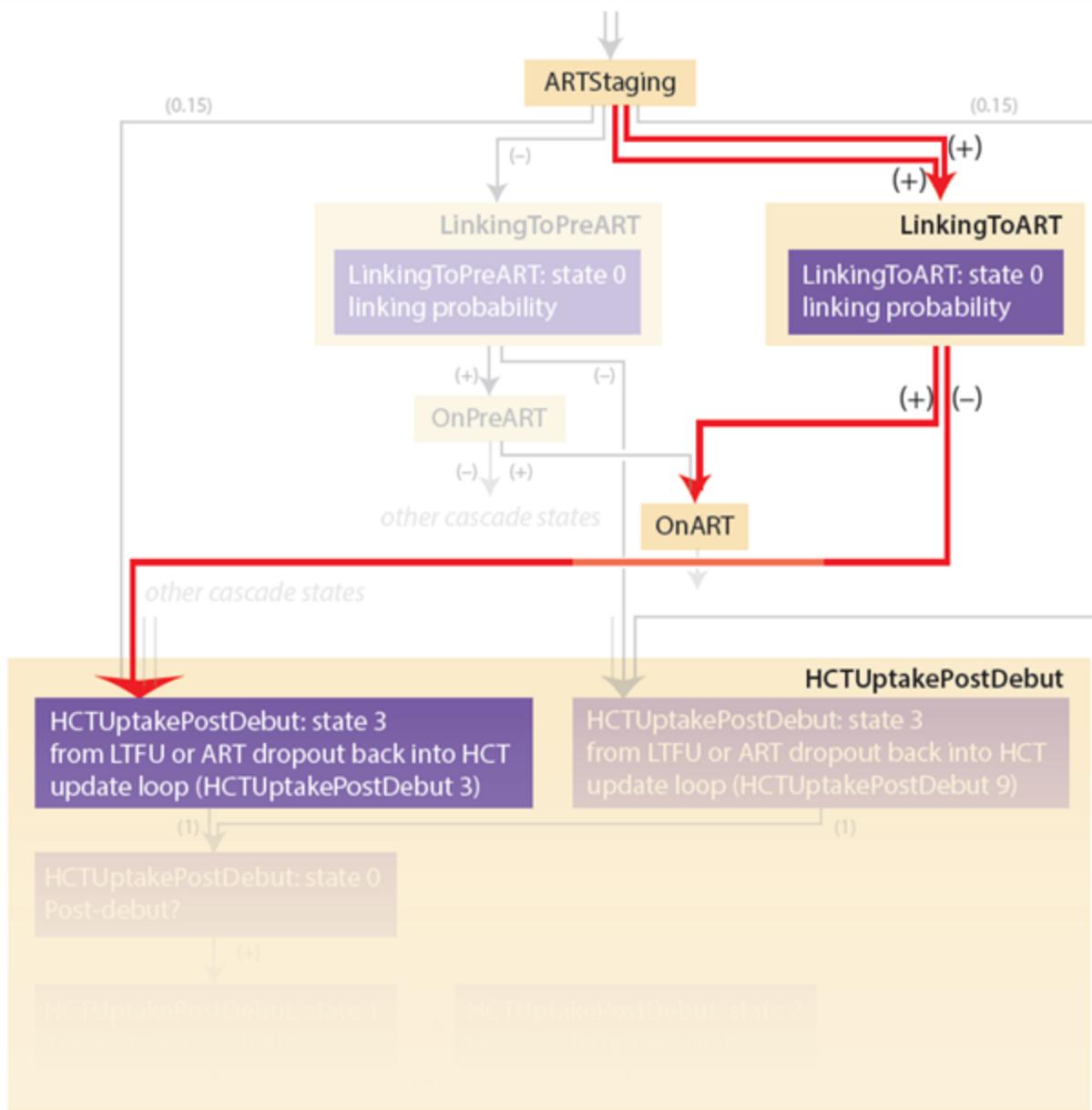
The probability of linking to pre-ART is time-variable, ramping from 46% to 70% with an inflection point in the year 2002. Those who do not link to pre-ART are lost to follow-up and enter the righthand block of **HCTUptakePostDebut**, discussed above, with a potential to re-initiate care later. Those who do link move to **OnPreART**.



In South Africa, the availability of ART was very limited prior to the start of the national treatment program in 2004. The pre-2004 influx of individuals reflects a demand for HIV care that preceded the availability for ART. The epidemic trend is not sensitive to the exact time trend used here, since individuals on pre-ART before 2004 were highly unlikely to receive ART and influence the epidemic trajectory.

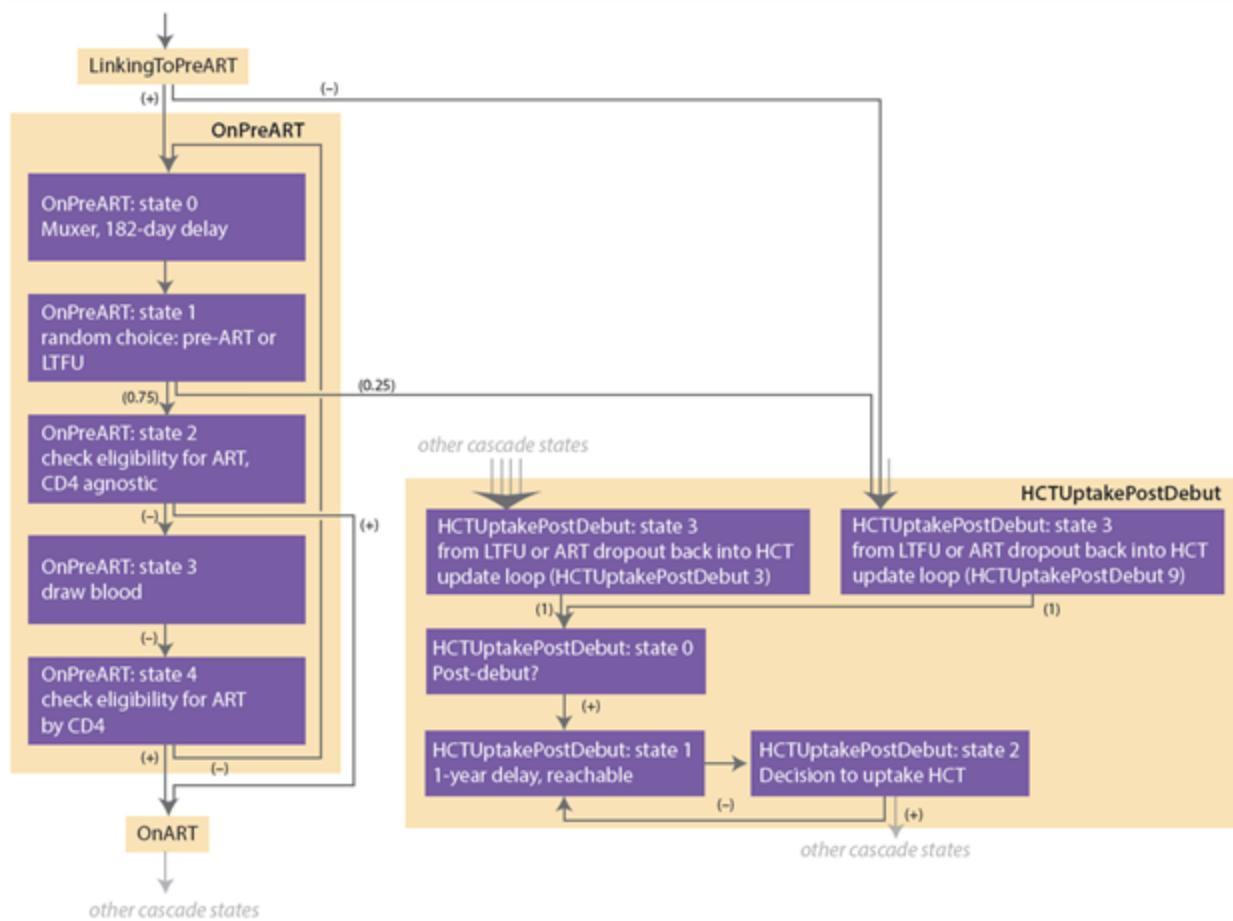
4-3-7-b. Linking to ART

The probability of linking to ART is time-variable, ramping from 0% to 90% with an inflection point in the year 2005. Those who do not link to ART are lost to follow-up and enter the lefthand block of HCTUptakePostDebut, discussed above, with a potential to re-initiate care later. Those who do link move to OnART.

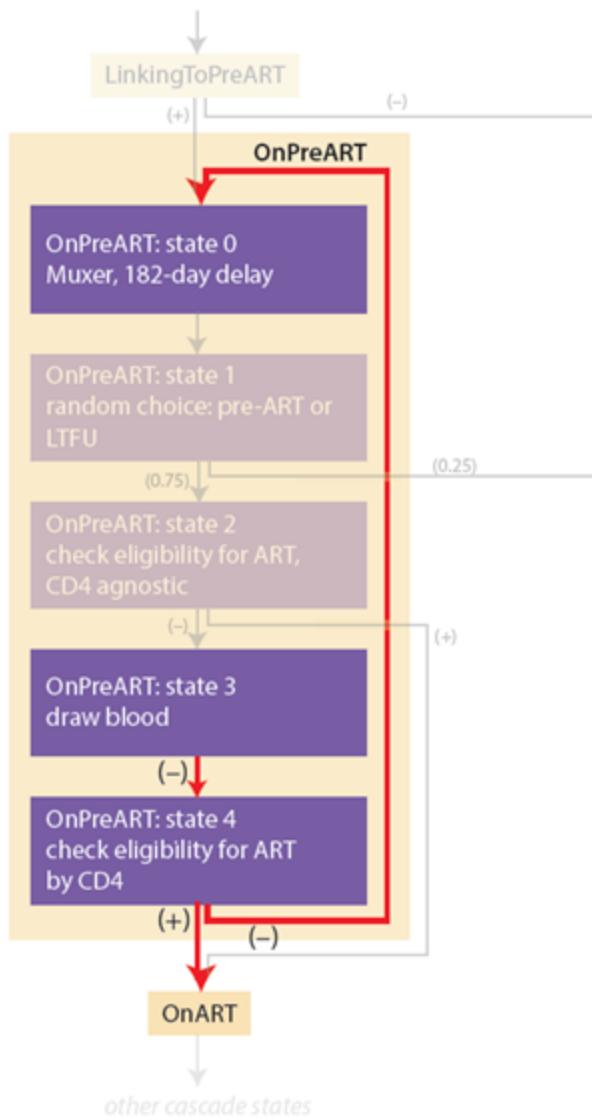


4-3-8. Pre-ART

Pre-ART is composed of five steps, similar to ART staging. The first step provides fixed a 6-month delay representing the recommended frequency of pre-ART monitoring. The second step contains a time-invariant probability of loss to follow-up upon each return appointment for pre-ART monitoring. It is configured using [HIVRandomChoice](#) to have a 25% probability of loss to follow-up, and links to the righthand entry point into HCTUptakePostDebut. The final three stages mirror those of ARTStaging: a CD4-agnostic eligibility check that leads to either OnART (if eligible) a phlebotomy step to record CD4 count (if ineligible by CD4-agnostic criteria). The final step checks eligibility by CD4 count, and leads to either OnART or another pre-ART monitoring visit 6 months later.

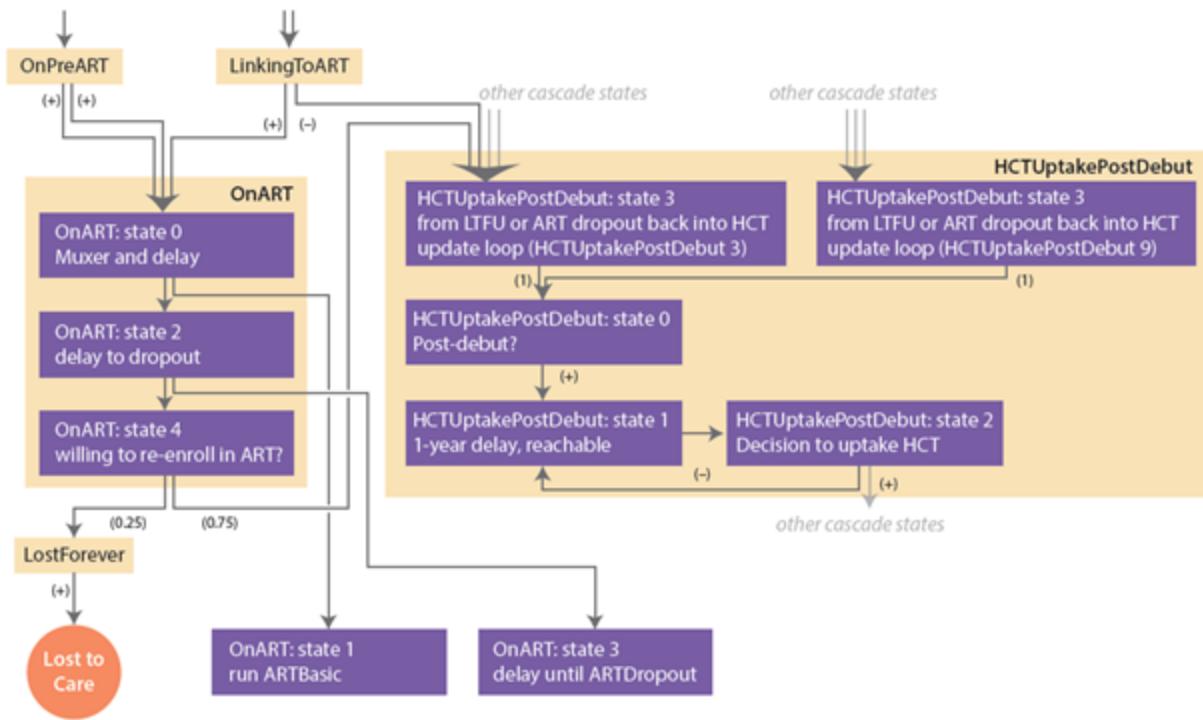


Unlike ARTStaging, PreART is a loop. If individuals are retained through all the stages and not found to be eligible for ART, they move from the last state back to the first state, as highlighted below.



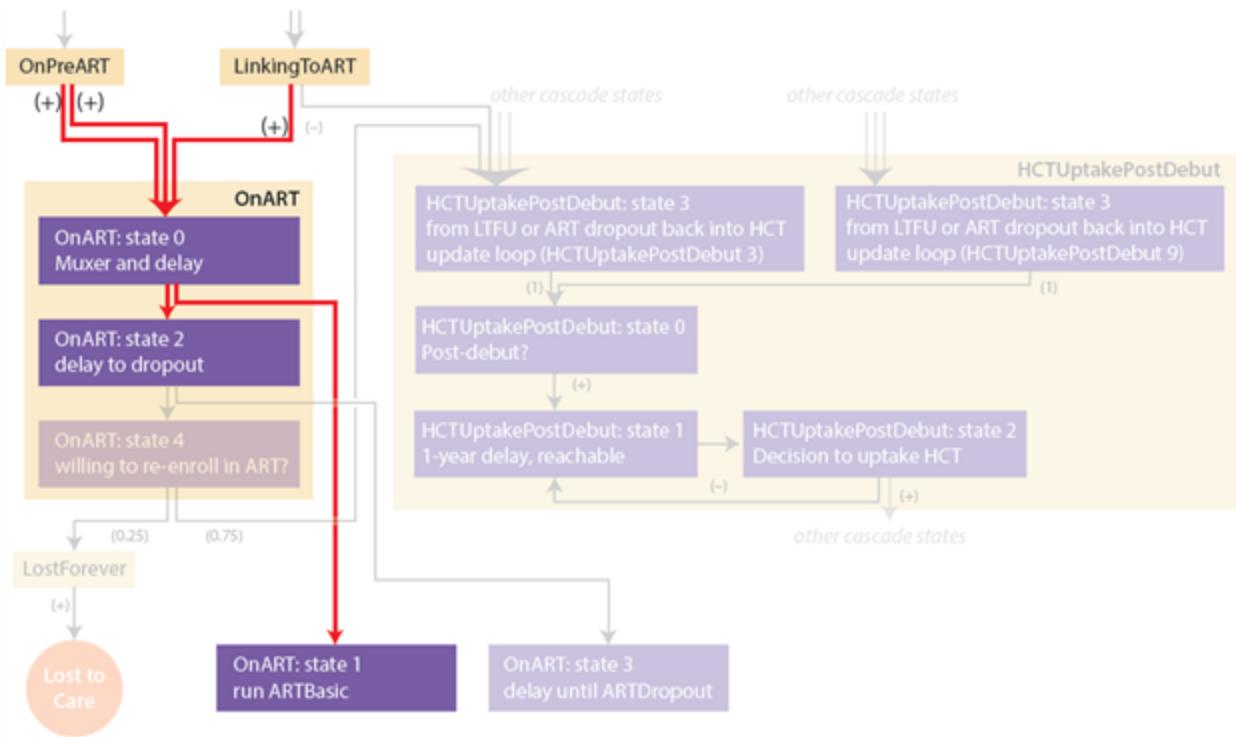
4-3-9. ART

The components of OnART deliver the final effect of the ART health care system on the individuals. The diagram below provides an overview of the inputs and outputs of OnART. There are three blocks that make up OnART: the first applies ART to the individual, the second configures the delay time until discontinuation of ART, and the third determines the proportion of those discontinued who could re-initiate ART, versus those who are LostForever.

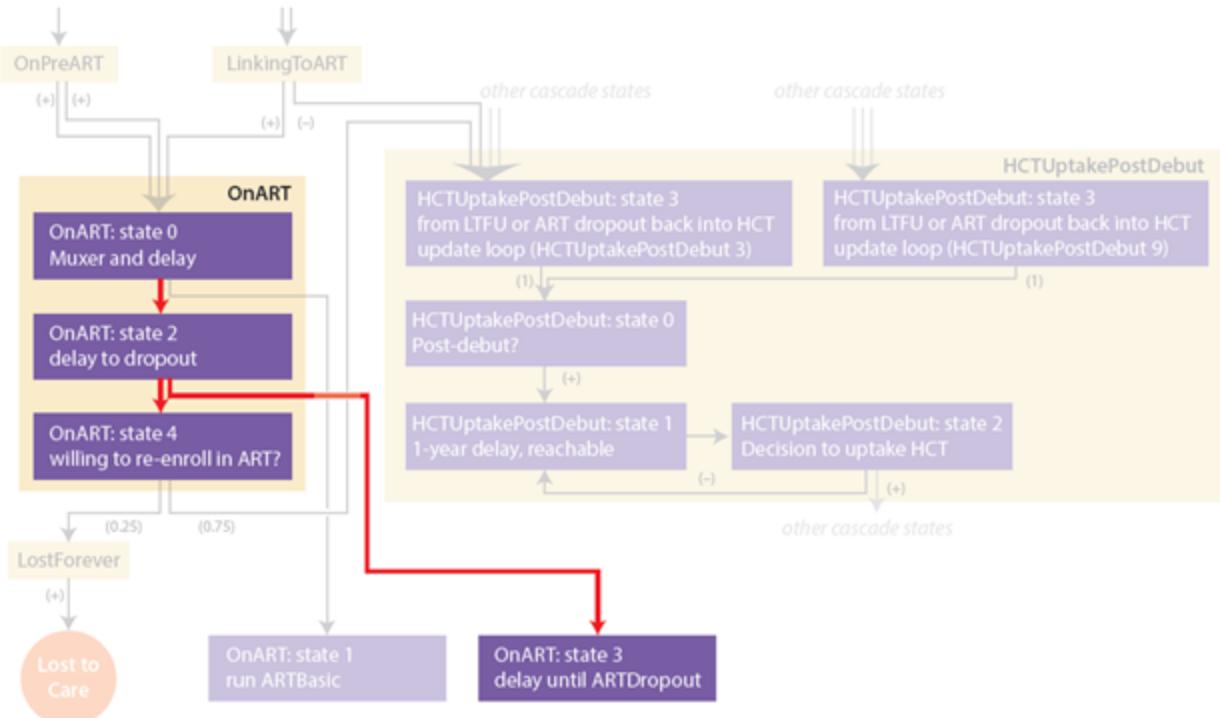


The first component of OnART is highlighted in the diagram below. It is triggered by LinkingToART and by the two eligibility blocks in OnPreART: CD4-agnostic and CD4-dependent. (Recall that LinkingToART consolidates the CD4-agnostic and CD4-dependent eligible individuals from ARTStaging, so only one link exists between LinkingToART and OnART.)

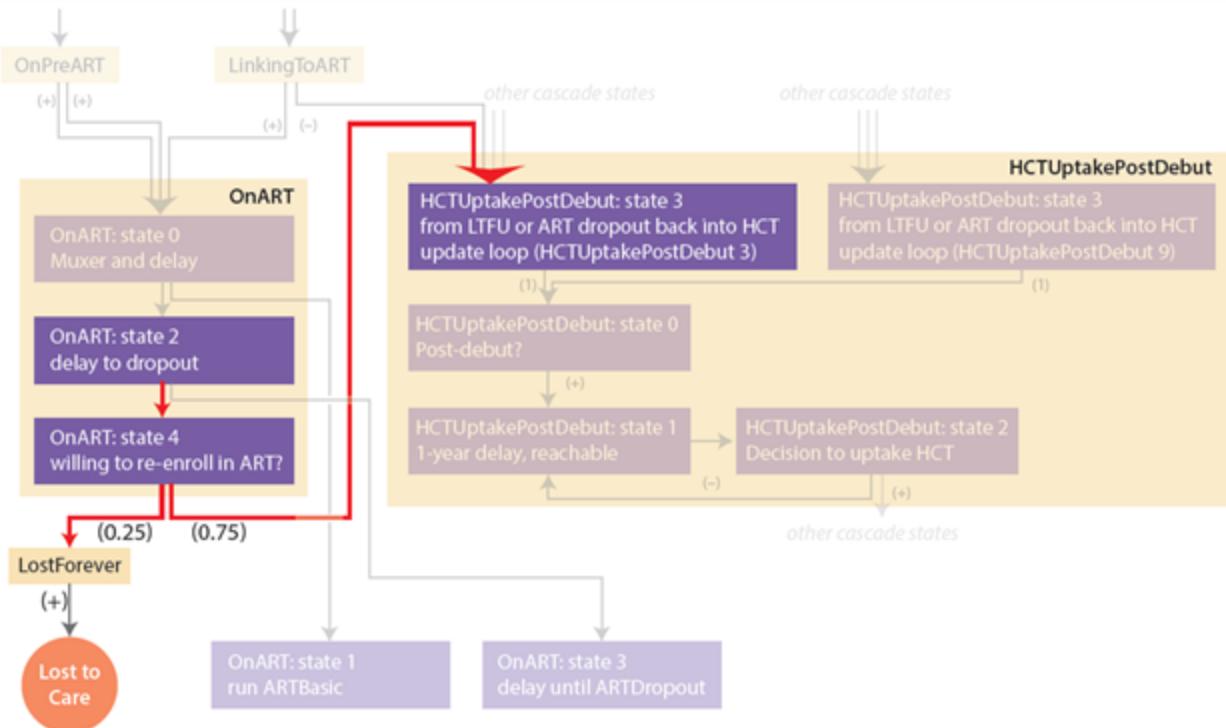
The effects of the first OnART block are four-fold. First, it creates a random delay, with a duration that is uniformly distributed between 1 and 120 days. This delay represents the time required for an individual to begin taking antiretroviral medications. Second, it prevents multiple initiations ART during this time, because it is a muxer and because its Cascade_State is listed in the Abort_States of many other stages of care. Third, after the delay time, it distributes the [ARTBasic](#) intervention. Fourth, it moved the individual into a delay state that determines the time until ART discontinuation.



ART discontinuation is assumed to occur at a rate of 20% per year, configured using an exponentially distributed delay time with a mean of 5 years. Scenario 5-2 describes how to make more complex assumptions about retention, including an initially high rate of discontinuation followed by a later low rate.



If an individual survives until the end of the middle delay block, then the third block is applied, which is a [HIVRandomChoice](#) between permanent discontinuation (`LostForever`) and the potential for re-initiation via the `HCTUptakePostDebut` mechanism described earlier. The RandomChoice is configured to allow re-initiation 75% of the time, but not all individuals who are given the chance to re-initiate will survive until re-initiation. Even those who do may suffer CD4 declines and AIDS progression, which increases mortality in the early period after ART re-initiation. Survival and disease progression during discontinuation and re-initiation of ART are described in [HIV Tutorial 2](#).



Congratulations! You have pieced together the building blocks of healthcare into a process for delivering ART, PMTCT, and VMMC. The next scenario will guide you through ways to change this baseline healthcare system, with an emphasis on future changes that could be used to represent future improvements in HIV care and prevention.

HIV Tutorial 5: Intervention Examples

In HIV Scenario 4, you learned about the building blocks of the health care system, and how to put them together to represent the scale-up in the guidelines, availability, and accessibility of HIV treatment and prevention services in sub-Saharan Africa. This tutorial will guide you through many possible ways to configure improvements to HIV programs that may be of interest to policy-makers, NGOs, and researchers.

For this tutorial, campaign override files (campaign_override.json) are added to the scenario directories. For the Quick Start tutorials, campaign override files only highlight the interventions that are of interest in a scenario and do not override the interventions in the campaign.json file. However, for the regression test scenarios in the EMOD source, campaign override files will override interventions when used with the regression_test.py script. See [Verifying the EMOD Executable](#) if you would like more information on regression tests.

5-1. Voluntary Medical Male Circumcision (VMMC)

Voluntary medical male circumcision (VMMC) is a one-time intervention that permanently reduces a male's susceptibility to HIV acquisition. By modifying the campaign.json input file, you can choose from a range of modes of access to VMMC. These include VMMC driven by existing levels of HIV testing in the model, a VMMC campaign targeted to all or a subset of the population, or health-seeking presentation for VMMC by individuals based on triggers such as their age.

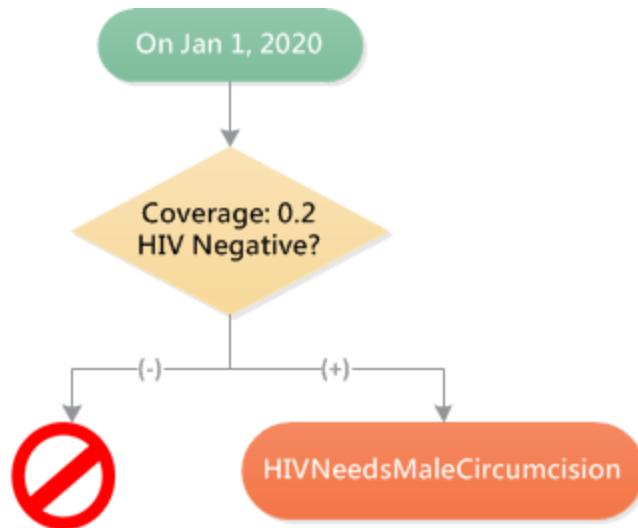
At the end of this scenario, a more complex configuration demonstrates expanded HIV testing for men that is integrated with both VMMC promotion and access to care for those diagnosed positive, including men who had previously been diagnosed and ART-experienced men who discontinued treatment.

5-1-a. One-Time VMMC Campaign

A simple way to model a VMMC intervention is to do so independently of current levels of HIV testing in men. For example, you might want to model the effect of providing VMMC to men in a particular year, without changing their HIV testing behavior or including the potential for HIV diagnosis and linkage to care for those diagnosed HIV positive.

Intervention scenario: On January 1, 2020, 20% of HIV-uninfected men receive VMMC.

To distribute the intervention, you must first distribute a diagnostic on Jan 1, 2020, to determine HIV status among 20% of males in the population. VMMC is then provided to those who have tested negative. Below is a diagram of the approach:



The intervention is implemented using a one-time diagnostic with a specified date, demographic coverage, sensitivity/specificity, and outcome. There are three diagnostics to choose from:

[SimpleDiagnostic](#) is available for all diseases supported by EMOD. When running `HIV_SIM`, it diagnoses with a desired sensitivity and specificity whether the individual is infected with HIV. A limitation of SimpleDiagnostic is that an action can only be taken upon positive diagnosis. In order to use SimpleDiagnostic to provide VMMC to HIV-negative men, you would have to set the sensitivity and specificity of the test to zero, which would invert the outcome of every test (providing a "positive" result for HIV-negative individuals).

[HIVSimpleDiagnostic](#) extends the generic SimpleDiagnostic to allow for different actions to be taken upon positive and negative diagnosis. This is ideal for a VMMC scenario, because a negative diagnosis needs to trigger a health action. HIVSimpleDiagnostic is also associated with a `Cascade_State` and can include `Abort_States` to prevent multiple entries into care.

[HIVRapidHIVDiagnostic](#) has the features of HIVSimpleDiagnostic, and also updates the individual's knowledge of HIV status. This could potentially change the individual's future access to ART, sero-sorting behavior, and future testing behavior. This diagnostic should be chosen only if you wish to include the effects of knowledge of status as part of the impact of the VMMC campaign.

This example uses HIVSimpleDiagnostic, which will not incorporate the impact of knowledge of status resulting from HIV testing in the VMMC campaign. This assumes that nothing happens as a result of a positive HIV diagnosis (`NoTrigger`), but that negative HIV diagnosis could lead to VMMC (`HIVNeedsMaleCircumcision`, which triggers an intervention that provides VMMC).

The diagnostic is distributed on January 1, 2020, by setting the `Start_Year` to 2020. The testing is targeted only to 20% of men by setting `Demographic_Coverage` to 0.2 and `Target_Gender` to Male. To configure a test that is always accurate and specific in diagnosing HIV-positive individuals, set `Base_Specificity` and `Base_Sensitivity` to 1.

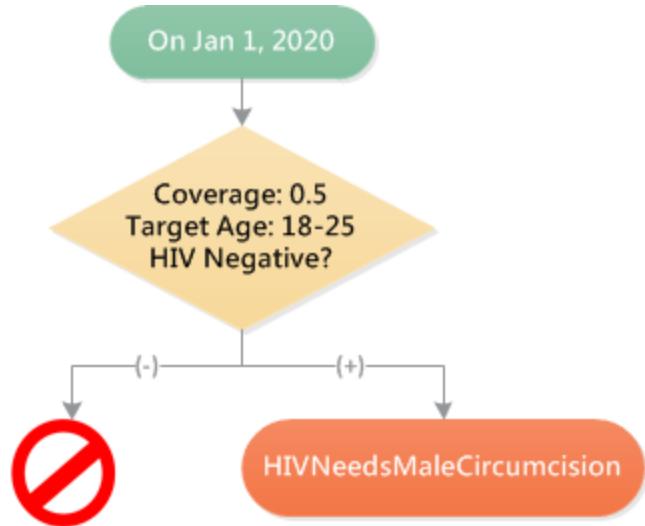
```
{
  "class": "StandardInterventionDistributionEventCoordinator",
  "Target_Demographic": "ExplicitAgeRangesAndGender",
  "Target_Gender": "Male",
  "Demographic_Coverage": 0.2,
  "Intervention_Config":
  {
    "class": "HIVSimpleDiagnostic",
    ...
    "Base_Specificity": 1,
    "Base_Sensitivity": 1,
    ...
    "Positive_Diagnosis_Event": "NoTrigger",
    "Negative_Diagnosis_Event": "HIVNeedsMaleCircumcision"
  }
}
```

Although you have chosen to target ExplicitAgeRangesAndGender, the ages range to be targeted has not been specified. By default, this will provide the intervention to all ages.

5-1-b. One-Time Age-Targeted VMMC Campaign

Intervention scenario: 50% of HIV-uninfected men between the ages of 18 and 25 become circumcised on Jan 1, 2020.

To target only a specific age range with VMMC, simply add the minimum and maximum ages to the campaign file where the HIVSimpleDiagnostic is specified. The overall structure of the campaign file remains the same:



For example, to target 50% of males between the ages of 18 and 25, configure the diagnostic as follows:

```
{
  "class": "StandardInterventionDistributionEventCoordinator",
  "Target_Demographic": "ExplicitAgeRangesAndGender",
  "Target_Age_Min": 18,
  "Target_Age_Max": 25,
  "Target_Gender": "Male",
  "Demographic_Coverage": 0.5,
  "Intervention_Config":
  {
    "class": "HIVSimpleDiagnostic",
    ...
    "Positive_Diagnosis_Event": "NoTrigger",
    "Negative_Diagnosis_Event": "HIVNeedsMaleCircumcision"
  }
}
```

5-1-c. Continuous Availability of VMMC for Adults and Infants

Instead of a one-time VMMC campaign, you may want to model continuous provision of VMMC services.

Intervention scenario: HIV-uninfected men receive VMMC at a continuous rate of 5%/year (on a continual basis over time) beginning on Jan 1, 2020.

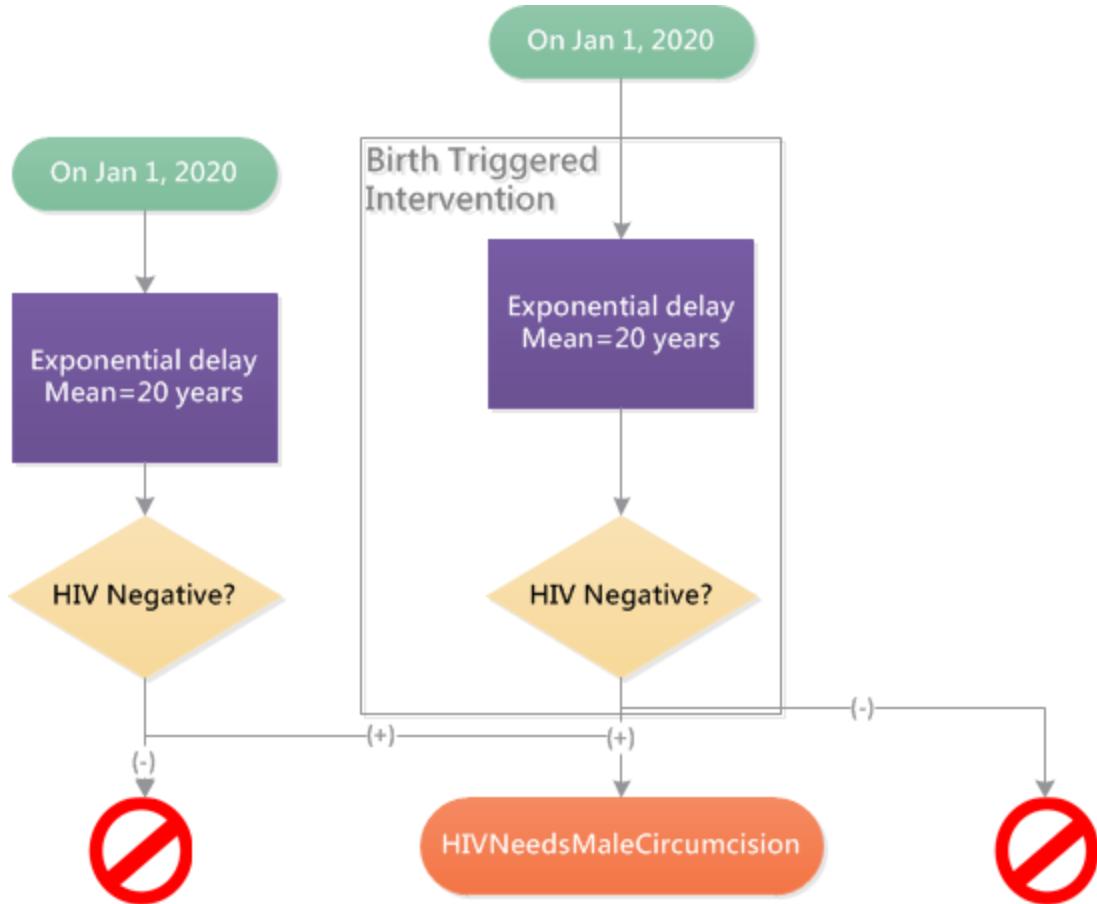
For individuals born before 2020, VMMC is distributed similarly to the one-time intervention, but with an added delay loop. The DelayedIntervention block below creates an exponentially distributed delay time of 20 years (specified as 7300 days), producing a continuous 5%/year rate of triggering HIVNeed-sMaleCircumcision.

```
{
  "class": "DelayedIntervention",
  ...
  "Delay_Distribution": "EXPONENTIAL_DURATION",
  "Delay_Period": 7300,
  "Actual_IndividualIntervention_Configs": [
    {
      "class": "HIVSimpleDiagnostic",
      ...
      "Negative_Diagnosis_Event": "HIVNeedsMaleCircumcision"
    }
  ]
}
```

For those born on or after 2020, the 20-year exponential delay is provided as a birth-triggered intervention by wrapping the exponential delay in a BirthTriggeredIV as follows:

```
{
  "class": "BirthTriggeredIV",
  "Actual_IndividualIntervention_Config":
  {
    "class": "DelayedIntervention",
    "Delay_Distribution": "EXPONENTIAL_DURATION",
    "Delay_Period": 7300,
    "Actual_IndividualIntervention_Configs": [
      {
        "class": "HIVSimpleDiagnostic",
        ...
        "Negative_Diagnosis_Event": "HIVNeedsMaleCircumcision"
      }
    ]
  }
}
```

The combination of current-population and birth-triggered interventions produces a continuous rate of circumcision, depicted below:



Note that for individuals born on Jan 1, 2020 (or the timestep that contains Jan 1, 2020), both the population-wide and the birth-triggered interventions are applied. These individuals will receive a doubled

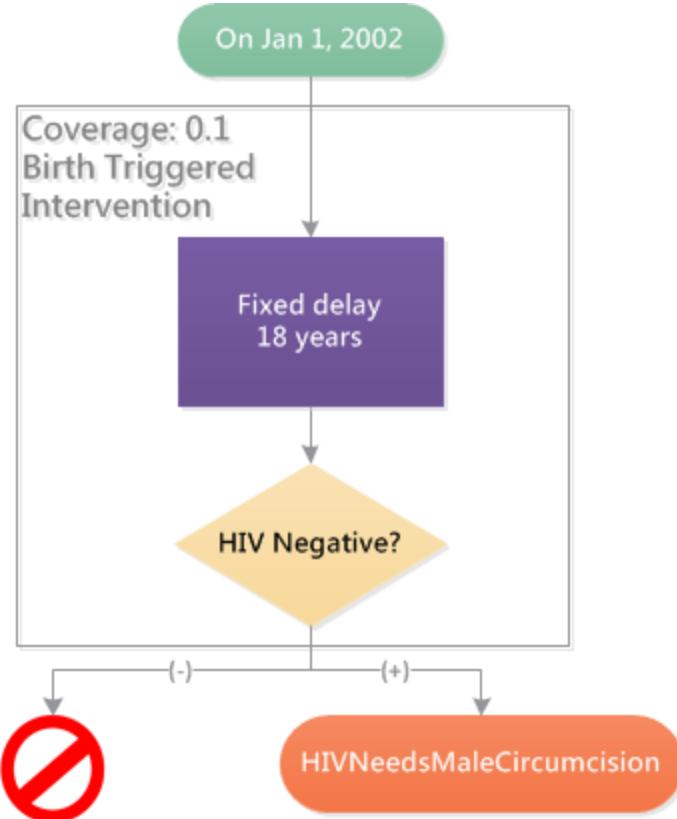
(10%/year) rate of VMMC. The time of the birth-triggered intervention can be applied one timestep later to avoid doubling the VMMC rate for these individuals.

5-1-d. Age-Triggered VMMC

In this scenario, you will learn how to trigger VMMC for individuals upon reaching a specified age.

Intervention scenario: Starting on Jan 1, 2020, 10% of HIV-uninfected men become circumcised upon reaching their 18th birthday.

A simple way to provide circumcision to 18-year-olds beginning in 2020 is to provide a birth-triggered intervention starting in 2002 - 18 years prior to the beginning of the circumcision campaign -- that contains a fixed 18-year delay. HIV status is checked after the 18-year delay to ensure that only HIV-uninfected men receive VMMC. The structure of the campaign is depicted in the diagram below:



In the campaign.json file, a birth-triggered delay of 6570 days, or 18 years, is provided starting in 2002:

```

"Start_Year": 2002,
...
{
  ...
  {
    ...
    "class": "BirthTriggeredIV",
    ...
  }
}
  
```

```

    "class": "DelayedIntervention",
    "Delay_Distribution": "FIXED_DURATION",
    "Delay_Period": 6570,
    ...
    {
        ...
        [
            ...
            "class": "HIVSimpleDiagnostic",
            ...
            "Negative_Diagnosis_Event": "HIVNeedsMaleCircumcision"
        ]
    }
}
}
}

```

This template can be extended to include variability in the exact age at which VMMC takes place. For example, if you wanted the age of VMMC to be uniformly distributed between the ages of 18 and 20, you could replace the FIXED_DURATION portion of the campaign with:

```

"Delay_Distribution": "UNIFORM_DURATION",
"Delay_Period_Min": 6570,
"Delay_Period_Max": 7300,

```

5-1-e. VMMC Driven by Existing Levels of Testing

In this scenario, you will use existing levels of HIV testing to increase VMMC by giving men who test negative a time-variable probability of VMMC uptake. Only men who were already testing for HIV in the baseline scenario would receive the VMMC intervention.

Intervention scenario: After January 1, 2020, all males who test negative during voluntary HIV counseling and testing consider voluntary male medical circumcision.

In the provided campaign.json file representing a baseline health care system, negative HIV diagnoses can occur in two places: among those presenting for repeat/voluntary testing at testing centers, and among those testing via other health care modalities such as antenatal, symptomatic, or partner testing. In this example, negative diagnoses in both of these tests have to potential to lead to VMMC.

Like in the previous example, the intervention should only go into effect after a specific date (January 1, 2020). Previously, because a new intervention was being provided, the start time could be configured by setting the Start_Year of HIV testing. This time, the time-dependent trigger must be configured differently, because VMMC will be triggered by pre-existing levels of HIV testing.

The time-based trigger is implemented using the [HIVPiecewiseByYearAndSexDiagnostic](#). Individuals who test negative are sorted both by gender and by the time of their HIV test. Only negative diagnosis among males ("Female_Multiplier": 0) testing after January 1, 2020, lead to VMMC.

To configure the time-based switch, you can use HIVPiecewiseByYearAndSexDiagnostic with an Interpolation_Order of zero and a Time_Value_Map that switches from 0% to 50% probability of VMMC.

```
{
  ...
  {
    ...
    {
      ...
      {
        "class": "HIVPiecewiseByYearAndSexDiagnostic",
        ...
        "Time_Value_Map" :
        {
          "Times": [ 1960,2020 ],
          "Values": [ 0, 0.5 ]
        },
        "Interpolation_Order": 0,
        "Female_Multiplier": 0,
        ...
      }
    }
  }
}
```

It is possible to configure a more gradual roll-out of VMMC by adding more "steps" to the "staircase" specified by the Time_Value_Map. The probability can also be made to vary linearly between the points of the Time_Value_Map by setting Interpolation_Order to 1.

5-1-f. Expansion of HIV Testing and VMMC

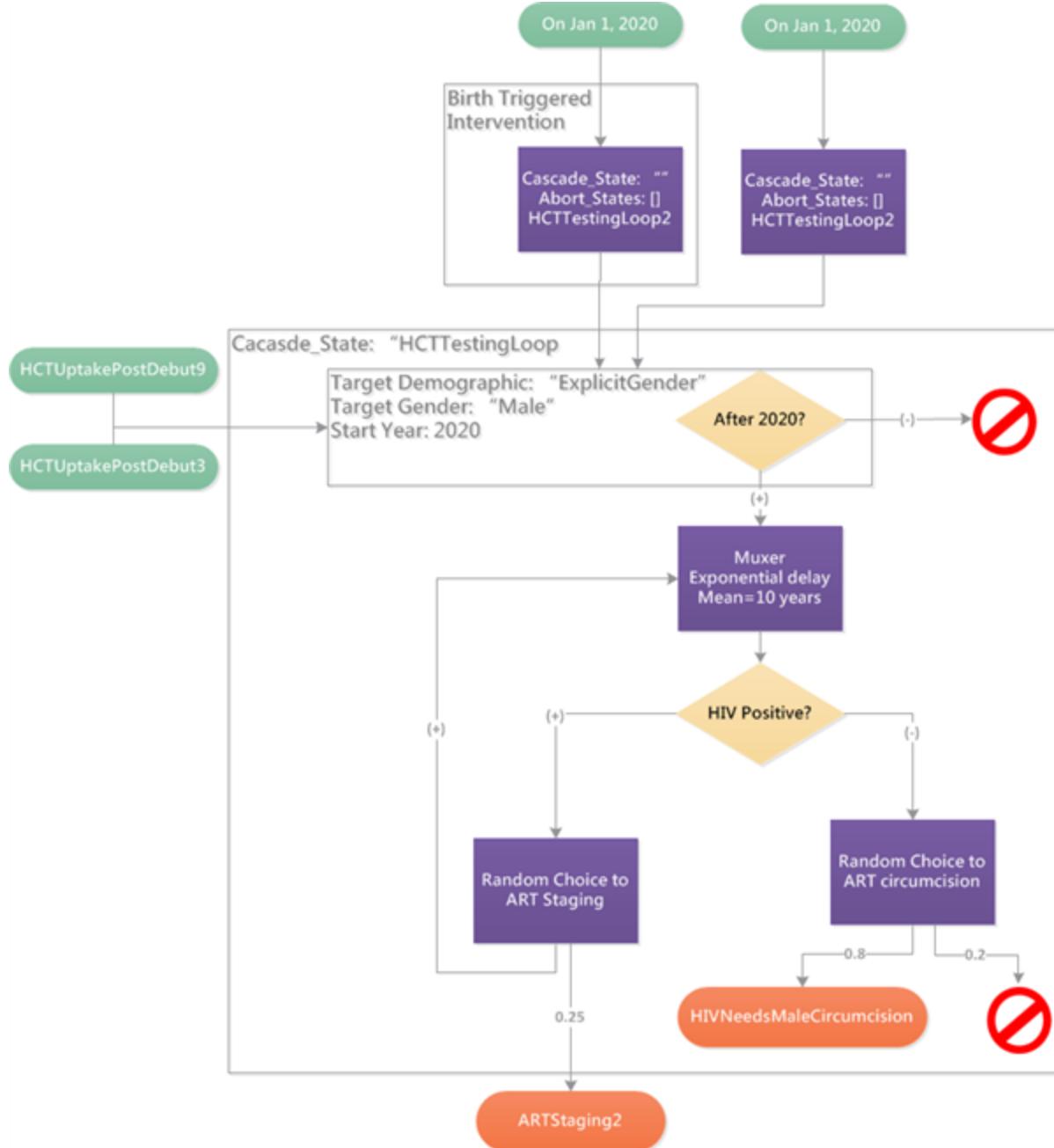
So far, you have seen how to provide VMMC through existing levels of testing, or through an isolated campaign that avoids association between VMMC-related testing and the potential for behavior change, changes in future testing behavior, and access to treatment.

This scenario shows how to increase HIV testing in a manner that can both link HIV-positive individuals to care and link HIV-negative men to VMMC services.

Intervention scenario: Starting on Jan 1, 2020, additional HIV testing is provided for all men at a rate of 10% per year (on a continual basis over time). Those testing positive are referred to an HIV clinic for staging if not already in care. Of those, 25% immediately appear for staging and 75% resume their pre-test behavior. Those testing negative immediately receive VMMC with 80% probability.

This is one of the more complex scenarios that is demonstrated. One approach to implementing the scenario is illustrated below. In this approach, testing at a rate of 10% per year is provided not only to treatment-naive men in 2020 and thereafter, but is also provided to men who discontinue care. Thus, the testing campaign also provides an avenue for men to re-initiate care that has been discontinued.

(These assumptions can be modified easily by changing the trigger conditions for the testing campaign, which is explained below). The overall approach is illustrated by the diagram below:



First, an event called HCTTestingLoop2 is broadcast to the entire the population in 2020, as well as at birth among those born after 2020 (using [BirthTriggeredIV](#) as shown previously in the "continuous VMMC campaign" scenario).

```
{
  "Start_Year": 2020,
```

```

...
{
  "Coverage": 1,
  ...
  {
    ...
    "Broadcast_Event": "HCTTestingLoop2"
  }
}
}

{
  "Start_Year": 2020,
  ...
  {
    "Demographic_Coverage": 1,
    "class": "BirthTriggeredIV",
    ...
    {
      ...
      "Broadcast_Event": "HCTTestingLoop2"
    }
  }
},

```

These individuals are then merged with individuals who have become lost to care, and a filter is applied to ensure that only those lost to care after 2020 are included, and that only males who have access to health care can proceed with the intervention.

In the excerpt below, the `Trigger_Condition_List` represents the merging of individuals who have received the expanded testing (HCTTestingLoop2), individuals who discontinued care after diagnosis but before initiating ART (HCTUptakePostDebut3), and ART-experienced individuals who have discontinued treatment (HCTUptakePostDebut9).

```

"Start_Year": 2020,
...
{
  "Target_Demographic": "ExplicitGender",
  "Target_Gender": "Male",
  ...
  {
    "Property_Restrictions_Within_Node":
      [
        { "Accessibility": "Yes" }
      ],
    ...
    "Trigger_Condition_List": [

```

```

        "HCTTestingLoop2",
        "HCTUptakePostDebut9",
        "HCTUptakePostDebut3"
        ...
    ],
    "Actual_IndividualIntervention_Config":
    {
        ...
        "Broadcast_Event": "HCTTestingLoop3"
    }
}
}

```

Those who pass the filter above broadcast the state HCTTestingLoop3, which in turn triggers HCTTestingLoop4 after an exponentially distributed 10-year delay. Note that this delay can also be triggered by a second event, HCTTestingLoop6, which represents males who failed to link to VMMC during a prior test, but could link later after repeat testing.

```

{
...
{
...
{
    "Trigger_Condition": "TriggerList",
    "Trigger_Condition_List": ["HCTTestingLoop3", "HCTTestingLoop6"],
    {
        ...
        "class": "HIVMuxer",
        "Abort_States": [ "LostForever", "OnART", "LinkingToART", "OnPreART", "LinkingToPreART", "ARTStaging" ],
        ...
        "Delay_Distribution": "EXPONENTIAL_DURATION",
        "Delay_Period": 3650,
        "Broadcast_Event": "HCTTestingLoop4"
    }
}
}
}

```

The Abort_States array of the [HIVMuxer](#) ensures that individuals who are already in HIV care or who have been "LostForever" to care do not enter care again through the testing campaign.

Finally, after the exponentially distributed 10-year delay (i.e., 10% per year testing rate), individuals receive an HIV diagnostic.

```
{
...
{
  ...
  {
    "Trigger_Condition": "HCTTestingLoop4",
    ...
    {
      "class": "HIVRapidHIVDiagnostic",
      ...
      "Positive_Diagnosis_Event": "HCTTestingLoop5",
      "Negative_Diagnosis_Event": "HCTTestingLoop6"
    }
  }
}
}
```

Positive diagnosis leads to a 25% probability of presenting for ART staging. The 75% who do not present for staging will continue to receive the 10%/year HIV testing intervention, which will provide another opportunity for linkage after an average of 10 years.

```
{
...
{
  ...
  {
    ...
    "Trigger_Condition": "HCTTestingLoop5",
    {
      ...
      "class": "HIVRandomChoice",
      "Choices":
        {
          "ARTStaging2": 0.25,
          "HCTTestingLoop3": 0.75
        }
    }
}
}
```

Negative diagnosis leads to an 80% probability of receiving VMMC.

```
{
...
{
  ...
}
```

```
{  
    ...  
    "Trigger_Condition": "HCTTestingLoop6",  
    {  
        ...  
        "class": "HIVRandomChoice",  
        "Choices":  
        {  
            "HIVNeedsMaleCircumcision": 0.8,  
            "NoTrigger": 0.2  
        }  
    }  
}
```

In addition to triggering VMMC in 80% of males, HCTTestingLoop6 also triggers resumption of testing at the 10%/year rate, since HCTTestingLoop6 is also in the Trigger_Condition_List for the exponentially distributed 10-year delay.

Congratulations! You have learned how to configure different outcomes for males who receive the new testing intervention: those who test positive could link to care or re-test later, and those who test negative could receive VMMC or re-test later. This relatively complex intervention scenario illustrates the power of the flexible campaign framework to explicitly define the way that an intervention connects to existing health care availability and how individuals lost to existing health care might interact with new programs.

5-2. Treatment Eligibility

An important question for ART programs is how universal eligibility for ART would change the patterns of ART access and retention. On one hand, earlier initiation could increase the risk of treatment discontinuation, especially if treatment is not perceived as being medically necessary. On the other hand, universal eligibility has the potential to simplify the treatment initiation process, and may reduce losses to care that are associated with the complexity of treatment initiation.

This scenario will guide you through the configuration of future treatment guidelines, and will show you how to modify assumptions about access to care after changes in treatment guidelines.

5-2-a. Configuring Expansion of Treatment Guidelines

You have already learned how to configure historical eligibility and access to treatment using the campaign.json file. This scenario will guide you through modifying future treatment guidelines to create projections.

Intervention scenario: Starting on January 1, 2020, everyone is eligible for ART.

The intention is to change future guidelines independently of any changes to the process of accessing care. However, in certain ways, the two cannot be considered entirely independent.

For example, in the [Scenario 4-3-6](#), you learned how CD4 testing and return for results is a frequent point at which patients are lost from care. In a world of universal eligibility, would CD4 testing be a prerequisite for treatment initiation?

In EMOD, it is simple to configure universal eligibility either with or without a prerequisite to complete CD4 testing before initiation.

Recall that in the last scenario, the campaign.json file included evaluation of eligibility for ART in two places: at initial staging, and at return visits during pre-ART monitoring. Each of those in turn had two steps. First, CD4-agnostic factors such as AIDS symptoms, age, and pregnancy are checked using a [HIVARTStagingCD4AgnosticDiagnostic](#). Then CD4-based eligibility is checked using a [HIVARTStagingByCD4Diagnostic](#).

If CD4 testing is to remain a prerequisite for treatment initiation (except among those with CD4-agnostic eligibility such as symptoms or pregnancy), then universal eligibility can be created by increasing the CD4 threshold to a large value beginning in 2020:

```
"class": "HIVARTStagingByCD4Diagnostic",
...
"Threshold": {
    "Times": [2004, 2011.8, 2015, 2020],
    "Values": [200, 350, 500, 1000000]
}
```

The 2020 values should be added to both initial staging and pre-ART monitoring, unless eligibility is intended to be different in those two situations.

If universal eligibility is to eliminate the need for CD4 testing as a prerequisite for treatment initiation, then eligibility should be added to the earlier, CD4-agnostic evaluation of eligibility called the [HIVARTStagingCD4AgnosticDiagnostic](#). A simple way to do this is to lower the WHO clinical stage threshold for eligibility:

```
"class": "HIVARTStagingCD4AgnosticDiagnostic",
...
"Adult_By_WHO_Stage": {
    "Times": [2004, 2011.8, 2020],
    "Values": [4, 3, 0]
}
```

Again, the 2020 values should be added for both initial staging and pre-ART monitoring, unless eligibility is intended to be different in these two situations.

The included campaign.json file contains both of the above changes: universal eligibility is applied in a CD4-agnostic manner as well as a CD4-dependent manner. This is equivalent to assuming that CD4 counts are not a prerequisite for universal eligibility, because the CD4-agnostic eligibility will always be applied to individuals first. To run the scenario with CD4-dependent eligibility, simple delete the 2020 values for eligibility Adult_By_WHO_Stage.

5-2-b. Impact of Expanded Guidelines on Retention

An important question about treatment expansion is its potential impact on retention. In this scenario, you will build upon the CD4-agnostic eligibility demonstrated above, and will learn how to configure a change in retention associated with early treatment initiation.

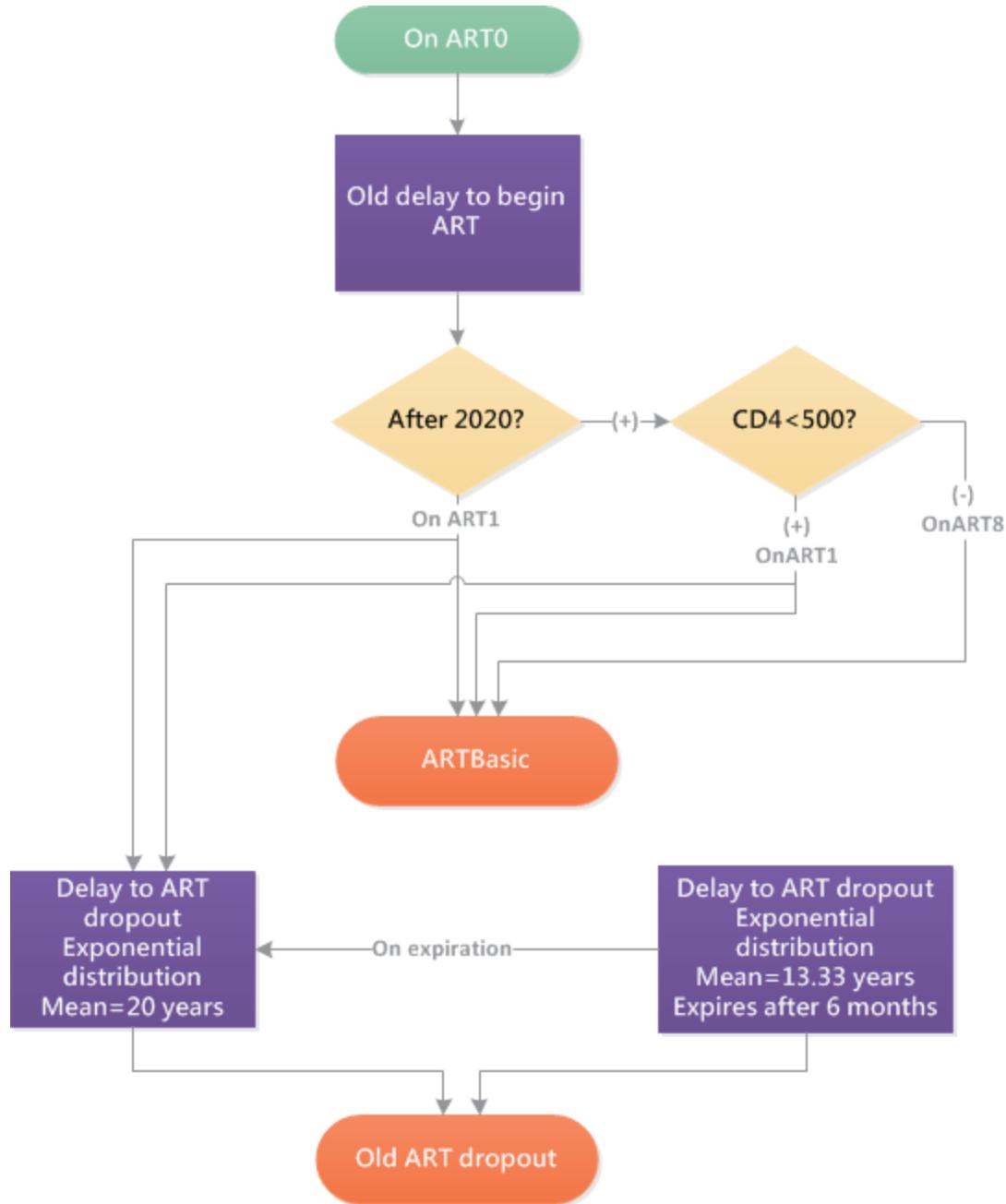
Intervention scenario: Starting on January 1, 2020, everyone is eligible for ART. The rate of treatment discontinuation is 50% higher (1.5x) in the first 6 months of treatment for those initiating with CD4>500 compared to CD4 350-500, but retention after 6 months for those initiating at CD4>500 is equal to retention for those initiating at CD4 350-500.

In [HIV Tutorial 4: Health Care](#), you learned how to configure a rate of treatment discontinuation by creating an exponential delay until discontinuation that is provided at the same time as ART initiation. For example, for a 5% per year discontinuation rate, an exponentially distributed delay of 20 years was provided.

For this scenario, a more rapid discontinuation rate of 7.5% per year is applied for six months to those initiating under expanded guidelines. It is only applied after 2020 and for those initiating with CD4>500.

After six months, the 7.5% per year rate "expires" and reverts to the original 5% per year rate.

The approach is illustrated below:



The diagram begins with the state **On ART0**, representing the delay until initiation of ART identical to the one in the previous scenario. Instead of **On ART0** triggering initiation of ART (through the intervention [ArtBasic](#)), it instead triggers a time-based filter using [HIVPiecewiseByYearAndSexDiagnostic](#). Starting on Jan 1, 2020, all those testing positive are initiated in ART or pre-ART in the same model timestep, with no delays, but still experience the same overall probabilities of loss to follow-up between testing and pre-ART/ART as before the elimination of delays.

```

"class": "HIVPiecewiseByYearAndSexDiagnostic",
...
  
```

```

"Time_Value_Map" :
{
  "Times": [ 1990, 2020 ],
  "Values": [ 0, 1 ]
},
"Interpolation_Order": 0,

```

Before 2020, this broadcasts OnART1, which, triggers the usual ARTBasic and 5%/year rate of discontinuation. After 2020, the HIVPiecewiseByYearAndSexDiagnostic broadcasts OnART7, which in turn checks CD4 count as follows:

```

"class": "CD4Diagnostic",
"CD4_Thresholds": [
{
  "Low": 0,
  "High": 500,
  "Event": "OnART1"
},
{
  "Low": 500,
  "High": 100000,
  "Event": "OnART8"
}
]

```

If the CD4 count is below 500 cells/uL, the event broadcasts OnART1, triggering the usual ARTBasic with 5%/year discontinuation. If CD4 is above 500 cells/uL, then it instead broadcasts OnART8.

OnART8 is configured to trigger ARTBasic just like OnART1. Indeed, they both link to the same intervention. Two triggers can be connected to one intervention using a `Trigger_Condition_List`:

```

"Trigger_Condition": "TriggerList",
"Trigger_Condition_List": ["OnART1", "OnART8"],
...
{
  "class": "ARTBasic"
}

```

OnART8 also triggers a temporarily applied exponential rate of 7.5% per year (i.e., one per 4866.67 days), which expires after 6 months (i.e., 183 days), as follows:

```

"Trigger_Condition": "OnART8",
...
{
  ...
}

```

```

    "Delay_Distribution": "EXPONENTIAL_DURATION",
    "Delay_Period": 4866.67,
    "Expiration_Period": 183,
    "Broadcast_Event": "OnART3",
    "Broadcast_On_Expiration_Event": "OnART9"
}

```

If discontinuation of care has not happened after six months, OnART8 will expire and trigger its `Expiration_Event`, OnART9, which joins back to the usual 5% per year discontinuation. Again, the discontinuation intervention is shared by OnART9 (for those who after 2020 with $CD4 > 500$) and OnART1 (those who initiated before 2020 or with $CD4 < 500$) using a `Trigger_Condition_List`:

```

"Trigger_Condition_List": ["OnART1", "OnART9"],
...
{
  ...
  "Delay_Distribution": "EXPONENTIAL_DURATION",
  "Delay_Period": 7300,
  ...
}

```

Thus the increased discontinuation rate of 7.5% per year is applied for only six months, after which individuals are merged back into their former patterns of health care access.

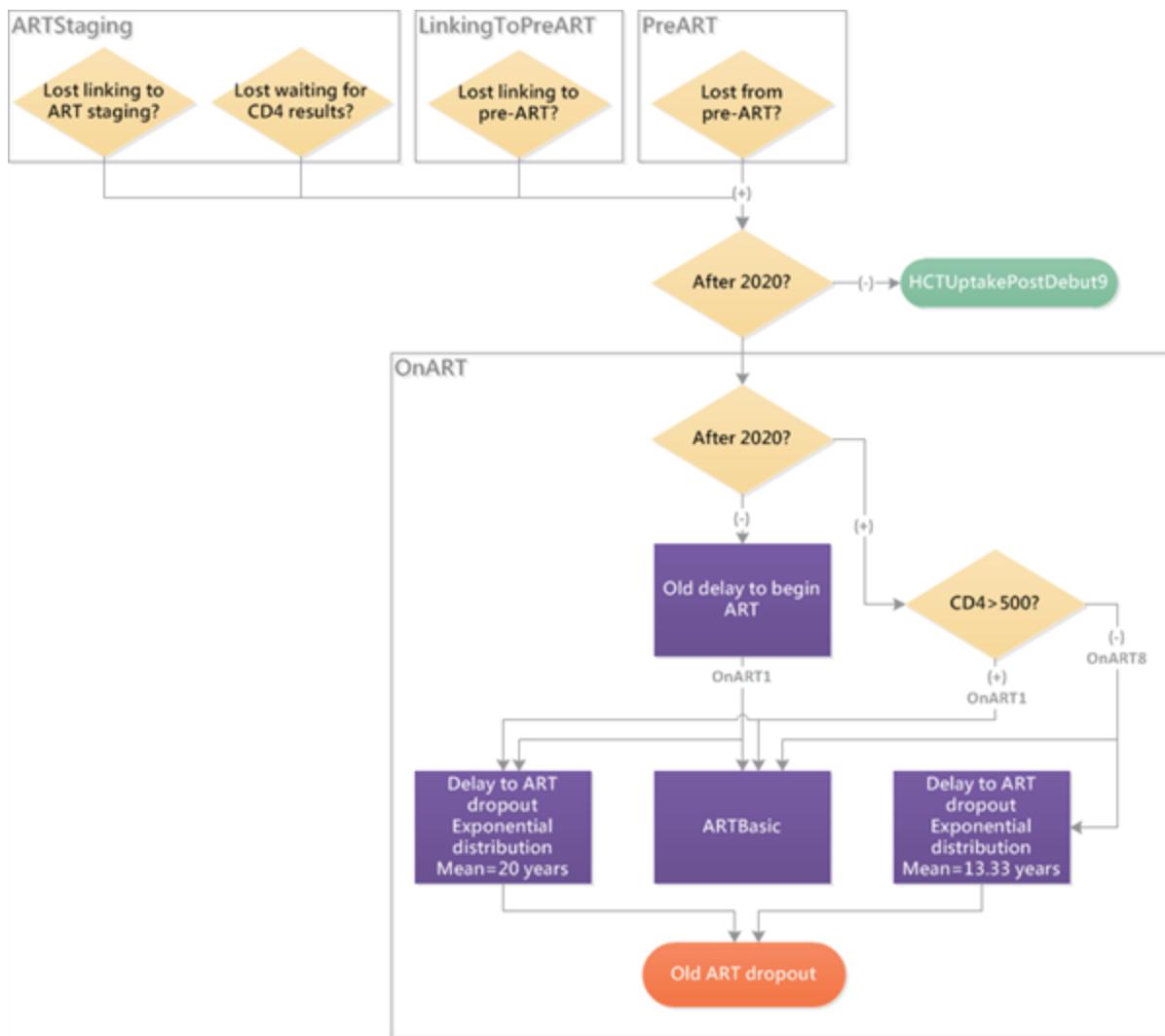
5-2-c. Impact of Expanded Guidelines on Linkage

Universal eligibility has the potential to simplify HIV treatment initiation, but will also increase the number of individuals requiring treatment. The overall effect of universal eligibility on health systems is not yet known.

This scenario will provide an opportunity to think about how the potential benefits of treatment simplification might compare to the potential risks of treatment interruption (due to factors such as patient readiness, capacity of the health care infrastructure, and supply of medications).

Intervention scenario: Starting on January 1, 2020, everyone is eligible for ART. After the guideline change, all patients can be initiated on ART on the day of presentation, skipping all loss to follow-up due to staging, adherence counseling, or linking from the testing clinic to the ART clinic. However, for those initiating with $CD4 > 500$, the rate of treatment discontinuation is 50% (1.5x) higher for the full time on treatment.

The implementation of this scenario is illustrated below:



In the previous scenario, you applied a 7.5% per year rate of discontinuation for only six months before reverting to the baseline 5% per year rate. In this scenario, the 7.5% per year rate is applied for the full duration of treatment. To make this change, simply omit the "Expiration_Period" from the exponential delay triggered by OnART8.

Next, after the year 2020, treatment initiation is simplified and the delay until initiation is removed. To do this, HIVPiecewiseByYearAndSexDiagnostic is added to check the date. After 2020, the delay in receiving ART is bypassed.

Lastly, the treatment simplification provides ensured linkage to ART for all who initiate after 2020. There are many ways to implement this. The included campaign.json file redirects all post-2020 losses to care between diagnosis and initiation to immediately re-initiate care.

5-2-d. Age-Targeted Treatment

Age- and gender-targeted interventions can allow you to configure health care interventions according to the demographic most likely to receive them. For example, they can be used to represent specific

outreach strategies, such as school-based programs or workplace-based programs.

Age targeting is performed using the [AgeDiagnostic](#) intervention, which can be used to connect health care events in an age- and gender-specific manner. This scenario will teach you how to use this feature to perform age and gender targeting.

To provide an example of age and gender targeting, you can extend the previous scenario (ART eligibility) to include age- and gender-specific criteria. You have already learned how to configure time-variable upper age limit that makes pediatric patients eligible for ART. This feature extends the functionality by allowing age ranges to be defined in a gender-specific way.

Intervention scenario: Starting on Jan 1, 2020, males under age 40 and females age 35 are eligible to initiate ART.

To implement the scenario, an HIVPiecewiseByYearAndSexDiagnostic is used to divert individuals who present for staging after January 1, 2020, similarly to the previous examples. After this time, individuals broadcast ARTStaging8, which links them to a male-specific and a female-specific AgeDiagnostic, as follows:

```
{  
    ...  
    "Target_Gender": "Male",  
    ...  
    {  
        ...  
        "Trigger_Condition": "ARTStaging8",  
        ...  
        {  
            ...  
            "Age_Thresholds": [  
                {  
                    "Low": 0,  
                    "High": 40,  
                    "Event": "LinkingToART0"  
                },  
                {  
                    "Low": 40,  
                    "High": 200,  
                    "Event": "ARTStaging4"  
                }  
            ]  
        }  
    }  
}
```

for males, and

```
{  
  ...  
  "Target_Gender": "Female",  
  ...  
  {  
    ...  
    "Trigger_Condition": "ARTStaging8",  
    ...  
    {  
      ...  
      "Age_Thresholds": [  
        {  
          "Low": 0,  
          "High": 35,  
          "Event": "LinkingToART0"  
        },  
        {  
          "Low": 35,  
          "High": 200,  
          "Event": "ARTStaging4"  
        }  
      ]  
    }  
  }  
}
```

for females.

5-3. HIV Testing

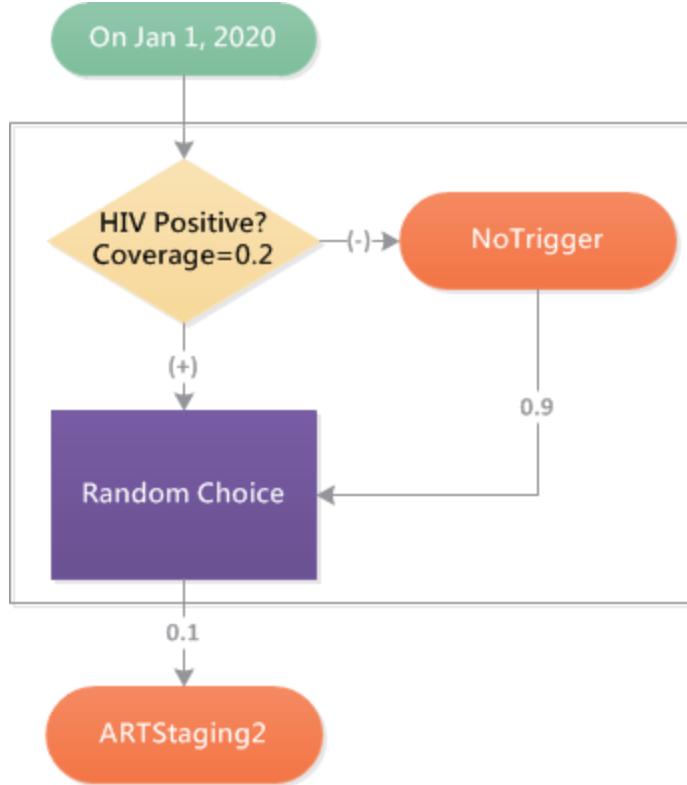
Many variations on the scale-up of HIV testing can be configured using campaign.json. In addition to the modalities that you have already learned (clinic-based voluntary testing, antenatal testing, couples testing, symptomatic testing, and infant testing), you can add any number of testing programs and configure them to represent a specific modality, such as mobile testing, community fairs, home-based testing, or self-testing.

This scenario will teach you how to add a one-time testing campaign as well as repeat testing behavior in which you can control the scale-up of testing and the distribution of delays between repeat tests. The model also gives you control of how individuals access care from each testing modality. You can control factors such as the proportion tested who access care, the distribution of delay time between testing and care, and the stage of care that becomes the entry point for those tested.

5-3-a. One-Time Testing Campaign

Intervention scenario: On Jan 1, 2020, a random 20% of the population receives an HIV test, resulting in a 10% probability of presenting to a clinic for staging.

To configure a the one-time testing campaign, you can use the approach illustrated below:



First, the testing is distributed to 20% of the population at random.

```

{
  ...
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Coverage": 0.2,
    "Intervention_Config":
    {
      "class": "HIVRapidHIVDiagnostic",
      ...
      "Positive_Diagnosis_Event": "ARTStaging7",
      "Negative_Diagnosis_Event": "NoTrigger"
    }
  }
}
  
```

Those testing negative broadcast NoTrigger, whereas those testing positive are linked to an [HIVRandChoice](#) with a 90% probability of NoTrigger and a 10% probability of ARTStaging2, as follows:

```

{
  ...
}
  
```

```
{  
  ...  
  {  
    ...  
    "Trigger_Condition": "ARTStaging7",  
    "Actual_IndividualIntervention_Config":  
    {  
      "class": "HIVRandomChoice",  
      ...  
      "Choices":  
      {  
        "NoTrigger": 0.9,  
        "ARTStaging2": 0.1  
      }  
    }  
  },  
  ...  
}
```

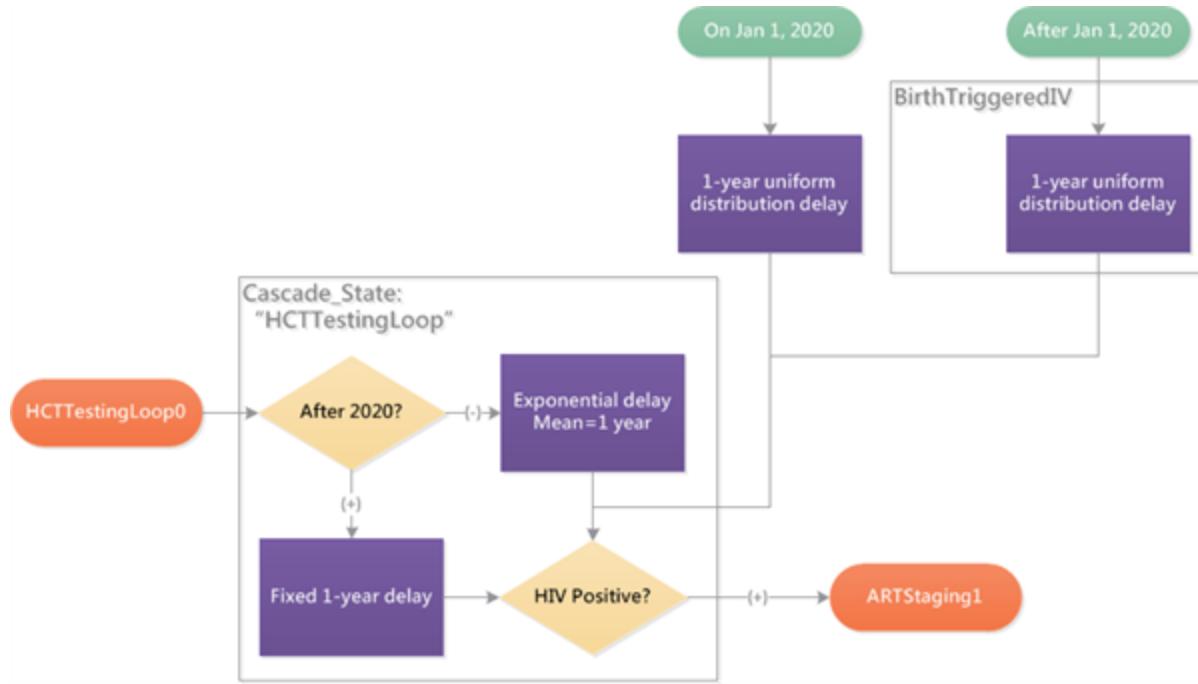
The block above can be modified to use the your customized linkage probability and point of entry into care. The linkage rate can also be made to be time-variable, and delays between testing and linkage can be added, by creating additional steps between HIVRandomChoice and ARTStaging2 (or other entry point to care).

5-3-b. Changing Existing Testing Patterns: Regular Annual Testing

In this scenario, you will learn how to alter existing patterns of testing. This can be used to represent changes in the utilization of existing health care infrastructure, or replacement of some health care infrastructure with different components.

Intervention scenario: Starting on Jan 1, 2020, everyone who is reachable by healthcare begins testing annually, beginning on a random day of the year and repeating with a fixed 1-year delay. For these individuals, the annual testing replaces any prior use of voluntary testing and counseling, although other forms of testing (symptomatic, antenatal, couples) can continue.

The approach is illustrated below:



To ensure that all individuals who are reachable by healthcare begin annual testing, a delayed testing intervention is distributed on January 1, 2020, according to the property "Accessibility": "Yes".

```
{
...
{
  ...
  "Property_Restrictions_Within_Node":
  [
    { "Accessibility": "Yes" }
  ],
  {
    ...
    {
      "class": "HIVDelayedIntervention",
      "Delay_Distribution": "UNIFORM_DURATION",
      "Delay_Period_Min": 0,
      "Delay_Period_Max": 365,
      "Broadcast_Event": "HCTTestingLoop1"
    }
  },
  ...
}
}
```

The delay is uniformly distributed between zero and 365 days to ensure that testing will occur on a random day of the year. The intervention is provided separately to individuals who are alive on January 1, 2020, and as a birth-triggered intervention to those who will be born in the future.

To complete the intervention, the delay time associated with repeat testing in the HCTTestingLoop is changed to a fixed 1-year delay after January 1, 2020, by linking an [HIVPiece-wiseByYearAndSexDiagnostic](#) (to check the date) to a new delay block with a fixed 365-day delay.

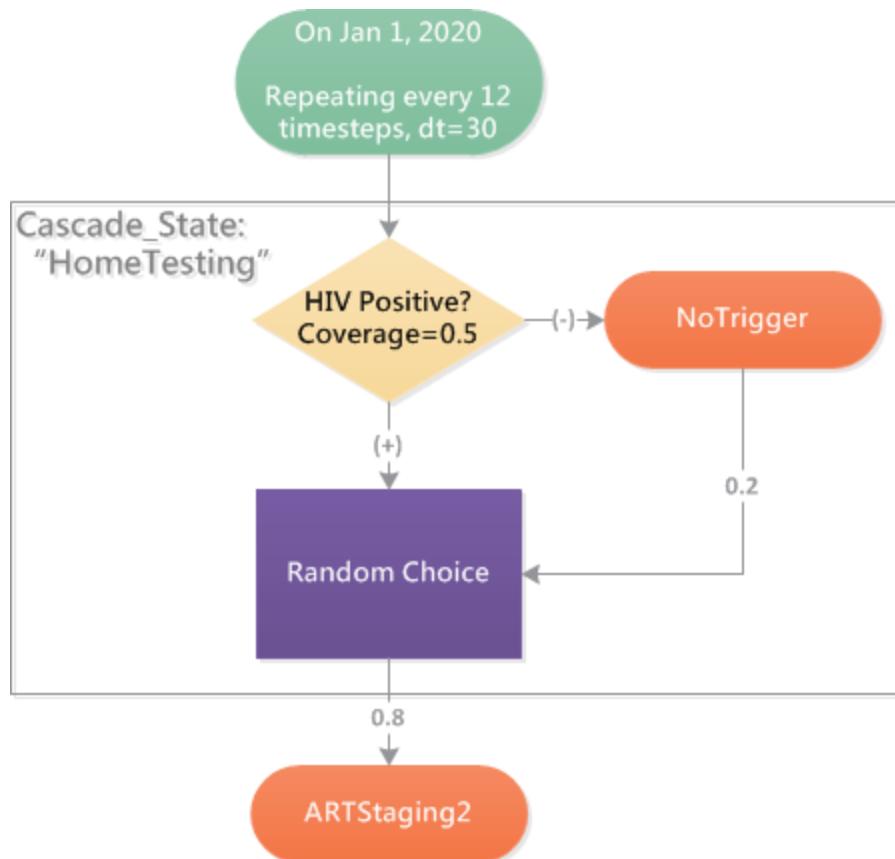
5-3-c. Community-Based Testing

The previous scenario taught you how to create annual testing on a random day of the year using a uniformly distributed delay, and repeat it using a delay loop. In this scenario, you will learn how to create synchronous testing on a specific day of the year. Synchronous testing could be used to represent an annual community-based testing event such as a community fair.

Another difference you'll see between this scenario and the prior one is that the community-based testing intervention will be provided in addition to, rather than in place of, facility-based testing.

Intervention scenario: Starting on Jan 1, 2020, and annually thereafter on the first of the year, 50% of the population receives home/community-based testing, of whom 80% immediately present for staging at existing clinics and 20% resume previous care-seeking behavior.

The approach illustrated below:



First, testing must be handed out annually on the same day of the year for all individuals. This is accomplished by making the intervention repeat itself annually by using the repetitions feature of the

[StandardInterventionDistributionEventCoordinator](#) (which is the class you've been using to hand out new interventions).



As of EMOD version 2.0, the repetitions feature requires `Timesteps_Between_Repetitions`, and cannot directly accept days or years between repetitions. If the simulation timestep is changed, the `Timesteps_Between_Repetitions` should also be changed to retain a specific rate of testing per unit of time.

In this example, the number of days per timestep is 30, so the nearest number of timesteps between repetitions is 12. A note is provided in the `campaign.json` file as a reminder:

```
{
...
  "Start_Year": 2020,
  ...
  {
    "class": "StandardInterventionDistributionEventCoordinator",
    "Demographic_Coverage": 0.5,
    "Number_Repetitions": 100,
    "NOTE": "Timesteps_Between_Repetitions is in units of DT, which here is one month.",
    "Timesteps_Between_Repetitions": 12,
    ...
    {
      "class": "HIVRapidHIVDiagnostic",
      ...
      "Positive_Diagnosis_Event": "ARTStaging7",
      "Negative_Diagnosis_Event": "NoTrigger"
      ...
    }
  }
},
```

Negative diagnosis leads to `NoTrigger`, which allows the individual to resume former behavior. Positive HIV diagnosis leads to a `RandomChoice` between `NoTrigger` and presentation for staging.

```
{
...
  {
    ...
    {
      ...
      "Trigger_Condition": "ARTStaging7",
      {
        ...
        "class": "HIVRandomChoice",
        "Choices":
```

```
        {
            "NoTrigger": 0.2,
            "ARTStaging2": 0.8
        }
    }
}
```

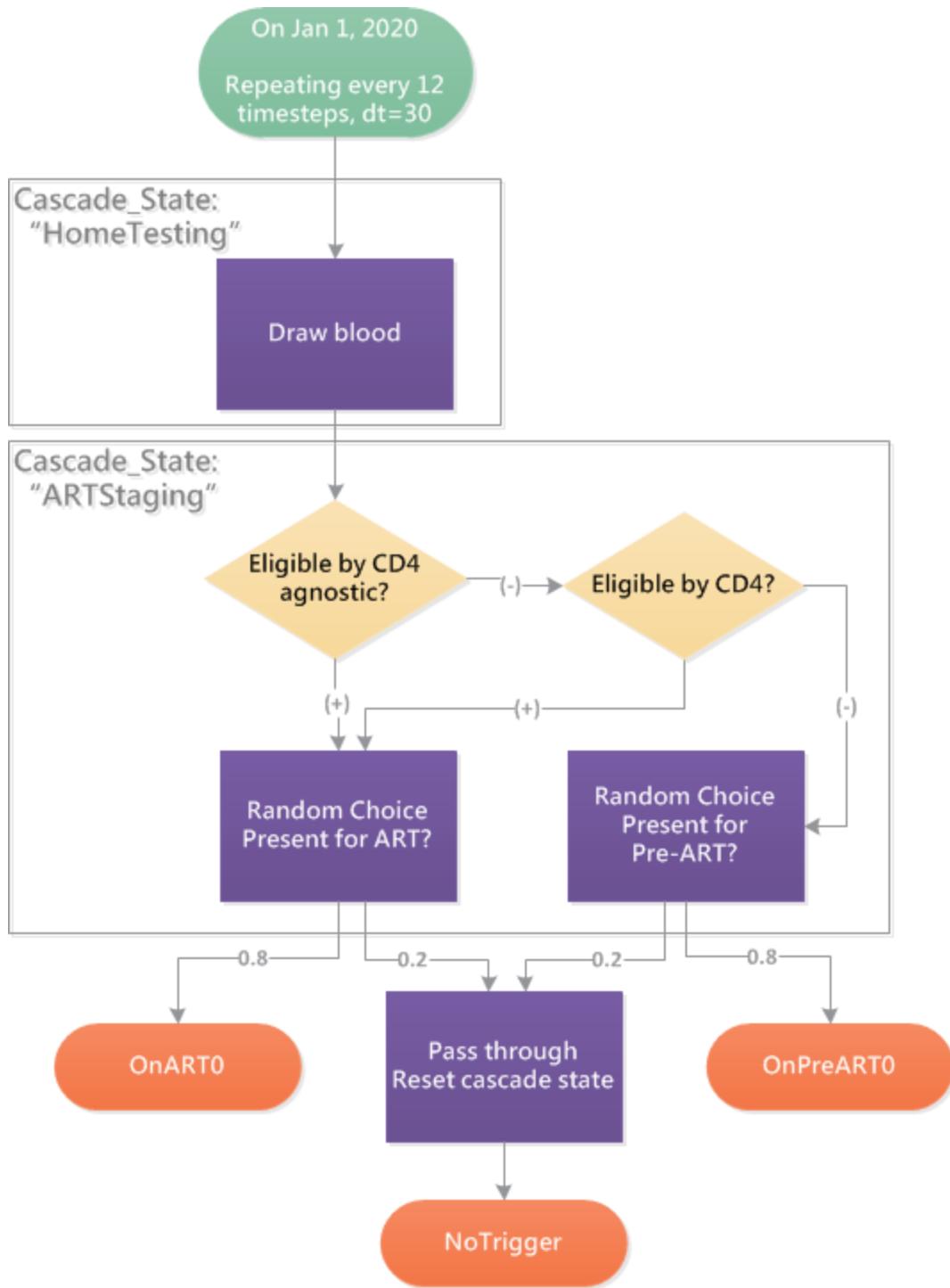
In previous interventions, you created similar delays by distributing an intervention that led to a fixed-time delay loop. Why was this approach not taken in this scenario? The reason is that individuals born after the start of the intervention would not have received the initial synchronized trigger. In other scenarios, their health-seeking has been linked to their date of birth using [BirthTriggeredIV](#). To synchronize their date of testing with the community testing day, the intervention itself must be provided repeatedly.

5-3-d. Community-Based Testing and Staging

Studies in sub-Saharan Africa have found home- and community-based testing with point-of-care determination of eligibility to be an effective¹ and cost-effective² form of treatment expansion. This scenario demonstrates how to extend a community-based or home-based testing intervention to include staging according to the treatment guidelines at the time of testing.

¹Barnabas RV, van Rooyen H, Tumwesigye E, Murnane PM, Baeten JM, Humphries H, et al. Initiation of anti-retroviral therapy and viral suppression after home HIV testing and counselling in KwaZulu-Natal, South Africa, and Mbarara district, Uganda: a prospective, observational intervention study. *The Lancet HIV*. 2014 Nov;1(2):e68-76.

²Smith JA, Sharma M, Levin C, Baeten JM, van Rooyen H, Celum C, et al. Cost-effectiveness of community-based strategies to strengthen the continuum of HIV care in rural South Africa: a health economic modelling analysis. *The Lancet HIV*. 2015 Apr;2(4):e159-68.



Just as the previous scenario created a parallel pathway to testing without changing facility-based testing behavior, this scenario creates a parallel pathway of testing, staging, and linkage to ART or pre-ART care.

5-3-e. Community-Based Testing and Staging with Delayed Presentation

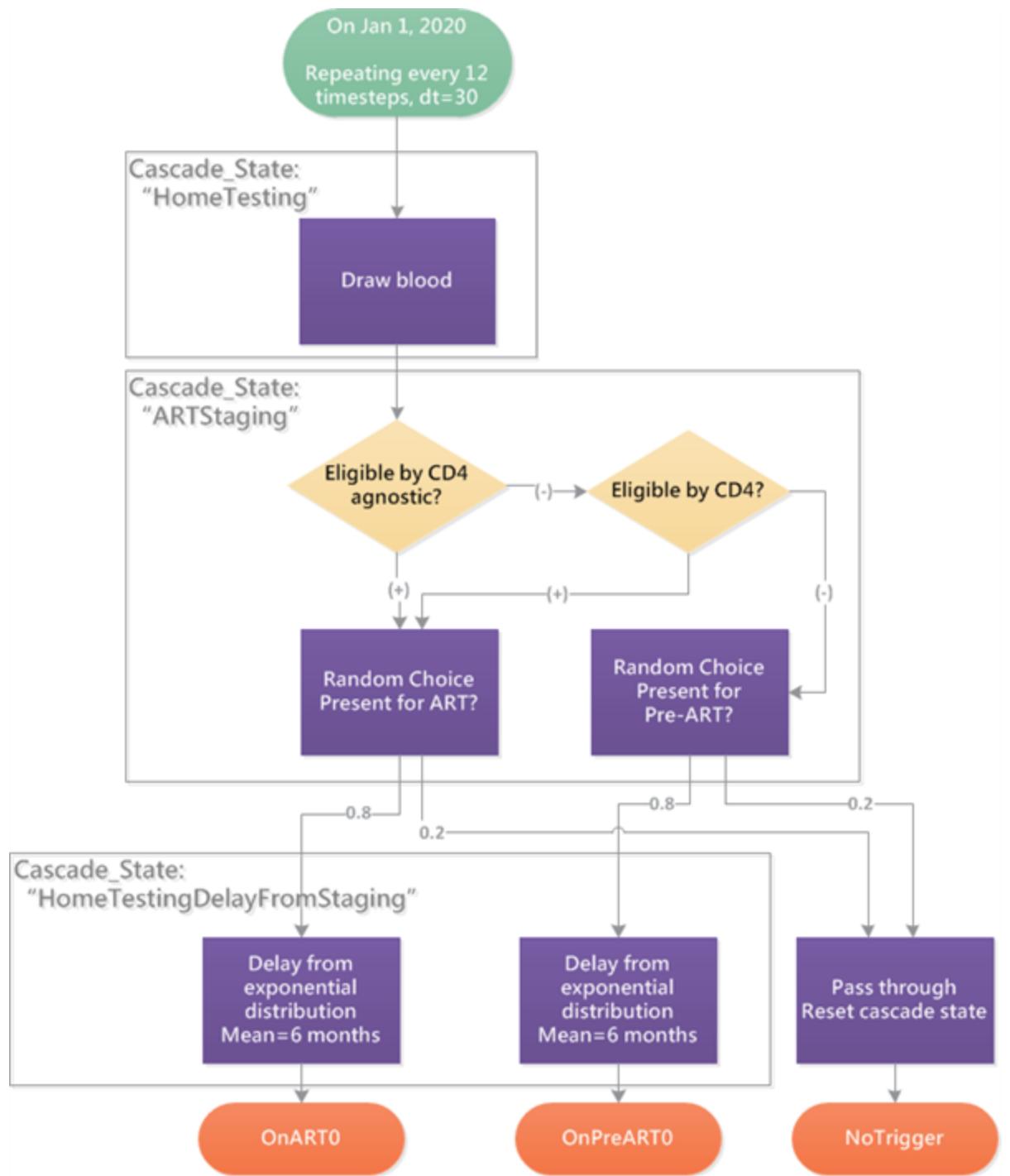
The previous scenario demonstrated how to create a parallel pathway of testing, staging, and linkage to represent community-based or home-based outreach. Using the building blocks you have already

learned, the scenario can be customized to reflect the desired patterns of participation and retention over time, by demographic category, and using different probability distributions to represent heterogeneity in behavior.

Studies of home-based or community-based outreach have been able to quantify the time required for patients to link to facility-based care. This scenario demonstrates how to configure an exponentially distributed delay time of 6 months.

Intervention scenario: Starting on Jan 1, 2020, and annually thereafter on the first of the year, 50% of the population receives home/community-based testing and staging, of whom 80% eventually present for pre-ART or ART (depending on outcome of staging) at existing clinics and 20% resume previous care-seeking behavior. For those who eventually present, their baseline care-seeking behavior may cause them to present earlier (e.g., via antenatal testing, becoming symptomatic, or even choosing to undergo voluntary re-testing at the clinic). For presentation driven by home/community-based testing, the delay time is exponentially distributed with a mean of 6 months.

The approach is illustrated below:



The six-month exponential delay until pre-ART:

```
{
...
{
...
{
```

```

    "Trigger_Condition": "ARTStaging14",
    {
        ...
        "class": "HIVDelayedIntervention",
        ...
        "Delay_Distribution": "EXPONENTIAL_DURATION",
        "Delay_Period": 182,
        "Broadcast_Event": "OnPreART0"
    }
}
}
}

```

is a separate block from the six-month delay until ART:

```

{
...
{
...
{
    "Trigger_Condition": "ARTStaging13",
    {
        ...
        "class": "HIVDelayedIntervention",
        ...
        "Delay_Distribution": "EXPONENTIAL_DURATION",
        "Delay_Period": 182,
        "Broadcast_Event": "OnART0"
    }
}
}
}

```

making it easy to customize the intervention for distinct delay times and distributions depending on whether the individual was found to be eligible for ART.

5-4. Retention

You have already learned how to configure the rates of retention between different stages of health care access, as well as after initiation of ART. The rates of linkage or discontinuation can be modified, made time-variable using one of the built-in distributions (such as the piecewise constant, piecewise linear, or sigmoid rates you have learned), or switched to a different trend at a specific time. The changes can also be targeted to specific sub-populations.

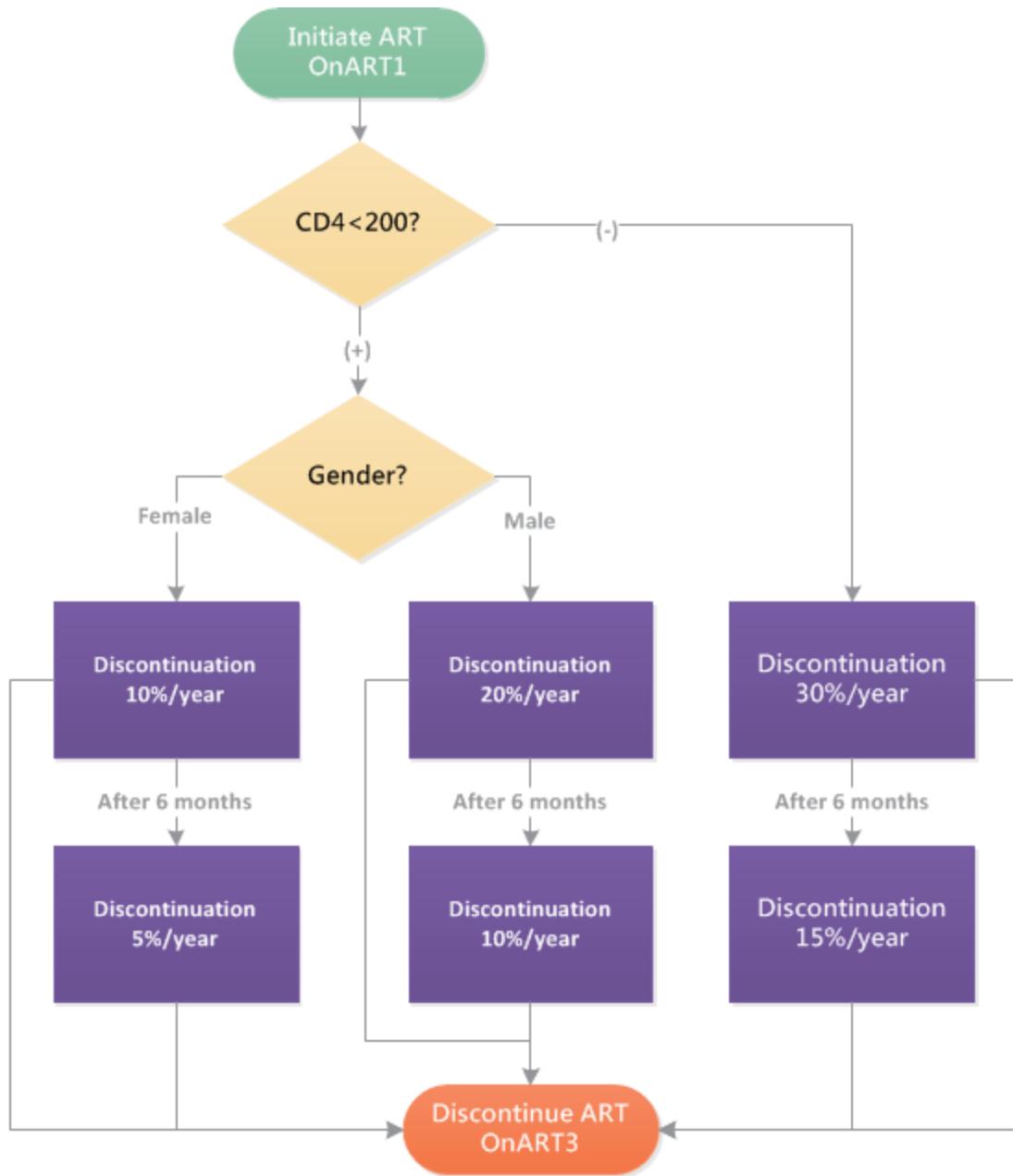
This scenario provides a few examples of configuring retention along the "leaky cascade" of care.

5-4-a. Complex Rate of Retention on ART: Dependence on Time, CD4 Count, and Demographics

The included campaign.json file includes ART discontinuation of 5% per year. This scenario demonstrates how to transform the simple assumption into a more complex set of assumptions. Note that changing these assumptions can potentially alter trends in mortality, number treated, and other information used in the setting-specific calibration of the model, and so may require re-calibration.

Intervention scenario: The rate of ART discontinuation for the first six months of treatment is 10% per year for females initiating with CD4 counts less than 200 cells/uL, 20% per year for males initiating with CD4 counts less than 200 cells/uL, and 30% per year for anyone initiation with a CD4 count above 200 cells/uL. After six months, the discontinuation rate drops by 50%.

The approach is illustrated below:



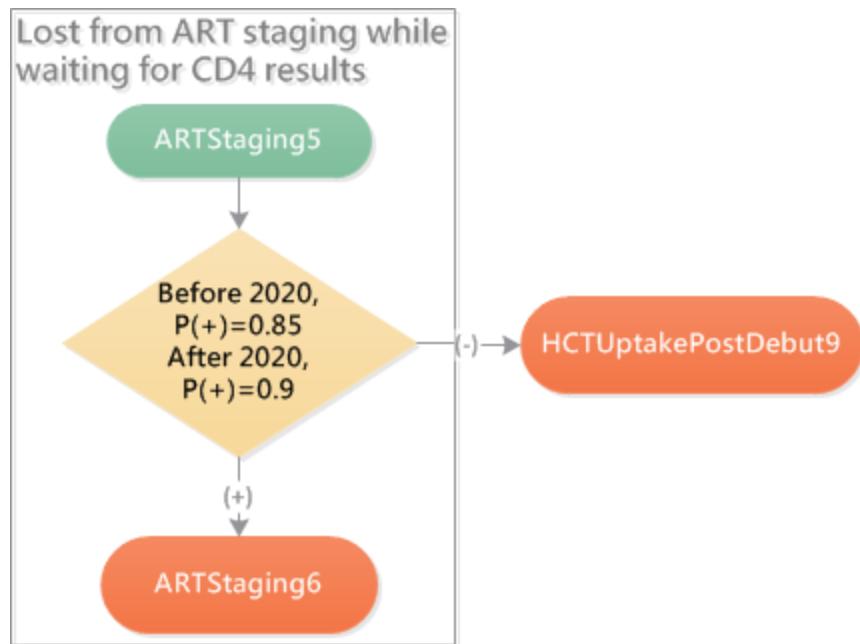
The implementation involves chaining together the building blocks you have learned earlier: demographic filters by gender, diagnostics by CD4 count, and rates that can expire and yield to other rates.

5-4-b. Point-of-Care CD4 Testing

This scenario will demonstrate how to configure potential improvements to linkage to care through instantaneous roll-out of point-of-care (PoC) CD4 testing.

Intervention scenario: Starting on Jan 1, 2020, 90% of individuals who have drawn blood for CD4 count are guaranteed to receive the CD4 result and become staged for ART, but may still fail to be linked to pre-ART or ART according to the current state of "leaks" in the cascade of care.

The scenario requires only a small modification to the existing "leaky cascade" of care in the provided campaign.json file. Using a time-based switch on January 1, 2020, the rate of return for CD4 results is increased to 90%.



The rest of the care cascade remains the same, so that losses at other stages of linkage are retained, and only CD4 diagnostic-related losses are eliminated.

5-4-c. Gradual Roll-Out of PoC CD4 Testing

The previous scenario assumed instantaneous roll-out of PoC CD4. This scenario demonstrates how to control the timing of PoC CD4 roll-out.

Intervention scenario: Starting on Jan 1, 2020, the proportion of individuals who are successfully staged after a CD4 diagnostic is performed rises linearly in time at a rate of 1% per year, before finally reaching 100%. Failure to be linked to pre-ART or ART may still occur due to other leaks in the care cascade.

As in the previous scenario, the care cascade is left unaltered except for the step of receiving CD4 results, which is allowed to vary in time. For a probability that changes linearly in time, use [HIVPiecewiseByYearAndSexDiagnostic](#) with `Interpolation_Order` set to 1.

```
{
...
{
  ...
  "Intervention_Config": {
    ...
  }
}
```

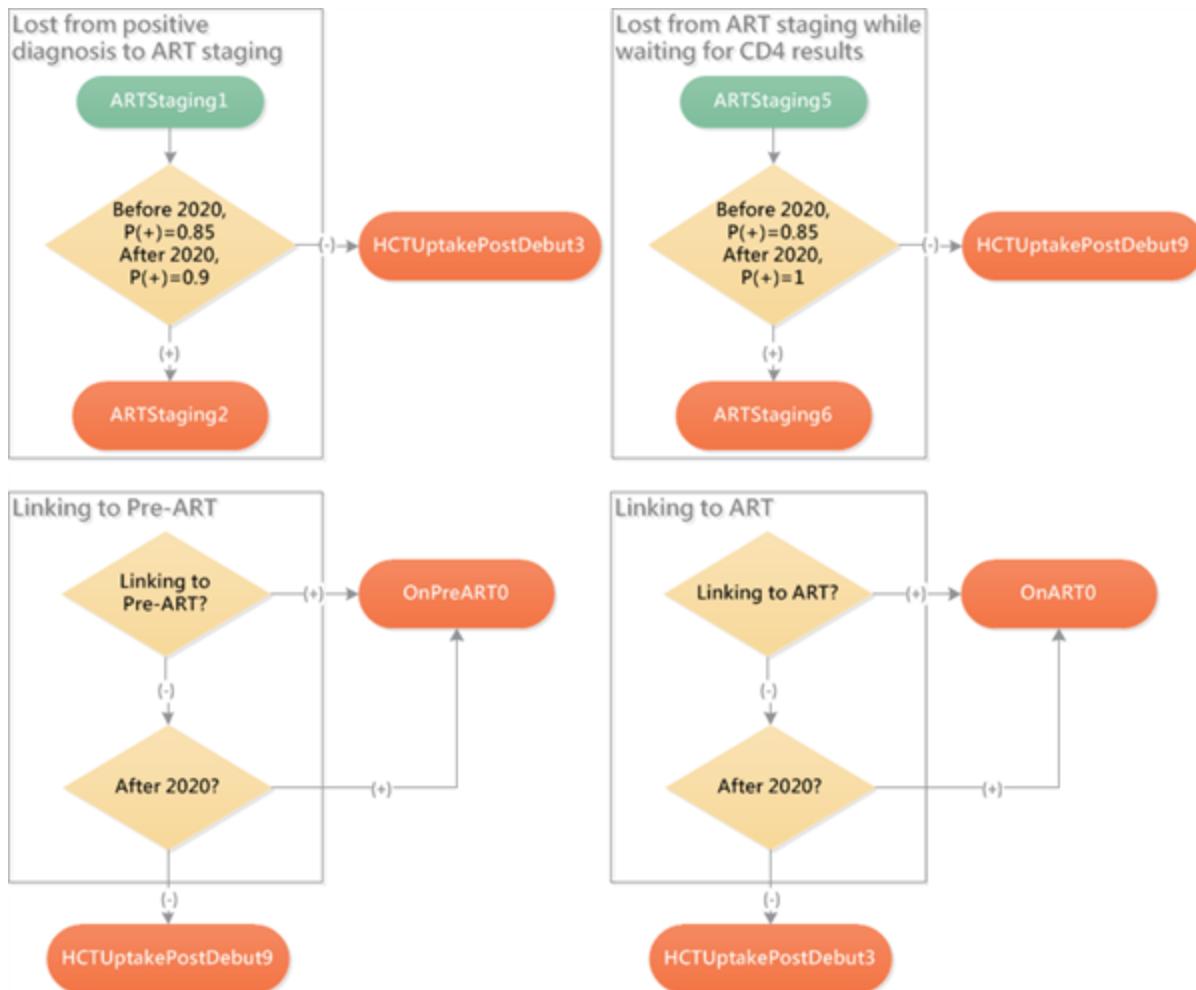
```
...
{
  "class": "HIVPiecewiseByYearAndSexDiagnostic",
  ...
  "Time_Value_Map":
  {
    "Times": [ 1990, 2020, 2035],
    "Values": [ 0.85, 0.85, 1.0]
  },
  "Interpolation_Order": 1,
  ...
}
}
```

5-4-d. 90% Linkage After Diagnosis

This scenario illustrates how an intervention can override trends in linkage along all stages of the care cascade to guarantee a specific rate of linkage between diagnosis and initiation of care.

Intervention scenario: Starting on Jan 1, 2020, 90% of individuals who have presented after testing HIV+ are staged and, depending on eligibility, are initiated into pre-ART or ART.

The scenario is implemented as illustrated below:



Losses at each stage of the case cascade are eliminated, except for the linkage rate from diagnosis to staging, which is raised to 90% using a piecewise step function.

```

{
...
{
...
{
...
  "Trigger_Condition": "ARTStaging1",
  ...
  {
    "class": "HIVPiecewiseByYearAndSexDiagnostic",
    ...
    "Time_Value_Map":
    {
      "Times": [ 1990, 2020 ],
      "Values": [ 0.85, 0.9 ]
    },
  }
}
}
  
```

```
    ...
    "Positive_Diagnosis_Event": "ARTStaging2",
    "Negative_Diagnosis_Event": "HCTUptakePostDebut3"
  },
},
},
},
```

The other stages of care initiation switch to 100% linkage, for an overall linkage rate of 90%.

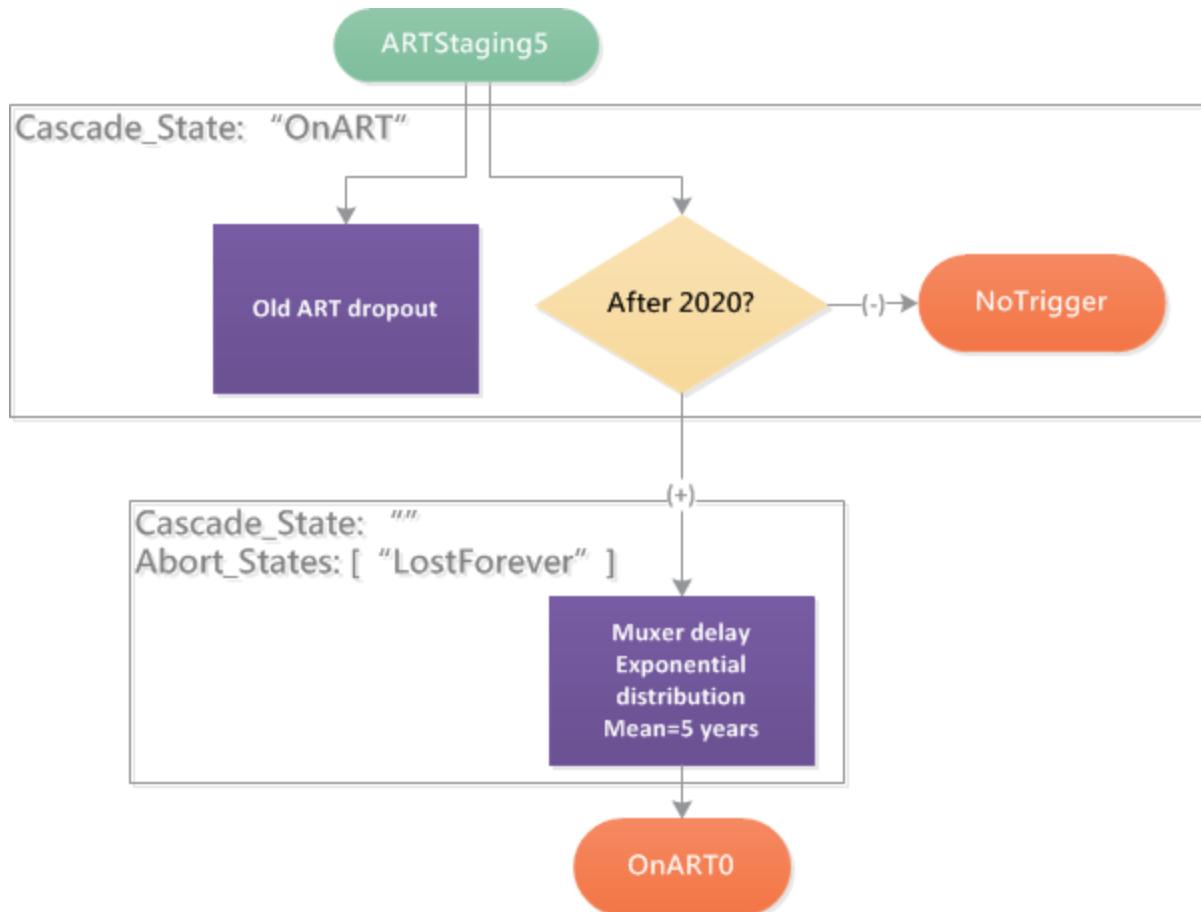
5-5. Re-Initiation of Care

5-5-a. Outreach to Re-Initiate Those Who Become Lost to Care

Some HIV clinics have resources to follow up with patients who have been lost from care. If the patient has not died or re-initiated care on his/her own, such an intervention might have a fixed success rate at returning the patient to care, or a more complex success rate that could depend on factors such as time out of care, time since the program began, or demographic factors. This scenario will demonstrate the fixed-rate case:

Intervention scenario: Outreach to individuals who discontinue ART after Jan 1, 2020 increases the rate of re-initiation by 20% per year.

The implementation is illustrated below:



For those who discontinue care after 2020, a 20% per year delay is applied until re-initiation of care. This rate competes with baseline rates of re-initiation as well as mortality. It effectively "boosts" the rate of return by a fixed amount, for those who remain alive out of care.

The exponential delay can be replaced with more complex assumptions. For example, multiple chained delays, in which one either triggers the next or expires to yield to the next, enables variability of return rate by time out of care.

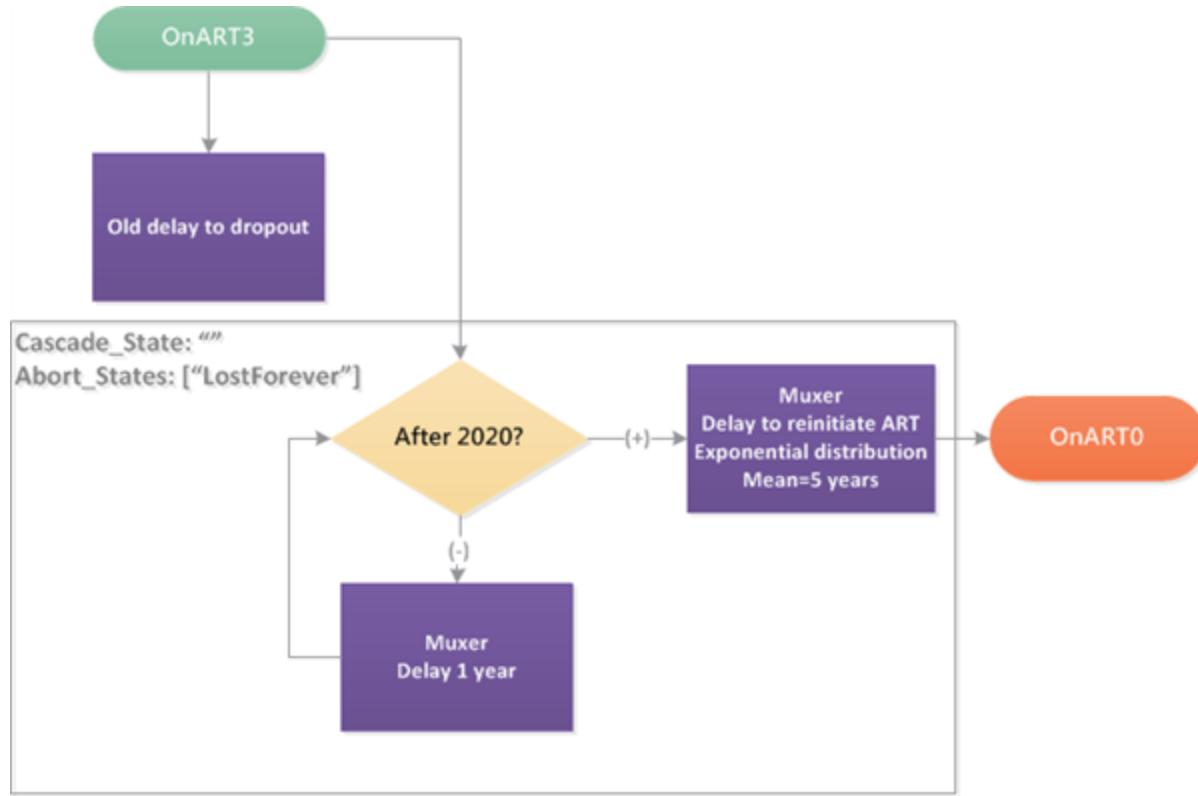
5-5-b. Outreach to Re-Initiate Those Already Lost to Care

In the previous scenario, you learned how to configure a return-to-care intervention for those who discontinue after a specified date. Suppose, instead, you wanted to increase re-initiation rates for all individuals, regardless of when they discontinued care.

Intervention scenario: Outreach increases the rate of re-initiation of ART by 20% per year, even if ART was discontinued prior to Jan 1, 2020.

Just as a real intervention would have to "find" individuals lost to care, the model would need a way to keep track of individuals who have previously discontinued ART. A simple way to achieve this is to track

this population from the beginning of the program, checking repeatedly whether the date of the intervention has occurred, as follows:



With this particular implementation, the rate of re-initiation does not grow for individuals who have discontinued and re-initiated ART multiple times, because the muxers ensure that individuals can only receive the benefit of the intervention once for a given interval out of care. The muxers can be changed to regular delay blocks if the intention is for the intervention's effect to be greater for those who have discontinued care multiple times (e.g., individuals being tracked by multiple facilities).

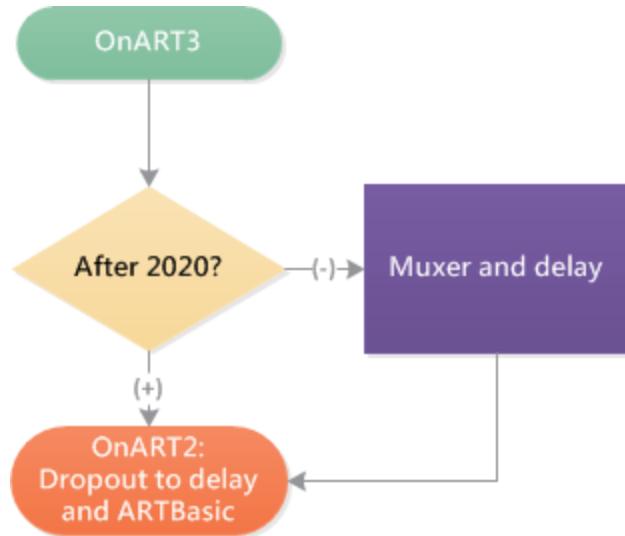
5-6. Delays in Receiving Care

5-6-a. Removing Delays in Health Care Access

In this scenario, you will learn how to switch off a health care delay at a specified time.

Intervention scenario: Starting on Jan 1, 2020, all those testing positive are initiated in ART or pre-ART in the same model timestep, with no delays, but still experience the same overall probabilities of loss to follow-up between testing and pre-ART/ART as before the elimination of delays.

The campaign.json file for this scenario includes a delay between linkage to ART care and initiation of antiretroviral medication through the intervention [ARTBasic](#). To eliminate this delay after a specified time, use the [HIVPiecewiseByYearAndSexDiagnostic](#) switch to selectively bypass the delay:



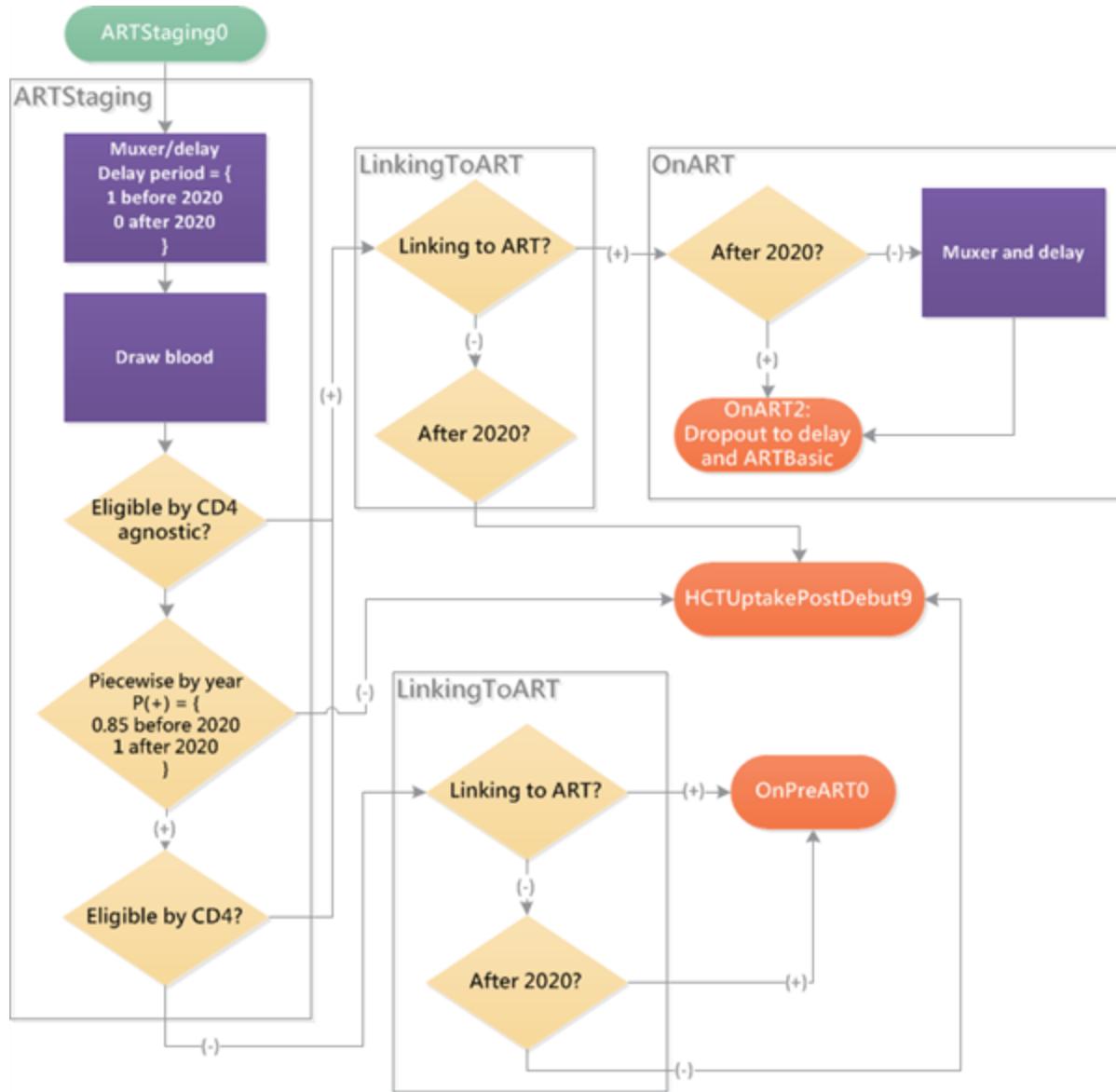
This motif can be used to bypass delays in a time-dependent manner.

5-6-b. Removing Delays and Ensuring Successful Linkage to Care

An idealized pattern of linkage to care would involve no delays and no losses to care between diagnosis and initiation of care. You will apply the motif that you learned in the previous scenario to bypass both delays and failures to link after a specified date.

Intervention scenario: Starting on Jan 1, 2020, all those testing positive are initiated in ART or pre-ART in the same model timestep, with no delays and also no loss to follow-up between testing and pre-ART/ART.

The bypasses and increases in retention along the care cascade are illustrated below:



Whereas a delay is bypassed by creating a direct link to the next event, losses to care can be bypassed by redirecting those who would have discontinued onward to the next stage of care.

5-7. HIV Prophylaxis

5-7-a. Uniform Efficacy

The examples so far have focused on programs for VMMC and ART, including their scale-up over time, sub-populations of interest, modalities of access, and patterns of retention/re-engagement. This scenario will provide you with a simple template for how to disseminate a prophylaxis intervention using existing levels of HIV testing in the healthcare system.

As with the VMMC examples earlier, this intervention can be extended to add additional HIV testing in different ways. Testing can be a one-time campaign, or can repeat at the desired frequency; repeat

testing can occur at fixed intervals, or at random intervals; testing can link only to prophylaxis, or it link to other forms of care and prevention.

The example provided here uses existing levels of testing to distribute HIV prophylaxis. The prophylaxis is assumed to provide a lifelong benefit of 60% reduction in HIV acquisition.

Intervention scenario: Starting on Jan 1, 2020, half of women ages 15 to 49 who receive a negative HIV diagnosis through existing health care modalities are provided with HIV prophylaxis with 60% efficacy at reducing HIV acquisition.

The intervention is distributed as follows:

```
{  
  ...  
  {  
    ...  
    "Target_Demographic": "ExplicitAgeRangesAndGender",  
    "Target_Age_Min": 15,  
    "Target_Age_Max": 49,  
    "Target_Gender": "Female",  
    "Demographic_Coverage": 0.5,  
    ...  
    {  
      ...  
      {  
        "class": "SimpleVaccine",  
        "Durability_Time_Profile": "BOXDURABILITY",  
        "Primary_Decay_Time_Constant": 30000,  
        "Vaccine_Type": "AcquisitionBlocking",  
        "Reduced_Acquire": 0.6  
      }  
    }  
  },  
},
```

5-7-b. Heterogeneous efficacy or adherence

Participants in clinical trials of HIV pre-exposure prophylaxis (PrEP) have shown heterogeneous levels of adherence to oral and topical products. In larger trials, efficacy has been stratified by level of adherence and found to be higher in sub-populations with higher adherence. It is possible that future products, such as vaccines or long-acting prophylaxis, will also have different levels of efficacy for different sub-populations.

To model this effect, you will divide recipients into sub-populations that receive different levels of benefit from HIV prophylaxis.

Intervention scenario: Starting on Jan 1, 2020, HIV prophylaxis is provided to all women between ages 15 and 49 who receive a negative HIV diagnosis through existing health care modalities. Half of women who receive prophylaxis have an 80% reduction in HIV acquisition, while half have only a 20% reduction in HIV acquisition.

First, an [HIVRandomChoice](#) intervention is applied to the target demographic (50% of females age 15 to 49 who have just been diagnosed HIV-negative) and used to separate sub-populations that will receive different levels of efficacy:

```
{
  ...
  {
    ...
    "Target_Demographic": "ExplicitAgeRangesAndGender",
    "Target_Age_Min": 15,
    "Target_Age_Max": 49,
    "Target_Gender": "Female",
    "Demographic_Coverage": 0.5,
    ...
    {
      ...
      {
        ...
        {
          "class": "HIVRandomChoice",
          "Choices":
          {
            "HCTUptakePostDebut4": 0.5,
            "HCTUptakePostDebut5": 0.5
          }
        }
      }
    }
  }
}
```

One of the efficacy groups receives an 80% prevention benefit.

```
{
  ...
  {
    ...
    {
      ...
      {
        ...
        {
          ...
          "Trigger_Condition": "HCTUptakePostDebut4",
          ...
        }
      }
    }
  }
}
```

```
        {
            "class":"SimpleVaccine",
            "Durability_Time_Profile":"BOXDURABILITY",
            "Primary_Decay_Time_Constant":30000,
            "Vaccine_Type":"AcquisitionBlocking",
            "Reduced_Acquire":0.8
        }
    }
}
```

The other group receives a 20% prevention benefit.

```
{
...
{
...
{
...
{
...
"Trigger_Condition": "HCTUptakePostDebut5",
...
{
    "class":"SimpleVaccine",
    "Durability_Time_Profile":"BOXDURABILITY",
    "Primary_Decay_Time_Constant":30000,
    "Vaccine_Type":"AcquisitionBlocking",
    "Reduced_Acquire":0.2
}
}
}
}
```

5-7-c. Long-acting product for HIV prophylaxis

In the previous examples, prophylaxis was configured to provide lifelong protection by configuring a long and constant duration of protection. This scenario will demonstrate how to configure temporary protection that lasts for a fixed period of time, and then decays with a configurable half-life.

Intervention scenario: Starting on Jan 1, 2020, half of women ages 15 to 49 who receive a negative HIV diagnosis through existing health care modalities are provided with a long-acting product that provides 90% effective protection against HIV for six months. After six months, protection decays with a half-life of one year.

The scenario uses the generic EMOD vaccine intervention, [SimpleVaccine](#), with a Durability_Time_Profile set to BOXDECAYDURABILITY. This gives a constant efficacy for a fixed amount of time, set by Primary_Decay_Time_Constant to 6 months = 183 days, followed by an exponentially decaying efficacy. The time constant of decay is set to 0.001899, giving a half-life of 365 days = 1 year.

```
{  
    ...  
    {  
        ...  
        {  
            ...  
            {  
                ...  
                {  
                    "class": "SimpleVaccine",  
                    "Durability_Time_Profile": "BOXDECAYDURABILITY",  
                    "Primary_Decay_Time_Constant": 183,  
                    "Secondary_Decay_Time_Constant": 0.001899,  
                    "Vaccine_Type": "AcquisitionBlocking",  
                    "Reduced_Acquire": 0.6  
                }  
            }  
        }  
    }  
}
```

Appendix A: Output File Descriptions

This appendix provides information about each output file available from STI and HIV simulations in EMOD v2.0. It includes instructions for how to enable the output file to be created, how to customize the output file if options are available to do so, what the file contains, and information about each data channel of the output file.

Age and Gender-Stratified HIV Epidemic

File name: [ReportHIVByAgeAndGender.csv](#)

Enabled by config.json parameter: Report_HIV_ByAgeAndGender

Customized by config.json parameters: Report_HIV_ByAgeAndGender_Start_Year, Report_HIV_ByAgeAndGender_Stop_Year

Used for simulation types: HIV

Purpose: Population size, HIV prevalence, new infections, and mortality in 1-year age bins and semi-annual time bins. Formatted as categories and counts of individuals, this output file works well with PivotCharts in Excel or equivalent functionality for aggregating counts with other data analysis software.

Usage tips: The parameters Report_HIV_ByAgeAndGender_Start_Year and Report_HIV_ByAgeAndGender_Stop_Year can be used to configure the time to start and stop logging data during the simulation. For example, if your simulation has a long burn-in period, you can set Report_HIV_ByAgeAndGender_Start_Year to a time after the burn-in period to avoid logging unnecessary data.

The parameter Report_HIV_Period is used to configure the time over which data is logged, in days. The time between rows of output is half the number of days configured in Report_HIV_Period. For example, if Report_HIV_Period, then data is written out semiannually.

For values such as population size or number infected, which are reported as a single “snapshot” in time, every other row of output can be dropped to provide midyear or year-end prevalence estimates. For values such as deaths or new infections, values are accumulated from the previous interval to the next. Thus, output rows can be summed in pairs to provide the total number of new infections over the course of a year, or from one mid-year to the next mid-year.

The output file processing scripts plotHIVSummary_15_49.py and plotHIVSummary_15_49.R perform these calculations with mid-year snapshots of “prevalent” values and year-end to year-end aggregation of “incident” values. Appendix B2 describes how to use the processing scripts and plot the results.

Data channel	Description
Year	The year at the end of the semiannual interval being recorded. E.g., 1980.5 means that the counts in this row were aggregated over the first half of 1980 or reported as a “snapshot” in the middle of the year 1980.
NodeId	Geographic node. As of v2.0, multi-node simulations are not supported for STI_SIM or HIV_SIM, so this is always set to 1.

Data channel	Description
Gender	0 for male, 1 for female
Age	Integer age from 0 to 99
Population	Total number of individuals in the age/gender category at the specified Year.
Infected	Number of HIV-infected individuals in the age/gender category at the specified Year.
Newly Infected	Number of newly infected individuals in the age/gender category, aggregated over the semiannual period leading up to the specified Year.
On_ART	Number of individuals receiving ART in the age/gender category at the specified Year.
Died	Number of deaths among individuals in the age/gender category, aggregated over the semiannual period leading up to the specified Year.
Died_from_HIV	Number of deaths due to HIV (as opposed to background mortality configured in the demographics file) among individuals in the age/gender category, aggregated over the semiannual period leading up to the specified Year.
Tested Past Year or On_ART	Number of individuals receiving ART or having tested in the past year, in the age/gender category at the specified Year.
Tested Ever	Number of individuals having ever been tested for HIV, in the age/gender category at the specified Year.

ART Initiation and Discontinuation

File name: [ReportHIVART.csv](#)

Enabled by config.json parameter: Report_HIV_ART

Used for simulation types: HIV

Purpose: Individual's ID, age, gender, CD4 count at ART initiation, and the time of ART initiation or discontinuation.

Data channel	Description
Year	Time of the event in units of calendar year, including fractions of years up to two decimal places.
ID	Number uniquely identifying the individual.
Gender	0 for male, 1 for female
Age	Age of the individual in units of days. Divide by 365 to obtain age in years.
CD4	CD4 count at ART initiation. If the individual is discontinuing ART, this will report the CD4 at initiation, not the current CD4 at discontinuation.
StartingART	1 if the individual is initiating ART, 0 if discontinuing ART

HIV Mortality

File name: [HIVMortality.csv](#)

Enabled by config.json parameter: Report_HIV_Mortality

Used for simulation types: HIV

Purpose: Provides information about the individual recorded at time of death, including disease status and CD4 count, medical history, and relationship history.

Data channel	Description
id	Number uniquely identifying the individual.
Death_time	Time of the event in units of days since the start of the simulation.
Death_was_HIV_cause	0 if death was due to background mortality configured in the demographics file, 1 if death was due to HIV.
Gender	0 for male, 1 for female.
Age	Age of the individual in years, including fractions of years (i.e., not rounded down to integer age).
Num_rels_just_prior_to_death	Integer number of relationships in which the individual was participating just prior to death.
Num_rels_lifetime	Integer number of lifetime relationships.
HIV_disease_state_just_prior_to_death	0 for uninfected, 1 for untreated acute HIV infection, 2 for untreated latent HIV infection, 3 for untreated late/AIDS stage, 4 for on ART.
Years_since_infection	The number of years since the individual was most recently infected. This can be reset if the infection is suppressed.

Data channel	Description
CD4_count_first_recorded	First CD4 count ever recorded with CD4 testing (the HIVDrawBlood intervention).
CD4_count_last_recorded	Most recent CD4 count recorded with CD4 testing (the HIVDrawBlood intervention).
CD4_count_current	Actual CD4 count at time of death (regardless of when CD4 testing was performed).
Days_since_CD4_blood_draw	Time lag between last CD4 test (the HIVDrawBlood intervention) and time of death.
Total_number_of_times_initiating_ART	Integer number of lifetime ART initiations.
Total_years_on_ART	Cumulative number of years on ART, including fractions of years.
Years_since_first_ART_initiation	Number of years since first ART initiation, including fractions of years.
Years_since_most_recent_ART_initiation	Number of years since most recent ART initiation, including fractions of years.

Data channel	Description
ART_status_just_prior_to_death	<p>Description of eligibility and status of ART at time of death. Possible values are:</p> <ul style="list-style-type: none"> • WITHOUT_ART_UNQUALIFIED • WITHOUT_ART_QUALIFIED_BY_BASELINE • ON_PRE_ART • LOST_TO_FOLLOW_UP • ON_ART_BUT_NOT_VL_SUPPRESSED • ON_VL_SUPPRESSED • ON_BUT_FAILING • ON_BUT_ADHERENCE_POOR • OFF_BY_DROPOUT
Cascade_State	<p>Cascade_State at time of death. Cascade_State is set by some interventions, and changed by the next intervention that sets a different Cascade_State.</p>
Ever_tested	<p>0 if individual has never received an HIVRapidHIVDiagnostic intervention, 1 if the individual has received it. Note that other diagnostics (such as SimpleDiagnostic and HIVSimpleDiagnostic) do not count toward Ever_tested.</p>
Ever_tested_positive	<p>0 if the individual has never received a positive HIV test via HIVRapidHIVDiagnostic, 1 if the individual has tested positive. Note that other diagnostics (such as SimpleDiagnostic and HIVSimpleDiagnostic) do not count toward Ever_tested_positive.</p>
Ever_received_CD4_result	<p>0 if the individual has never received a CD4 test via the HIVDrawBlood intervention, 1 if individual has received a CD4 test.</p>
Ever_in_ART	<p>0 if the individual has never received the ARTBasic intervention, 1 if the individual has received it.</p>
Currently_in_ART	<p>0 if the individual was not receiving the ARTBasic intervention at time of death, 1 if the individual was receiving it at time of death.</p>

HIV Disease Progression

File name: [ReportHIVInfection.csv](#)

Enabled by config.json parameter: Report_HIV_Infection

Used for simulation types: HIV

Purpose: Logs every individual's state at each timestep.

Data channel	Description
Column	Description
Year	Time of the timestep in units of calendar year, including fractions of years up to two decimal places.
Id	Number uniquely identifying the individual.
MCWeight	Not currently supported. This column will always show a Monte Carlo weight of 1.
Age	Age of the individual in years, including fractions of years (i.e., not rounded down to integer age).
Gender	0 for male, 1 for female.
getProbMaternalTransmission	The hypothetical probability of MTCT, if the individual were to give birth at the present time and not receive any interventions such as PMTCT or ART. Not applicable for males or for females of non-childbearing age.
TimeSinceHIV	The number of days since the individual became infected. If the individual was infected by an Outbreak intervention with the Incubation_Period_Override parameter set to zero, the infection is “fast forwarded.” In this case, TimeSinceHIV is the effective time of infection is in the past, and the TimeSinceHIV is adjusted accordingly.
CD4count	Current CD4 count (regardless of when CD4 testing was performed),

Data channel	Description
PrognosisCompletedFraction	The proportion of the total untreated HIV survival time that has already been lived. Only relevant when not on ART.
Prognosis	The remaining untreated survival time until AIDS-related death. Only relevant when not on ART.
Stage	0 for uninfected, 1 for untreated acute HIV infection, 2 for untreated latent HIV infection, 3 for untreated late/AIDS stage, 4 for on ART.
ViralLoad	Not currently supported.
WHOStage	The individual's WHO stage, linearly interpolated between integer values. Round down to obtain integer value for WHO clinical stage. This is set to -1 for uninfected individuals.
Infectiousness	Gets the individual's infectiousness, which depends on disease stage and ART, and includes effects of heterogeneous infectiousness.
ModAcquire	Multiplicative modifier on disease acquisition; will be 1 for HIV. Configured in <code>Immunity_Acquisition_Factor</code> .
ModTransmit	Multiplicative modifier on disease transmission. Configured in <code>Immunity_Transmission_Factor</code> .
ModMortality	Multiplicative modifier on disease death. Configured in <code>Immunity_Mortality_Factor</code> .

Data channel	Description
ArtStatus	<p>The options are as follows:</p> <ul style="list-style-type: none"> • 1 if the individual is not currently receiving ART • 5 if the individual is on ART, but their viral load is not yet suppressed • 6 if the individual is on ART, and their viral load is suppressed • 7 if the individual is on ART but is experiencing virological failure • 8 if the individual has had poor adherence to ART • 9 if the individual has dropped out of ART <p>0, 2-4 and 10 are not currently supported for this release.</p>
InfectivitySuppression	<p>Multiplier acting on Base_Infectivity to determine the per-act transmission probability of a virally suppressed HIV-positive individual. This can be reduced from ART_Viral_Suppression_Multiplier due to ARTBasic's Days_To_Achieve_Viral_Suppression.</p>
DurationOnART	<p>The number of days since the individual most recently started ART.</p>
ProbMaternalTransmissionModifier	<p>The better maternal suppression multiplier provided by PMTCT or zero.</p>
OnArtQuery	<p>0 if the individual is not on ART, 1 if the individual is on ART.</p>
CoInfectiveFactor	<p>The per-act transmission multiplier for an individual with the co-infection flag. If the individual does not have the flag, the value will be 1.</p>
DebutAge	<p>The age of sexual debut (in days).</p>
IsCircumcised	<p>0 if not circumcised, 1 if circumcised. Only applicable for males.</p>

Data channel	Description
InterventionReducedAcquire	The multiplier, based on interventions like SimpleVaccine , used to reduce the probability that an individual will acquire an infection.
InterventionReducedTransmit	The multiplier, based on interventions like SimpleVaccine , used to reduce the probability that an individual will transmit an infection.
InterventionReducedMortality	The multiplier, based on interventions like SimpleVaccine , used to reduce the probability that an individual will die due to an infection.

Health Events and Interventions

File name: [ReportEventRecorder.csv](#)

Enabled by config.json parameter: Report_Event_Recorder

Customized by config.json parameters: Report_Event_Recorder_Events, Report_Event_Recorder_Ignore_Events_In_List, Report_Event_Recorder_Individual_Properties

Used for simulation types: All

Purpose: Log events from individuals (e.g. Birth, Pregnant, DiseaseDeath, HIVSymptomatic, ...) and from any interventions you have used.

Usage tips: First, decide if you want to list the events that should be recorded, or if you want to record all events except the ones you list.

Use Report_Event_Recorder_Events to list events. They can either be individual events such as Births, “whitelisted” events such as ARTStaging0 through 9, or your custom events listed in config.json’s Listed_Events.

For example:

```
"Report_Event_Recorder_Events": [
    "HCTTestingLoop0",
    "HCTTestingLoop1",
    "HCTTestingLoop2",
    "Births",
    "ARTStaging1"
],
```

If Report_Event_Recorder_Ignore_Events_In_List is set to 0, then only these events will be recorded. If it is set to 1, then all events except these will be recorded.

In addition to the default data channels listed below, it is also possible to list whether an individual has been assigned any particular [Individual Property](#). To do so, add the name of the Individual Property to the array Report_Event_Recorder_Individual_Properties.

For more information about configuring the event recorder, see the EMOD parameter reference guide.

Data channel	Description
Year	Time of the event in units of calendar year, including fractions of years up to two decimal places.

Data channel	Description
Event_Name	The event being logged. If Report_EventRecorderIgnoreEvents_In_List is set to 0, then the event name will be one of the ones listed under Report_EventRecorderEvents. Otherwise, it will be the name of any other event that occurs and is not listed under Report_EventRecorderEvents.
Individual_ID	Number uniquely identifying the individual.
Age	Age of the individual in units of days. Divide by 365 to obtain age in years.
Gender	0 for male, 1 for female.
Infectiousness	The per-act probability of transmission, including intrahost factors like stage and ART, but excluding condoms.
<custom channels>	If any Individual Properties are listed under the config.json array Report_EventRecorderIndividualProperties, they will appear as additional columns between the Infectiousness and HasHIV columns of the CSV file.
HasHIV	This column is included for HIV simulations only. N if the individual is not infected, Y if the individual is infected with HIV.
OnART	This column is included for HIV simulations only. N if the individual is not on ART, Y if the individual is on ART.
CD4	Current CD4 count (regardless of when CD4 testing was performed).
WHO_Stage	The individual's WHO stage, linearly interpolated between integer values. Round down to obtain integer value for WHO clinical stage. This is set to -1 for uninfected individuals.
CascadeState	The individual's state in the simulation's cascade of care. This state is determined by the interventions used in the campaign event. The possible states are listed in Valid_Cascade_States.

Formation of Relationships

File name: [RelationshipStart.csv](#)

Enabled by config.json parameter: Report_Relationship_Start

Used for simulation types: STI, HIV

Purpose: Provide information about each relationship and its members, evaluated at the time of relationship formation.

Description: Includes the relationship type, start time, scheduled end time, and detailed information about each participant (referred to as participant “A” and participant “B”) -- ID, gender, age, infection status, circumcision status for males, co-infections, number of active, recent, and lifetime relationships, and [Individual Properties](#).

Data channel	Description
Rel_ID	A unique identifier for the relationship (different from the IDs of the participants).
Rel_start_time	The time (in days) during the simulation when the relationship started.
Rel_scheduled_end_time	The time (in days) during the simulation that the relationship was scheduled to end. This is determined when the relationship is created based on the type of relationship and its Weibull distribution parameters.
Rel_type (0 = transitory 1 = informal 2 = marital)	The type of relationship between individuals A and B; 0 for transitory, 1 for informal, 2 for marital.
Original_node_ID	The ID of the node where the relationship was started.
<A or B>_ID	This column is repeated for each individual in the relationship. Number uniquely identifying the individual.
<A or B>_is_infected	This column is repeated for each individual in the relationship. 0 for not infected, 1 for infected.

Data channel	Description
<A or B>_gender	This column is repeated for each individual in the relationship. 0 for male, 1 for female.
<A or B>_age	This column is repeated for each individual in the relationship. Age of the individual in units of years.
<A or B>_total_num_active_rels	This column is repeated for each individual in the relationship. The total number of active relationships the individual is currently in.
<A or B>_num_active_transitory_rels	This column is repeated for each individual in the relationship. The total number of transitory relationships the individual is currently in.
<A or B>_num_active_informal_rels	This column is repeated for each individual in the relationship. The total number of informal relationships the individual is currently in.
<A or B>_num_active_marital_rels	This column is repeated for each individual in the relationship. The total number of marital relationships the individual is currently in.
<A or B>_num_lifetime_rels	This column is repeated for each individual in the relationship. The total number of relationships the individual has had during their lifetime.
<A or B>_num_rels_last_6_mo	This column is repeated for each individual in the relationship. The total number of relationships the individual has had in the last 6 months.
<A or B>_extra_relational_bitmask	This column is repeated for each individual in the relationship. Indicates which types of relationships that individual is allowed to have when they have more than one active relationship. 0 for transitory, 1 for informal, 2 for Marital.
<A or B>_is_circumcised	This column is repeated for each individual in the relationship. 0 for not circumcised, 1 for circumcised.
<A or B>_has_STI_coinfection	This column is repeated for each individual in the relationship. 0 if the partner does not have an STI co-infection, 1 if they do have an STI co-infection.

Data channel	Description
<A or B>_is_super-spreader	This column is repeated for each individual in the relationship. 0 for when the partner is not a superspread, 1 for when they are a super-spreader. Whether or not an individual is determined to be a super spreader is determined by Probability_Person_Is_Behavioral_Super_Spreader.
<A or B>_IndividualProperties	This column is repeated for each individual in the relationship. The IndividualProperties associated with each partner. This string may contain multiple key-value pairs. Each key and value are separated by a hyphen, and each pair is separated by a semicolon.
<A or B>_CD4_count	This column is repeated for each individual in the relationship. The CD4 count for each partner.
<A or B>_viral_load	This column is repeated for each individual in the relationship and will be included for HIV simulations only. This is not currently supported. -1 implies that the partner is not infected. 10000 implies that the partner is infected.
<A or B>_HIV_disease_stage	This column is repeated for each individual in the relationship and will be included for HIV simulations only. The stage of infection for each individual.
<A or B>_STI_CoInfection	This column is repeated for each individual in the relationship and will currently be included for HIV simulations only. 0 for when the partner does not have an STI co-infection; 1 for when they do have an STI co-infection.
<A or B>_HIV_Tested_Positive	This column is repeated for each individual in the relationship and will be included for HIV simulations only. 0 if the partner has never tested positive for HIV, 1 if the partner has ever tested positive. The HIVRapidHIVDiagnostic intervention is used to test whether an individual has HIV.

Data channel	Description
<A or B>_HIV_Received_Results	<p>This column is repeated for each individual in the relationship and will be included for HIV simulations only.</p> <p>Represents the results received by the individual from the latest test for HIV (HIVRapidHIVDiagnostic). UNKNOWN implies that the individual has never received the results from a test. NEGATIVE implies that the most recent results received by the individual were negative. POSITIVE implies that the most recent results received by the individual were positive for HIV. Whether or not an individual receives the results is determined by HIVRapidDiagnostic's Probability_Received_Result parameter.</p>

Dissolution of Relationships

File name: [RelationshipEnd.csv](#)

Enabled by config.json parameter: Report_Relationship_End

Used for simulation types: STI, HIV

Purpose: Provide information about each relationship and its members, evaluated at the time of relationship dissolution.

Description: Includes the relationship type, start time, scheduled end time, actual end time (which may differ from the scheduled end time, e.g., due to the death of a partner), participant IDs, and ages at the time of dissolution.

Data channel	Description
Rel_ID	A unique identifier for the relationship (different from the IDs of the participants).
Rel_start_time	The time (in days) during the simulation when the relationship started.
Rel_scheduled_end_time	<p>The time (in days) during the simulation that the relationship was scheduled to end.</p> <p>This is determined when the relationship is created based on the type of relationship and its Weibull distribution parameters.</p>
Rel_actual_end_time	<p>The actual end time of the relationship, in days since the start of the simulation.</p> <p>This may differ from the scheduled end time, e.g., due to the death of a partner.</p>
Rel_type (0 = transitory 1 = informal 2 = marital)	0 for transitory relationship, 1 for informal relationship, 2 for marital relationship.
male_ID	This label is currently used to uniquely identify one of the partners in the relationship. In a future release, this will be updated to partner A, as same-sex partners are allowed in the model.
female_ID	This label is currently used to uniquely identify one of the partners in the relationship. In a future release, this will be updated to partner B, as same-sex partners are allowed in the model.

Data channel	Description
male_age	Currently indicates the age (in years) for one of the partners in the relationship. In a future release, this will be updated to partner A, as same-sex partners are allowed in the model.
female_age	Currently indicates the age (in years) for one of the partners in the relationship. In a future release, this will be updated to partner B, as same-sex partners are allowed in the model.

Transmission of disease within relationships

File name: [TransmissionReport.csv](#)

Enabled by config.json parameter: Report_Transmission

Used for simulation types: STI, HIV

Purpose: Provide information about each relationship and its members, evaluated at the time of disease transmission within the relationship.

Description: Includes the time/date of transmission and information about the transmitter and recipient (age, gender, current and lifetime number of relationships, infection stage, circumcision status for males, co-infections, and disease-specific biomarkers if applicable).

Data channel	Description
SIM_TIME	The time (in days) during the simulation that the infection was transmitted.
YEAR	Time of the simulation timestep in units of calendar year. For STI simulations, this is the simulation time divided by 365. For HIV simulations, this is the simulation time divided by 365 plus Base_Year.
SRC_ID	Number uniquely identifying the transmitting individual.
SRC_INFECTED	0 for not infected, 1 for infected. This should always be 1.
SRC_GENDER	0 for male, 1 for female.
SRC_AGE	Age of the infecting individual in years, including fractions of years (i.e., not rounded down to integer age).
SRC_current_relationship_count	The total number of relationships (all types) that the transmitting individual was in at time of transmission.
SRC_lifetime_relationship_count	The total number of relationships (all types) that the transmitting individual has had until the current time.
SRC_relationships_in_last_6_months	The number of relationships (all types) that the transmitting individual has had in the previous 6 months.

Data channel	Description																				
SRC_FLAGS	<p>Indicates which types of relationships that individual is allowed to have when they have more than one active relationship. These are encoded in a 3-digit bitmask. In order, the digits correspond to marital, informal, and transitory relationships.</p> <p>The following table lists the possible combinations:</p> <table border="1"> <thead> <tr> <th>Binary</th><th>Description</th></tr> </thead> <tbody> <tr> <td>000</td><td>No extra relationships are allowed.</td></tr> <tr> <td>001</td><td>Only extra Transitory relationships are allowed.</td></tr> <tr> <td>010</td><td>Only extra Informal relationships are allowed.</td></tr> <tr> <td>100</td><td>Only extra Marital relationships are allowed.</td></tr> <tr> <td>011</td><td>Extra Informal and Transitory relationships are allowed.</td></tr> <tr> <td>101</td><td>Extra Marital and Transitory relationships are allowed.</td></tr> <tr> <td>110</td><td>Extra Marital and Informal relationships are allowed.</td></tr> <tr> <td>111</td><td>Extra relationships are allowed for all types. Superspreaders will have all types enabled.</td></tr> <tr> <td>Years_since_infection</td><td>The number of years since the individual was most recently infected. This can be reset if the infection is suppressed.</td></tr> </tbody> </table>	Binary	Description	000	No extra relationships are allowed.	001	Only extra Transitory relationships are allowed.	010	Only extra Informal relationships are allowed.	100	Only extra Marital relationships are allowed.	011	Extra Informal and Transitory relationships are allowed.	101	Extra Marital and Transitory relationships are allowed.	110	Extra Marital and Informal relationships are allowed.	111	Extra relationships are allowed for all types. Superspreaders will have all types enabled.	Years_since_infection	The number of years since the individual was most recently infected. This can be reset if the infection is suppressed.
Binary	Description																				
000	No extra relationships are allowed.																				
001	Only extra Transitory relationships are allowed.																				
010	Only extra Informal relationships are allowed.																				
100	Only extra Marital relationships are allowed.																				
011	Extra Informal and Transitory relationships are allowed.																				
101	Extra Marital and Transitory relationships are allowed.																				
110	Extra Marital and Informal relationships are allowed.																				
111	Extra relationships are allowed for all types. Superspreaders will have all types enabled.																				
Years_since_infection	The number of years since the individual was most recently infected. This can be reset if the infection is suppressed.																				
SRC_CIRCUMSIZED	0 for not circumcised, 1 for circumcised (for the transmitting individual).																				
SRC_STI	0 for when the transmitting individual does not have an STI co-infection; 1 for when the transmitting individual does still have an STI co-infection at the time of the transmission event.																				

Data channel	Description
SRC_SUPERSPREADER	0 for when the transmitting individual is not a superspread, 1 for when they are a superspread. Whether or not an individual is determined to be a super spreader is determined by Probability_Person_Is_Behavioral_Super_Spread.
SRC_INF_AGE	Not currently supported. This will always display -42.
DEST_ID	Number uniquely identifying the infected individual.
DEST_INFECTED	0 for not infected, 1 for infected. The receiving individual may or may not be infected.
DEST_GENDER	0 for male, 1 for female.
DEST_AGE	Age of the receiving individual in years, including fractions of years (i.e., not rounded down to integer age).
DEST_current_relationship_count	The total number of relationships (all types) that the receiving individual was in at time of transmission.
DEST_lifetime_relationship_count	The total number of relationships (all types) that the receiving individual has had until the current time.
DEST_relationships_in_last_6_months	The number of relationships (all types) that the receiving individual has had in the previous 6 months.
DEST_FLAGS	Indicates which types of relationships that individual is allowed to have when they have more than one active relationship. See SRC_FLAGS for explanation of bitmask.
DEST_CIRCUMSIZED	0 for not circumcised, 1 for circumcised (for the receiving individual).
DEST_STI	0 for when the transmitting individual does not have an STI co-infection; 1 for when the receiving individual does have an STI co-infection at the time of the transmission event.
DEST_SUPERSPREADER	0 for when the receiving individual is not a superspread, 1 for when they are a superspread. Whether or not an individual is determined to be a super spreader is determined by Probability_Person_Is_Behavioral_Super_Spread.

Data channel	Description
SRC_CD4	<p>This column will be included for HIV simulations only.</p> <p>The current CD4 count of the transmitting individual.</p>
SRC_VIRAL_LOAD	<p>This column will be included for HIV simulations only.</p> <p>Not currently supported . 10000 implies that the individual is infected.</p>
SRC_STAGE	<p>This column will be included for HIV simulations only.</p> <p>0 for uninfected, 1 for untreated acute HIV infection, 2 for untreated latent HIV infection, 3 for untreated late/AIDS stage, 4 for on ART. -1 implies the transmitting individual does not have HIV.</p>
DEST_CD4	<p>This column will be included for HIV simulations only.</p> <p>The current CD4 count of the receiving individual.</p>
DEST_VIRAL_LOAD	<p>This column will be included for HIV simulations only.</p> <p>Not currently supported. 10000 implies that the individual is infected.</p>
DEST_STAGE	<p>This column will be included for HIV simulations only.</p> <p>0 for uninfected, 1 for untreated acute HIV infection, 2 for untreated latent HIV infection, 3 for untreated late/AIDS stage, 4 for on ART. -1 implies the receiving individual does not have HIV.</p>

Coital Acts

File name: [RelationshipConsummated.csv](#)

Enabled by config.json parameter: Report_Coital_Acts

Used for simulation types: STI, HIV

Purpose: Provide information about each coital act, evaluated at the time of the coital act.

Description: Includes time, relationship and participant IDs, whether a condom was used, and each participant's age, gender, infection status, circumcision status, co-infection status, and treatment status.

Data channel	Description
Time	The time (in days) during the simulation that the infection was transmitted.
Rel_ID	A unique identifier for the relationship (different from the IDs of the participants).
<A or B>_ID	This column is repeated for each individual in the relationship. Number uniquely identifying each individual.
<A or B>_Gender	This column is repeated for each individual in the relationship. 0 for male, 1 for female.
<A or B>_Age	This column is repeated for each individual in the relationship. Age of the individual in years.
<A or B>_Is_Infected	This column is repeated for each individual in the relationship. 0 for not infected, 1 for infected.
Did_Use_Condom	0 if no condom was not used during this coital act, 1 if a condom was used.
<A or B>_Num_Current_Rels	This column is repeated for each individual in the relationship. The total number of active relationships in which the individual is currently participating.

Data chan- nel	Description
<A or B>_ Is_Cir- cumcised	<p>This column is repeated for each individual in the relationship.</p> <p>0 for not circumcised, 1 for circumcised. Only relevant for males.</p>
<A or B>_ Has_Coln- fection	<p>This column is repeated for each individual in the relationship and will currently only be displayed for HIV simulations.</p> <p>0 if the individual does not have an STI co-infection, 1 if the individual currently has an STI co-infection.</p>
<A or B>_ HIV_Infec- tion_Stage	<p>This column is repeated for each individual in the relationship and will currently only be displayed for HIV simulations.</p> <p>0 for uninfected, 1 for untreated acute HIV infection, 2 for untreated latent HIV infection, 3 for untreated late/AIDS stage, 4 for on ART. -1 indicates that the individual does not have HIV.</p>
<A or B>_ Is_On_ART	<p>This column is repeated for each individual in the relationship and will currently only be displayed for HIV simulations.</p> <p>0 if the individual is not on ART, 1 if the individual is currently receiving ART.</p>

Age-Stratified Epidemic Information

File name: [BinnedReport.json](#)

Enabled by config.json parameter: Enable_Demographics_Reporting

Used for simulation types: all

Purpose: Age-stratified records (in 5-year age bins) of the population size, number of infections, number of new infections, and disease-related deaths over time, reported at each time step.

For more information about this output file, please see the [Binned Report File](#) in IDM's online documentation.

Data channel	Description
Population	The population size within the indicated age bin.
Infected	The number of infected individuals within the indicated age bin.
New Infections	The number of individuals newly infected on this timestep within the indicated age bin.
Disease deaths	The number of individuals who died on this timestep within the indicated age bin.

Age-Stratified Demographic Information

File name: [DemographicsSummary.json](#)

Enabled by config.json parameter: Enable_Demographics_Report

Used for simulation types: all

Purpose: Age-stratified records (in 5-year age bins) of the population size, number of births, number of non-disease deaths (those not associated with the disease being modeled), gender ratio, and other demographic summary statistics, reported at each time step.

For more information about this output file, please see the [Demographics Summary File](#) in IDM's online documentation.

Data channel	Description
Gender Ratio (fraction male)	The fraction of individuals who are male.
Statistical Population	Total population size at this timestep, summed over nodes and including Monte Carlo weighting if used.
Average Age	Mean age of the population.
New Natural Deaths	Number of deaths on this timestep driven by "background mortality," i.e., factors not related to the disease being simulated.
Possible Mothers	Number of females between the ages of 14 and 45.
Pseudo-Population	The number of individuals who are explicitly simulated in the model. If Monte Carlo weights are always set to 1, then this is equal to the Statistical Population which includes Monte Carlo weights.
New Births	The number of individuals born on this timestep. Includes Monte Carlo weight.
Population Age <5	The number of individuals under age 5. Includes Monte Carlo weight.
Population Age 10-14	The number of individuals age 10-14. Includes Monte Carlo weight.

Data channel	Description
< and so on for 5-year age bins up to 99>	
Population Age >100	The number of individuals over age 100. Includes Monte Carlo weight.

Diagnostic Outputs for Software Developers

File name: [Inset Chart.json](#)

Enabled by config.json parameter: Enable_Default_Reportng

Used for simulation types: all

Purpose: Information about the simulation at each time step, customized for model development (compared to other output files that are more tailored for scientific research).

For more information about this output file, see the [Inset Chart File](#) in IDM's online documentation.

Data channel	Description
Infected	Number individuals infected with the disease being simulated.
New Infections	Number of new infections with the disease being simulated.
Cumulative Infections	Cumulative number of infections since the start of the simulation.
Disease Deaths	Number of disease-related deaths (TBD - cumulative? on this timestep?)
Prevalence (Females, 15-49)	Disease prevalence among females age 15-49.
Single Post-Debut Women, Prevalence (Males, 15-49)	Disease prevalence among females age 15-49 who are older than the age of sexual debut.
Prevalence among Sexually Active (Adults)	Disease prevalence among all adults who are older than the age of sexual debut (TBD - or have had a sex partner? or have had a coital act?)
Post-Debut Population	Population of individuals who have reached/surpassed the age of sexual debut.
Single Post-Debut Men	Population of males who have reached/surpassed the age of sexual debut, and are not in a relationship.
Paired People	Population of individuals who are in relationships.

Data channel	Description
Number of Individuals Ever in a Relationship	Population of individuals who have ever been in a relationship.
Active Transitory Relationships	Number of active transitory relationships.
Active Informal Relationships	Number of active informal relationships.
Active Marital Relationships	Number of active marital relationships.
Statistical Population	Population size, including Monte Carlo weighting if used.
Births	Cumulative births since the start of the simulation.
Campaign Cost	Cumulative cost of interventions calculated as the sum of unit costs. Unit cost for each intervention is configured in campaign.json.

Appendix B: Scripts for Plotting Model Results

The STI/HIV tutorials include scripts to help analyze data produced by the EMOD simulations.

These scripts are provided in a variety of languages, including Python, R, MATLAB and Mathematica. While many of the scripts are specific to the individual STI and HIV scenarios, there are four common scripts used by most tutorials. The scripts can be used as is, or you can use them as templates to create your own. The common scripts are located in Scenarios\Scripts directory.

After running the model, locate the scenario folder which should contain the output folder. From the Windows file explorer, type “cmd” in the address bar to open a command window. Then type python or Rscript with the appropriate command line arguments to run each script.

Details of each script are provided in the following sections.

InsetChart Channel Viewer

Python Script names: plotAllCharts.py

Purpose: Plot all of the data in the InsetChart.json output file

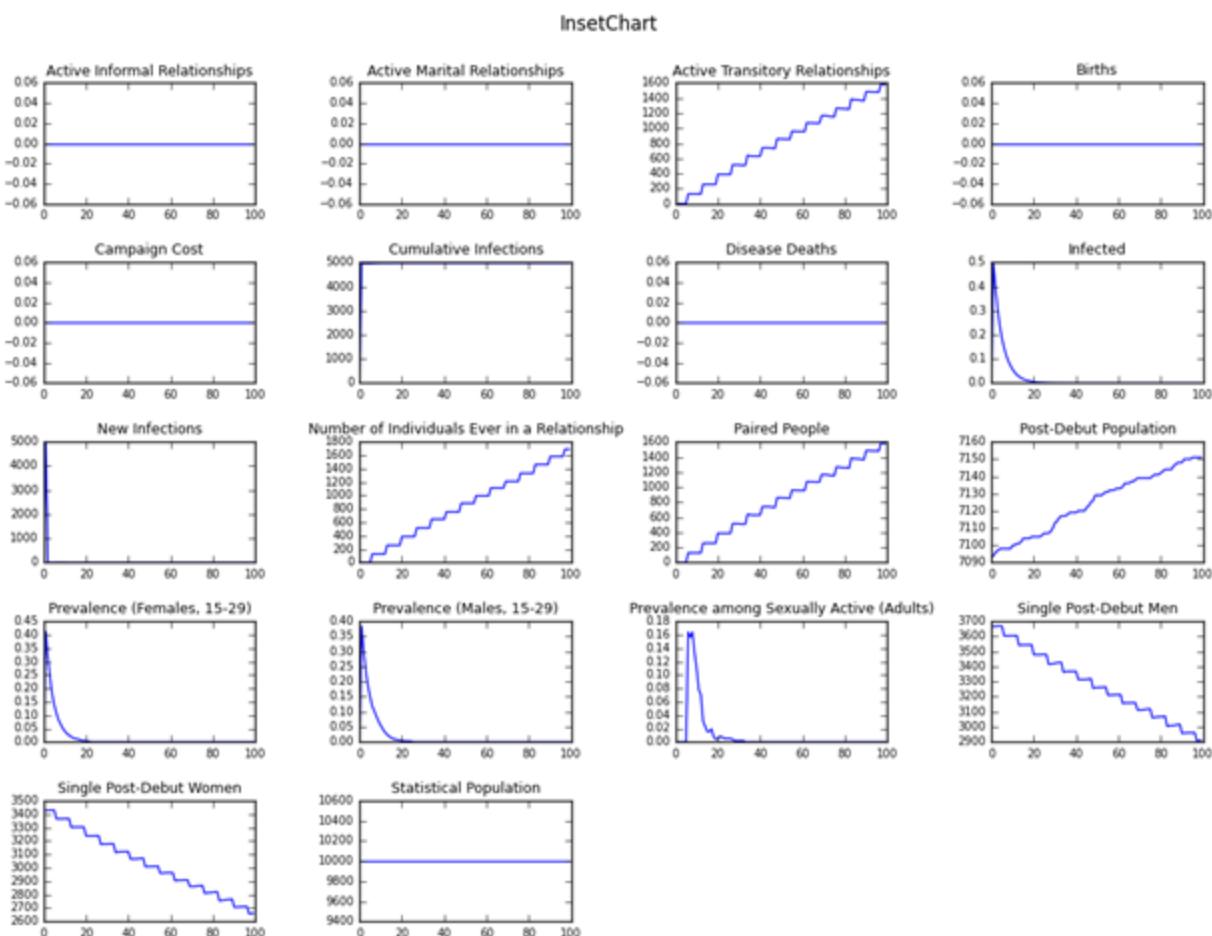
Usage: From the command line, invoke python with three arguments. The first is the path to the script, the second is the path to the InsetChart.json file, and the third is a descriptive name for the resulting plot.

You can also run the scripts from your preferred Python interface.

Example: > `python ..\..\..\Scripts\plotAllCharts.py output\InsetChart.json "InsetChart"`

Required files: InsetChart.json

Example figure:



Prevalence, Incidence, Mortality, and Number on ART

Python Script name: plotHIVSummary_15_49.py

R Script name: plotHIVSummary_15_49.r (R)

Purpose: Plot HIV prevalence, incidence, mortality, and ART coverage over time and by gender for those aged 15-49

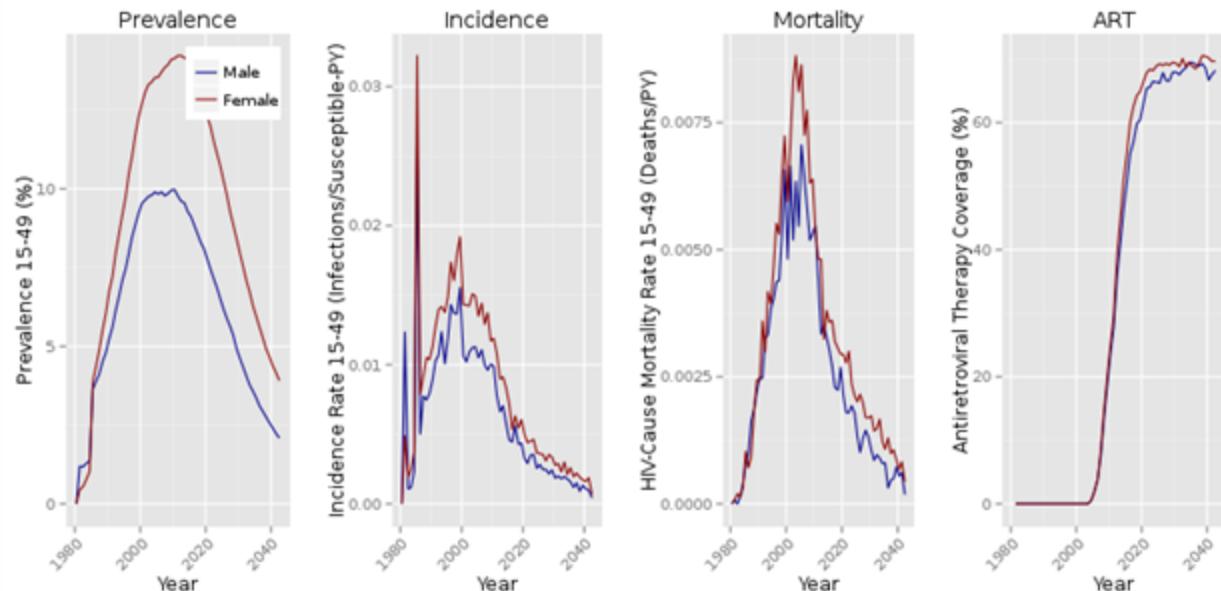
Usage: From the command line, invoke python or Rscript with two arguments. First is the path to the appropriate plotHIVSummary_15_49 script, and second is the path to ReportHIVByAgeAndGender.csv.

Example for Python: > `python.exe plotHIVSummary_15_49.py ReportHIVByAgeAndGender.csv`

Example for R: > `Rscript plotHIVSummary_15_49.R ReportHIVByAgeAndGender.csv`

Required files: ReportHIVByAgeAndGender.csv

Example figure:



Population by Age

Python Script name: plotBinnedPopulation.py

R Script name: plotBinnedPopulation.r

Purpose: Plot the population in 5-year bins over time

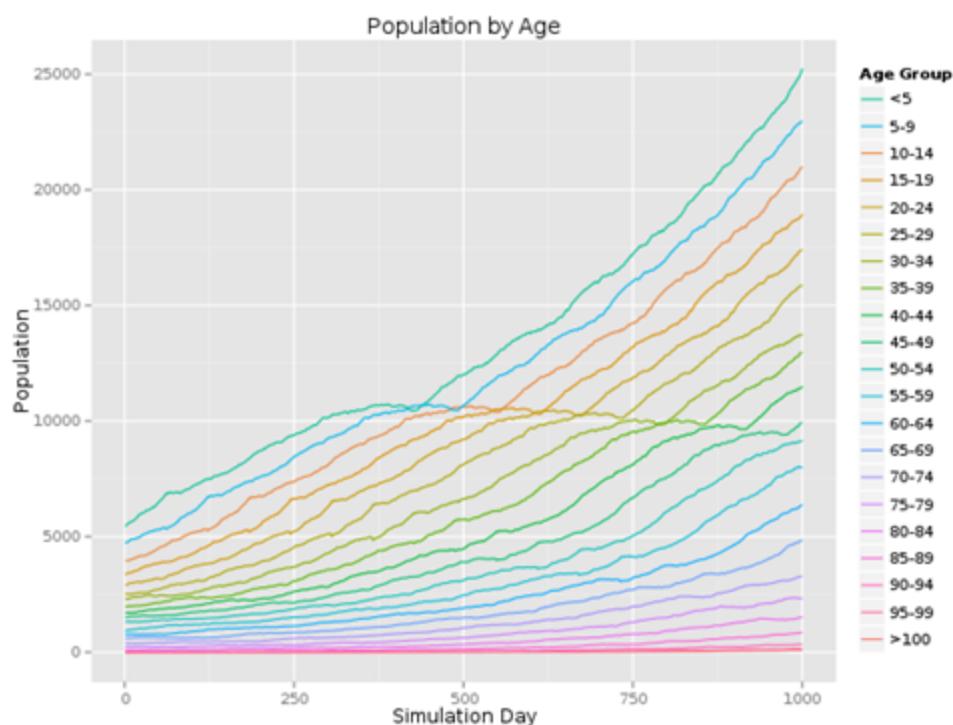
Usage: From the command line, invoke python or Rscript with two arguments. First is the path to the appropriate plotBinnedPopulation script, and second is the path to BinnedReport.json.

Example for Python: > `python.exe plotBinnedPopulation.py BinnedReport.json`

Example for R: > `Rscript plotBinnedPopulation.R BinnedReport.json`

Required files: BinnedReport.json

Example figure:



Log of Events and Interventions Applied to Individuals

Python Script name: plotEventRecorder.py

R Script name: plotEventRecorder.r

Purpose: Log events from individuals (e.g. Birth, Pregnant, DiseaseDeath, HIVSymptomatic) and from any interventions you have used.

Usage: From the command line, invoke python or Rscript with two arguments. First is the path to the appropriate plotEventRecorder script, and second is the path to ReportEventRecorder.csv.

Example for Python: > **python.exe plotEventRecorder.py ReportEventRecorder.csv**

Example for R: > **Rscript plotEventRecorder.R ReportEventRecorder.csv**

Required files: ReportEventRecorder.csv

Example figure:

