User guide to the Spectrum-STI Module

Estimating national STI burdens and trends for high-risk and low-risk population groups

9 June 2020

Spectrum-STI versions 5.88 beta 23 and later

World Health Organization

Avenir Health

Foreword

The Spectrum-STI Module is a computer program developed to generate country estimates of prevalence levels and time trends for active syphilis, gonorrhea and chlamydia. Spectrum-STI is a statistical trend fitting model and whilst appropriate for looking at past trends, it should not be used for generating future long term projections.

Spectrum-STI has been developed by Avenir Health with financial support from WHO.

Acknowledgements

This manual was written by Jane Rowley (London UK), Eline Korenromp and Guy Mahiané (Avenir Health), with input from John Stover, Jill Wyman, Kendall Hecht and Robert McKinnon (Avenir Health), and Melanie Taylor (WHO).

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Acronyms and Abbreviations

WHO	World Health Organization
STI	Sexually Transmitted Infection
RPR	rapid plasma reagin (syphilis diagnostic assay)
TPHA	*Treponema pallidum* haemagglutination assay
DemProj	Demographic Projection, module of Spectrum
AIM	AIDS Impact Module, within Spectrum
M	Male
F	Female
FSW	Female sex workers
MSM	Men who have sex with Men
CI	confidence interval(s)
ANC	Antenatal Care
Ob/Gyn	Obstetrics and Gynecology
GAM	Global AIDS Monitoring
IBBS	Integrated Bio-Behavioural Survey
EPP	Epidemic Projection Package, sub-module of Spectrum AIM
HIV	Human Immunodeficiency Virus
PWID	People who inject drugs
RP	Reported prevalence
US CDC	United States Centers for Disease Control
PEPFAR	U.S. President's Emergency Plan for AIDS Relief

1 Introduction

The Spectrum-STI Module is part of the Spectrum system of modelling tools developed by Avenir Health. All of the Spectrum modules have been designed to produce information useful for policy formulation and dialogue (see Spectrum Manual for more information, http://www.avenirhealth.org/software-spectrum.php).

Spectrum-STI was designed to look at national trends over time in adults in the prevalence and incidence of sexually transmitted infections [1-7]. The three STIs currently included in the STI module are *Chlamydia trachomatis* (chlamydia), *Neisseria gonorrhoeae* (gonorrhea) and *Treponema pallidum, subspecies pallidum* (syphilis).

Spectrum-STI generates prevalence and incidence estimates for:

- **Syphilis:** 'probable active' syphilis infection, defined as primary plus secondary stages of infection. In prevalence surveys this corresponds to being concurrently rapid plasma reagin (RPR)-positive and *Treponema pallidum* haemagglutination assay (TPHA)-positive. This is the same definition used by the WHO[1] and the Institute of Health Metrics and Evaluation in their regional and global syphilis estimates.
- **Gonorrhea and chlamydia:** Urogenital infections only. Both infections can also rectal or oropharyngeal infections, but these are not included in the estimates.

The STI module is run in parallel with the Spectrum module DemProj (short for: Demography projection). DemProj projects the growth over time of national populations. It is also recommended that the Spectrum AIDS Impact Module (AIM) is run in parallel to the STI module.

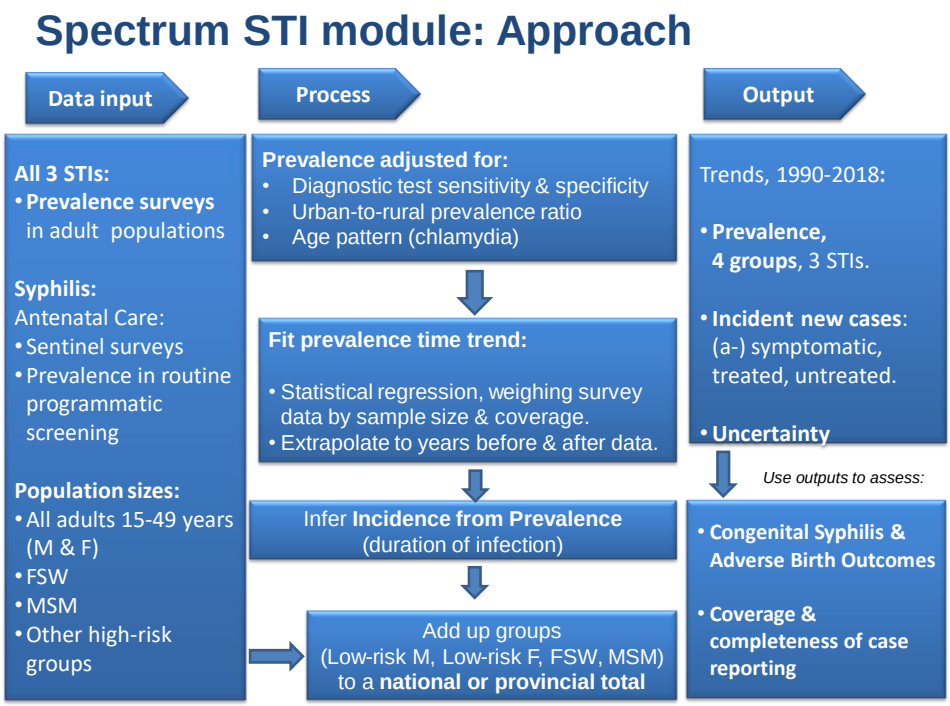
- **DemProj:** DemProj is the Spectrum module underlying all Spectrum disease modules. It projects the population for an entire country by age and sex, based on assumptions about fertility, mortality, and migration. Urban and rural projections can also be prepared. These estimates and projections are based on the United Nations Population Division's World Population Prospects, 2019 Revision. Data to generate estimates for almost all countries in the world are part of the Spectrum data file.

- **AIDS Impact Model (AIM):** AIM is the Spectrum module that projects the impact of the HIV/AIDS epidemic. It is optional but recommended when running the STI module especially in countries where HIV is affecting background mortality and age structure. It is also useful if a user wants to compare trends in HIV and STIs using the same projection file.

Figure 1.1 provides an overview of Spectrum-STI.

Please note, that the computer program uses the term "projection" to describe a country "estimation'. Spectrum-STI is a statistical trend fitting model and hence is designed to look at past trends not future. The use of the term "projection" in the computer program does not mean that the module is appropriate for making future projections. This is just the terminology used in all of the Spectrum modules.

Figure 1.1


Spectrum STI module: Approach
Data input
Process
Output
All 3 STIs:
• Prevalence surveys in adult populations
Syphilis:
Antenatal Care:
• Sentinel surveys
• Prevalence in routine programmatic screening
Population sizes:
• All adults 15-49 years (M & F)
• FSW
• MSM
• Other high-risk groups
Prevalence adjusted for:
• Diagnostic test sensitivity & specificity
• Urban-to-rural prevalence ratio
• Age pattern (chlamydia)
Fit prevalence time trend:
• Statistical regression, weighing survey data by sample size & coverage.
• Extrapolate to years before & after data.
Infer Incidence from Prevalence (duration of infection)
Add up groups (Low-risk M, Low-risk F, FSW, MSM) to a national or provincial total
Trends, 1990-2018:
• Prevalence, 4 groups, 3 STIs.
• Incident new cases: (a-) symptomatic, treated, untreated.
• Uncertainty
Use outputs to assess:
• Congenital Syphilis & Adverse Birth Outcomes
• Coverage & completeness of case reporting

2 Estimation Methods

Spectrum-STI Version 5.88 generates national prevalence estimates from estimates for different population groups. In the default version there are four population groups:

- Low-risk women
- Low-risk men
- Female Sex Workers (FSW)
- Men who have sex with Men (MSM)

In addition, users have the option to introduce other population groups for which they have one or more prevalence data point and a population size estimate (see Section 5.4).

2.1 Prevalence trend estimates for populations with data: Statistical methods

2.1.1 Syphilis

Spectrum-STI provides two alternative statistical estimation methods to fit the available syphilis data in a population group over time:

- Logistic regression;
- Segmented polynomials for incidence.

Logistic regression is the default method set for syphilis for all groups when a new Spectrum-STI projection file is created. This method is much quicker to run than the segmented polynomial regression, but will always give a monotonous increase or decrease in prevalence throughout the time period estimated. This approach should be used for initial test runs, data editing and quality checking.

In the segmented polynomial (spline) for incidence approach, prevalence is fitted through the underlying infection incidence. This allows for flexible time trends, including smooth reversals in prevalence, and year-on-year fluctuations in prevalence are constrained as incidence cannot drop below zero [2,3]. In Spectrum-STI the spline is restricted to having at most 2 knots, which means that there can be at most three epidemic phases over the projection horizon. When there are fewer than 3 data points, the spline produces results similar to logistic regression: the slope is dropped in the estimation and only a constant intercept is estimated, producing a time-constant estimate in case of only 1 data point, and a monotonous rise or decline in case of 2 data points.

For both statistical methods, the data are scaled by dividing by sample size, so that the sample size does not influence the estimated prevalence level or trend but does influence confidence bounds. The 95% confidence intervals (CI) for prevalence are then derived by bootstrapping, and the median of the bootstrapped prevalence is the final estimate.

In addition, Spectrum-STI extrapolates syphilis trend estimates in a population to a user specified length of time before the first prevalence data point and after the last data point (see Section 4.2). Before and after these dates, prevalence is assumed to be constant.

2.1.2 Gonorrhea and chlamydia

Gonorrhea and chlamydia prevalence in each population group are estimated over time as a moving average through the standardized and weighted prevalence data. Prior to doing the estimation, each prevalence data point is divided by sample size so that sample size does not influence the estimated prevalence level or trend but does influence the confidence bounds. When generating the moving average, the relative contribution of each data point to the estimate for a particular year reflects how close it is to the year being estimated. Each year further away results in its contribution falling by a fixed percentage (called the annual dilution factor), which is set at 20% as default (see Sections 4.3 and 4.4).

This estimation method is applied throughout the period with any data available; for years before the first data point and after the last data point, the estimate is flat-lined at the value of that earliest year with data and latest year with data, respectively.

95% confidence intervals (CI) are derived by bootstrapping, combining uncertainties in each survey's observed prevalence, and in the male-to-female prevalence ratio, urban-to-rural prevalence ratio, and high-risk to low-risk population prevalence ratio.

2.2 Estimating incidence

For gonorrhea and chlamydia, and for syphilis when prevalence trends were estimated using logistic regression, incidence estimates for each population group are derived from the prevalence trend estimates and the relationship between prevalence, incidence and duration of infection (also see Annex 2.2).

The 95% CIs on incidence bounds reflect both the uncertainty (estimated by bootstrap) in prevalence, and an additional uncertainty on the duration of infection, set at ±50%.

When syphilis estimates are generated using the segmented polynomials for incidence approach both prevalence and incidence estimates are generated directly.

2.3 Pooling data & generating trend estimates

Table 2.1 summarizes how the prevalence data are pooled to generate the trend estimates for low-risk women, FSW, low-risk men, and MSM.

Table 2.1 Approaches used to generate estimates.

	Syphilis:	**Gonorrhea and chlamydia:**
Low-risk women	Estimated by pooling data from low-risk population groups (e.g., ANC survey, ANC routine screening, surveys in low-risk women, blood donors). Prevalence data can also be included that does not disaggregate between women and men (e.g. routine blood donor screening results, or general population surveys). If there are no data from low-risk women, but an estimate was generated for low-risk men, then the prevalence in low-risk women is estimated from the low-risk men's prevalence, using the male-to-female prevalence ratio. If there are no data from low-risk women or men but there is an estimate for FSWs or another female high-risk group, then the high-risk to low-risk ratio is used. Otherwise no estimate generated.	Estimated by pooling prevalence data from low-risk women (e.g., ANC, pregnant women in the community/outside ANC, clinic attendees, Ob/Gyn clinic attendees, community, military, students, young, workers, blood donors, and mixed groups). If there are no data for low-risk women, but there is an estimate for FSW or another female high-risk group, then high-risk to low-risk female ratio is used. Otherwise no estimate generated.
FSW	Estimated from FSW prevalence data If there are no FSW prevalence data but there is a low-risk estimate for women, then the FSW prevalence is generated from the low-risk estimate using the high-risk to low-risk prevalence ratio for women. Otherwise no estimate generated.	Estimated from FSW prevalence data. If there are no FSW prevalence data but there is a low-risk estimate for women, then the FSW prevalence is generated from the low-risk estimate using the high-risk to low-risk prevalence ratio for women. Otherwise no estimate generated.
Low-risk men	Estimated by pooling data from low-risk men (e.g., clinic attendees, community, military recruits, students, young, workers, blood donors).	Estimated by pooling prevalence data from low-risk men. If there are no data or the available data are not active (Use data = N or Spectrum-STI Weight set at 0) then

	Syphilis:	Gonorrhea and chlamydia:
	If there are no data or the available data are not active (Use data = N or Spectrum-STI Weight set at 0) then the prevalence in low risk men is estimated from the prevalence in low-risk women using the male-to-female prevalence ratio. If there is no low risk female or low-risk male data but there is data and an estimate for MSM or, if no MSM data, another male key group, then the high-risk to low-risk ratio used. Otherwise no estimate generated.	the prevalence in low risk men is estimated from the prevalence in low-risk women using the male-to-female prevalence ratio. If there is no low risk female or low-risk male data but there is data and an estimate for MSM or, if no MSM data, another male key group, then the high-risk to low-risk ratio used. Otherwise no estimate generated
MSM	Estimated by pooling MSM prevalence data. If there are no MSM prevalence data but there is a low-risk estimate for men, then the MSM prevalence is generated from the low-risk estimate using the high-risk to low-risk prevalence ratio for men. Otherwise no estimate generated.	Estimated by pooling MSM prevalence data. If there are no MSM prevalence data but there is a low-risk estimate for men, then the MSM prevalence is generated from the low-risk estimate using the high-risk to low-risk prevalence ratio for men. Otherwise no estimate generated.

When there are insufficient data for a region to generate an estimate for a particular population or infection Spectrum-STI is structured to estimate prevalence using male-to- female ratios (Table 2.2) or high-risk to low-risk prevalence ratios (Table 2.3). These ratios are based on the estimates used in the WHO 2012 and 2016 Global Estimates and expert discussions [8,9].

Table 2.2 Male-to-Female prevalence ratio. Ratios are assumed to be time constant.

	Value	Lower-bound	Upper-bound
Syphilis	1.0	0.667	1.33
Gonorrhea	0.86	0.53	1.07
Chlamydia	0.80	0.60	1.00

Table 2.3 High-risk group to low-risk group prevalence ratio. Ratios are assumed to be time constant.

STI	Population group	Sex	Value	Lower-bound	Upper-bound
Syphilis	FSW	Women	10.0	7.5	15.0
	OtherHighRisk-Women	Women	10.0	5.0	20.0
	MSM	Men	10.0	7.5	15.0
	OtherHighRisk-Men	Men	10.0	5.0	20.0
Gonorrhea	FSW	Women	10.0	7.5	15.0
	OtherHighRisk-Women	Women	10.0	5.0	20.0
	MSM	Men	10.0	7.5	15.0
	OtherHighRisk-Men	Men	10.0	5.0	20.0
Chlamydia	FSW	Women	5.0	3.8	7.5
	OtherHighRisk-Women	Women	5.0	1.5	6.0
	MSM	Men	10.0	7.5	15.0
	OtherHighRisk-Men	Men	10.0	5.0	20.0

2.4 Aggregating groups to generate a national estimate

Once the prevalence trend estimation is done for each group, Spectrum-STI aggregates the groups into a national estimate by weighting the prevalence in each population group by its population size. The number of low-risk adult women and men are estimated by subtracting from the overall (men and women) population the sizes of all the other groups entered (e.g., FSW, MSM).

The uncertainty distributions (95% Cis) for the national estimates are calculated by combining the respective variances as if they were independent.

3 Installing and Using Spectrum-STI

3.1 Installing Spectrum-STI

Spectrum-STI will run on any computer running Windows 95 or later Windows versions. It requires about 70MB of hard disk space[1].

To install Spectrum-STI:

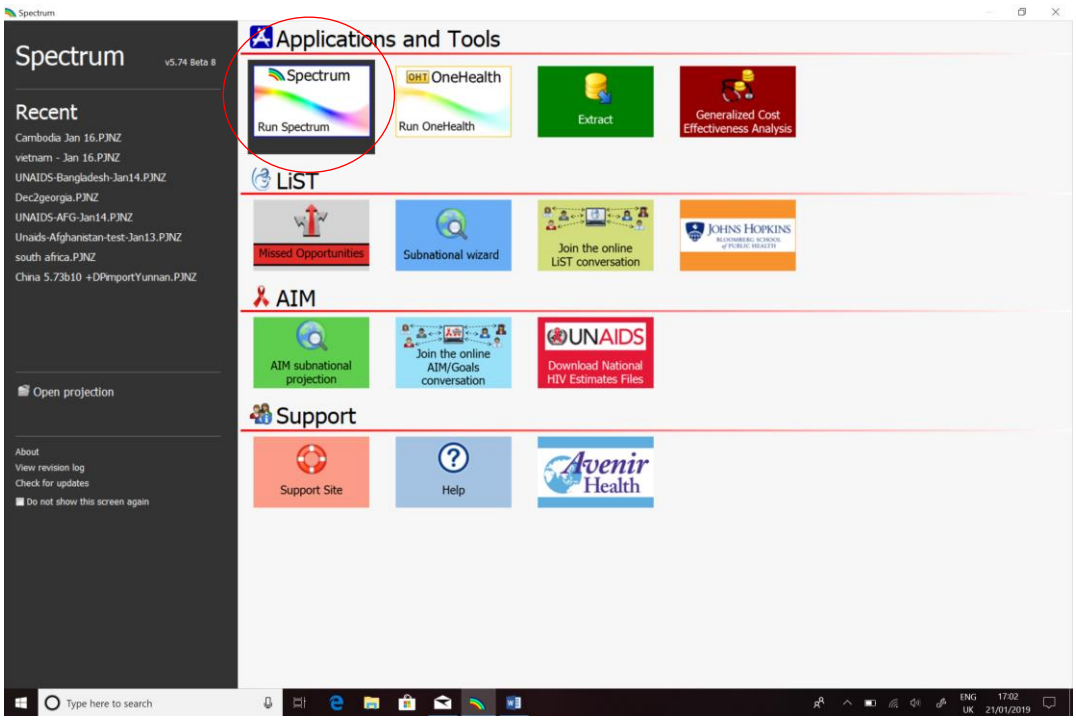
1. Download the latest version of the Spectrum software (e.g., Spectrum Beta 5.88 from http://spectrumbeta.futuresinstitute.org/.
2. Install Spectrum by double clicking on the file named **"specInstall.exe".** This will start the installation program. Follow the instructions on the screen to complete the installation. The program will, by default, install into C:\Program Files (x86)\Spectrum5.
3. For ease of use *pin* the Spectrum application icon to the taskbar, via Windows Explorer, folder C:/Program files x86/Spectrum5 – right-click on the 'Application' file.

3.2 Opening Spectrum

Open Spectrum by clicking on the Spectrum Icon (rainbow) in the Taskbar:

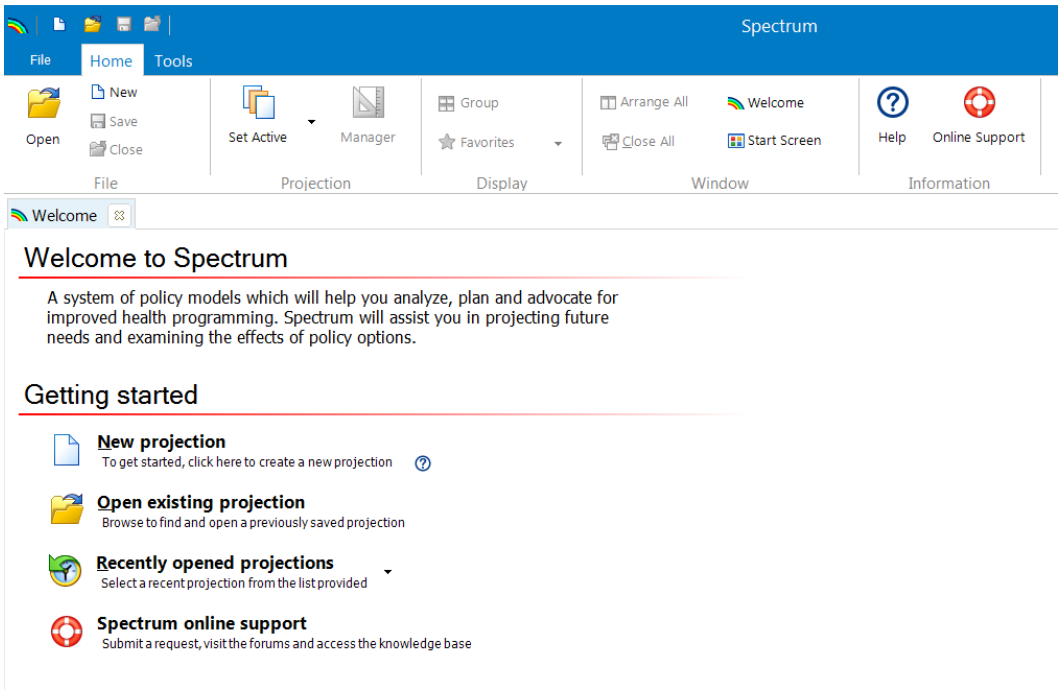
This will bring up the Opening screen.

To run Spectrum click on the Spectrum icon under "Applications and Tools'.



[1] If you have trouble installing Spectrum-STI, it may be that you do not have the appropriate permission to install programs on your computer and you will need to seek permission and/or help from your institution's IT administrator.

This will take you to the Welcome page.



3.3 Changing the language

The first time Spectrum is run after being installed the displays will be in English. You can change to another language, by selecting "File" in the blue task bar and then "Options" from the bottom task bar and then under "Appearance" chose "Language" from the Spectrum menu and select the language you want to use and click on the "Ok" button.

The STI module is available in English and Spanish. Other UN languages (e.g., French and Russian) have part of the windows translated, but the STI-specific parts are only available in English and Spanish. Note, if a language other than English, French, Spanish or Portuguese are selected you must have the proper fonts or version of Windows to display the language correctly.

3.4 Accessing Help and Online Support

To access Help and Online Support you need to be in the Home screen. If you are not on the home screen (i.e., you are in the STI Module) you will need to click on "Home".

Help: As of May 2020, online Help content is available for the STI module in English. Help is available for the other modules, e.g. DemProj and AIM for HIV, in several languages.

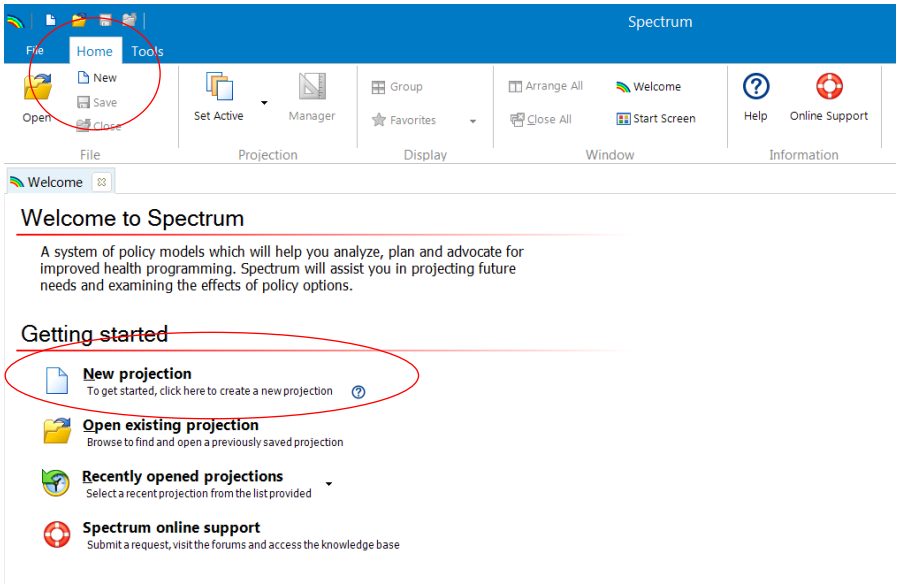
Online Support: Users can request online support from Avenir Health with the Spectrum-STI module, as for any Spectrum module – this is accessed from within the Spectrum application.

When switching to another language, Spectrum's 'Help' functionality gets translated via a download from the internet provided you have access to the internet when doing the language switch. If you do not have access to the internet the Help text will remain in English.

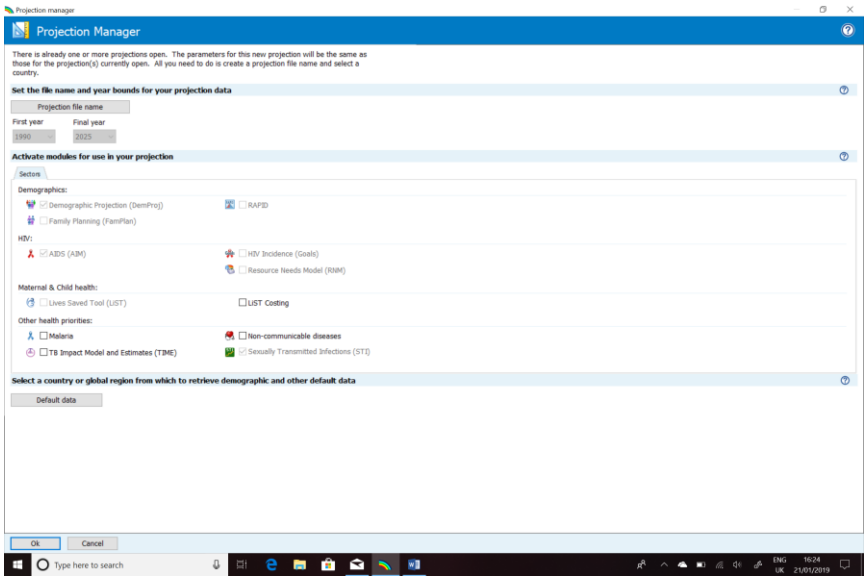
3.5 Creating a new STI estimation/ projection

You can create a new estimation or projection in two ways from the Welcome page.

1. Select "New projection" under Getting Started or
2. Select the Home tab and click on" New".



The Projection manager dialogue box will then open:



To generate a new estimation you need to:

1. Set the file name and year boundaries for the projection.

- Projection file name: This is the name and path for the data files associated with this projection. This name is also used to identify the projection across the Spectrum user interface. The file will take the form of *.PJNZ.
- Boundary Years: Set the first year of the projection to a year before the first known prevalence data point; or if you don't know that yet, to an early historic year. We recommend that you change these to 1990 and 2025. The last year should be set to 2025 – to allow short-term projections of the ongoing and near-future trend.

TIP:
Once a projection file has been created, it is not possible to add other Spectrum modules or to change the start or end year. If you have data from before 1990, or anticipate that these will come forward, then set the first boundary year of the projection accordingly. Outputs/Results can easily be adjusted to show fewer years (e.g. the years with actual country data).

2. Activate the relevant modules for the projection by clicking on the relevant check boxes. At a minimum you will need to activate 2 modules.

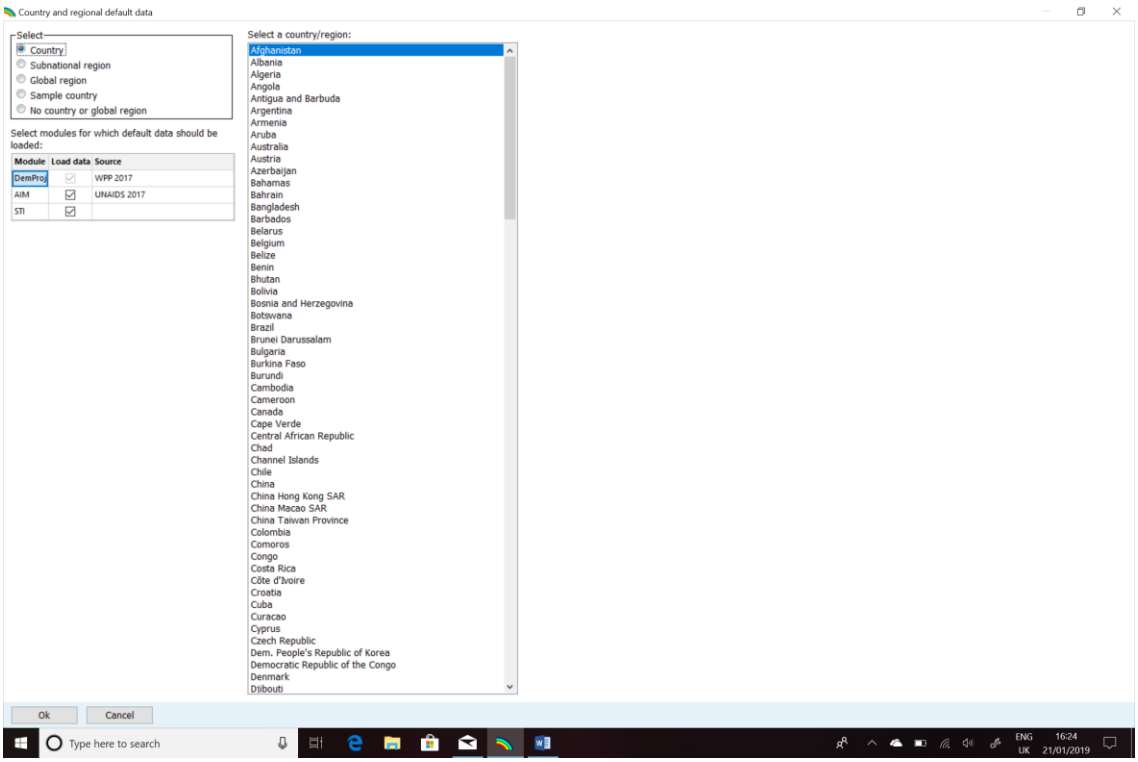
- Demographic Projection (DemProj) under Demographics.
- Sexually Transmitted Infections (STI) under Other health priorities.

In addition, we would recommend that you activate

- AIDS (AIM) under HIV. This module projects the impact of the HIV/ AIDS epidemic. It is optional but recommended especially in countries where HIV is affecting background mortality and age structure.

Do **NOT** activate any other modules.

3. Select a country or global region by clicking the "Default Data" button and selecting a country from the list on the screen and click on the "OK" button. This will take you back to the Projection Manager Screen.



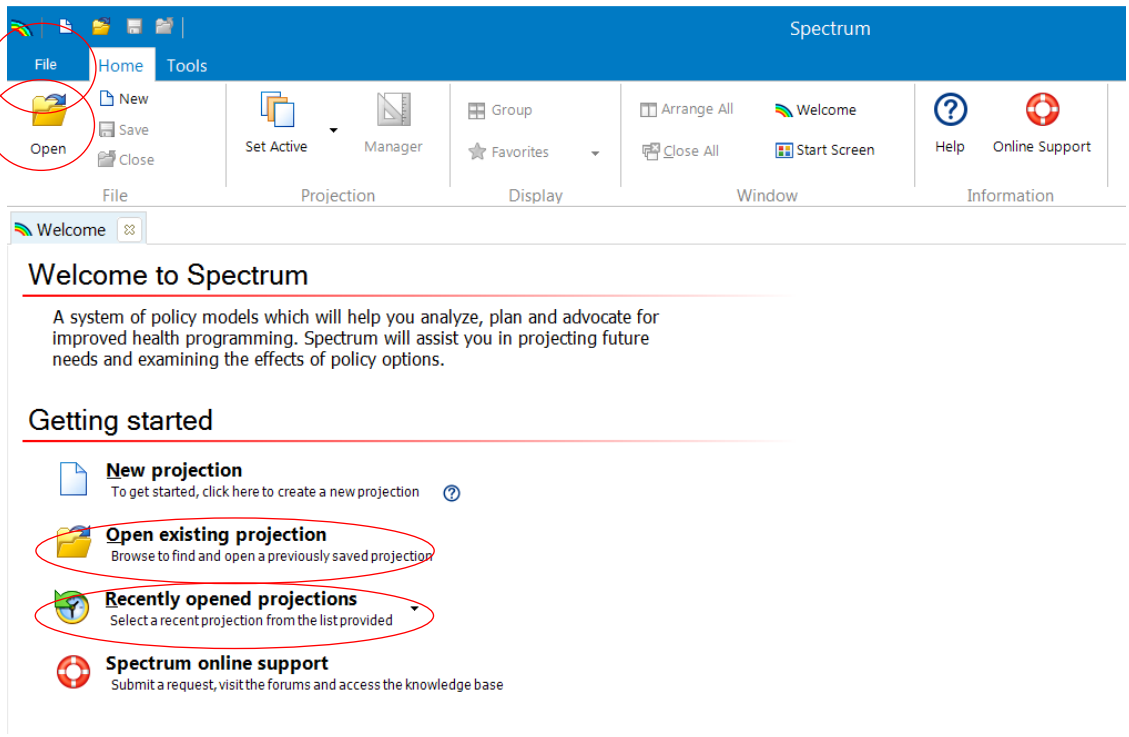
4. Click on the OK button at the bottom of the Projection Manager screen.

Spectrum-STI will now create the projection and load the default demographic, HIV and STI data available for the country. Note, an Internet connection is required for this process. It typically takes up to a minute or two for the data to load. Whilst this is happening the bottom-left corner provides time-changing updates (*Creating demography*, then *Creating AIM*… etc.,) indicating that Spectrum-STI is loading the data. When it is finished processing the program will return to the File management page and the bottom-left corner will say 'Ready'.

3.6 Opening an existing estimation/ projection

An existing projection can be opened in a number of ways.

1. Click on “Open existing projection” or on “Recently opened projections”.
2. Under the Home tab click on "Open". A window will open, so that you can navigate to the directory and find the desired projection.
3. Click on the “File” tab in the upper left corner of the Spectrum window. This will open a drop down menu. Either, click "Open projection" navigate to the directory and find the desired projection, or click on one of the projections listed under Recent projections on the right side of the drop down menu.

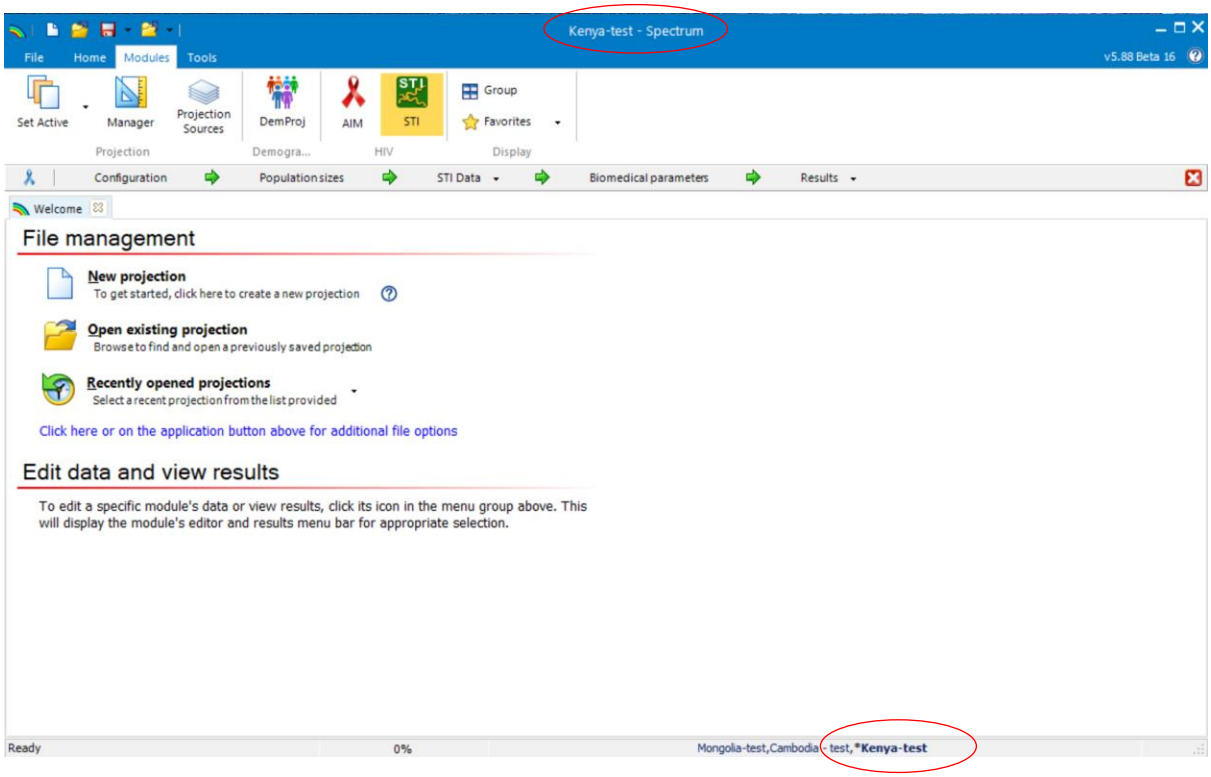


3.7 Setting the active estimation/ projection

You can determine which projection is active, by looking at the top-centre of the Spectrum window. The file name of the active projection will be displayed in the blue bar. In the example shown below, *'Cambodia.'* is the active projection. If only one projection is open, that is automatically the active projection. To see all projections that are open, look at the bottom-right of the Spectrum window. If more than one projection is open, all of the projection file names are displayed there. The active projection file is the one in bold with a star in front of the name.

TIPS:

- If a projection is “active” then any edits made to the STI file (Configuration, STI Data, Biomedical parameters or results) will affect this projection only. They will *not* affect any other projections that are open but are not active.
- To select another projection to be set as active, use the Set Active button in the menu bar or click on the appropriate file name in the status bar.

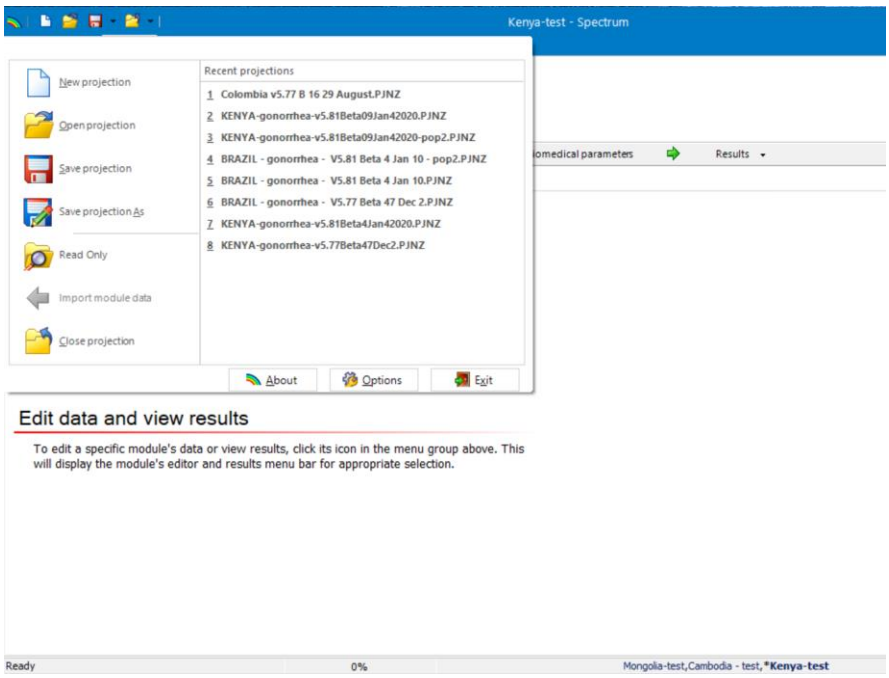


3.8 Saving an estimation/ projection

There are two easy ways to save a projection.

1. Click on the "Home" tab on the top menu and then click on "Save".
2. Click on the "File" tab in the upper left corner of the Spectrum window. This will open a drop down menu. Choose "Save projection" to keep the same projection name and location. You also have the option to click "Save projection As" in the drop down menu. Use this option if you want to change the projection name or the folder path where the projection file is saved.

If more than one projection is open, you will be given the option to save one or all of the projections.



3.9 Closing an estimation/ projection

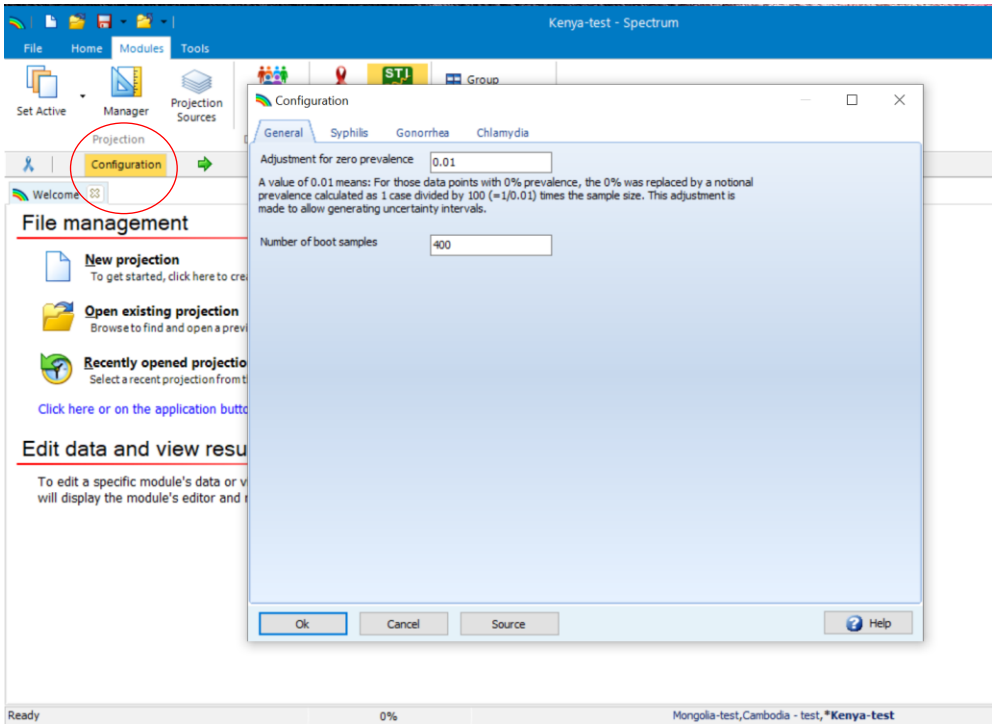
The easiest way to close an estimation/ projection is either:

- Click on “Home” in the top menu, then select "Close" and follow the instructions (see above). This gives you the option to choose one or all projections to close. You select the projection you want to close, by clicking the projection name or "All projections";
  or
- Click on “File” tab in the upper left corner of the Spectrum window. When the File tab is clicked, a drop down menu appears and choose "Close projection" and follow the instructions. This gives you the option to choose one or all projections to close. You select the projection you want to close by clicking the projection name or "All projections".

You can also close a projection – and the program – by clicking on the “X” box in the top upper right corner of the Spectrum window.

4. STI Module: Configuration parameters

Click on the Configuration menu item and the configuration data editor will appear. There are four Configuration menu sheets. All of the parameters in the four sheets can be changed. However, we recommend that you do not change any of these parameters. The default values reflect best-practice, global values as proposed by Avenir Health, WHO and specialist advisors. The source box provides a list of related references. If you do make any changes, you will need to click on the "Ok" box to save them.

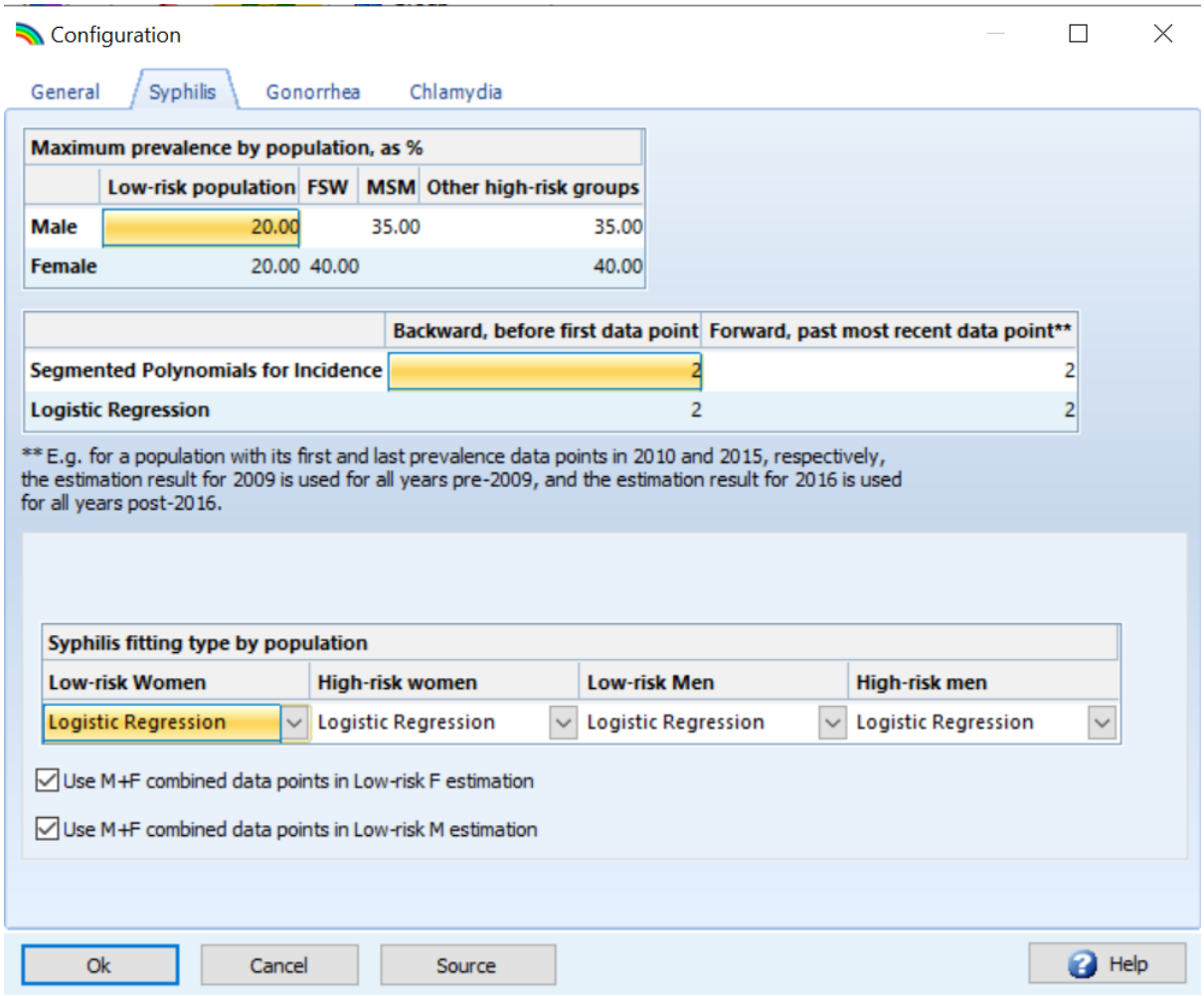


4.1 General

Adjustment for zero prevalence: If a study reported a prevalence of 0 this value is replaced by the "adjustment for zero prevalence" times the sample size to allow for logistic regression and generation of uncertainty intervals.

Number of bootstraps: The default value is set to 400. Simulations suggest that this number is typically enough to obtain a good approximation of both incidence and prevalence over time, using their respective medians. For the final estimates, (i.e. after the data sets have been finalized and weights assigned) the number of bootstraps can be increased to 1,000 to smooth the curves.

4.2 Syphilis

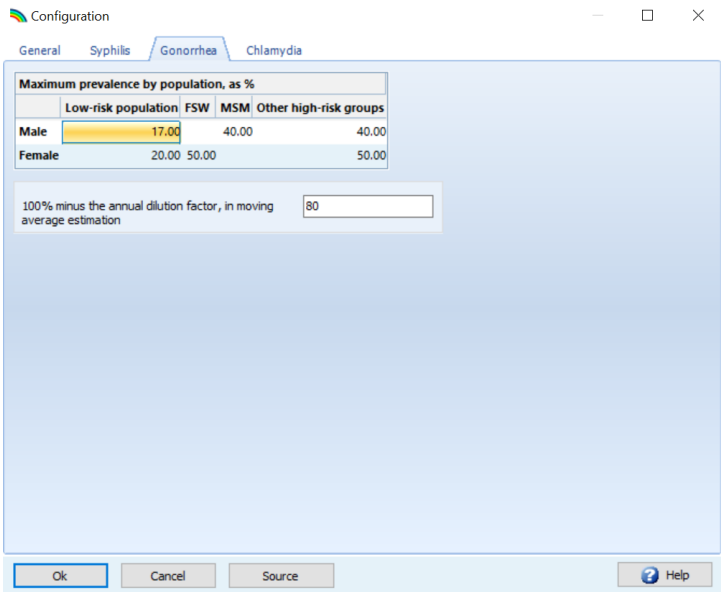


Maximum prevalence by population: The estimated point prevalence and the upper bound of the 95% CI for each population group are restricted. The default maximum values are based on empirical data from across low- and middle-income countries since 1990.

Extrapolation period: Users can specify how long before and after the first and last data point, respectively, Spectrum-STI extrapolates the time trend estimation. Before and after these dates, prevalence is assumed to be constant.

Syphilis Fitting type by population: For syphilis there are two options for curve fitting. The default model is logistic regression (see Section 2.1.1). Users can also specify if they want to include data points that are not disaggregated by sex in the low-risk female and/or the low-risk male estimations. If the boxes are checked then data from studies that present data for males and females combined (M + F) are included in the estimates.

4.3 Gonorrhea

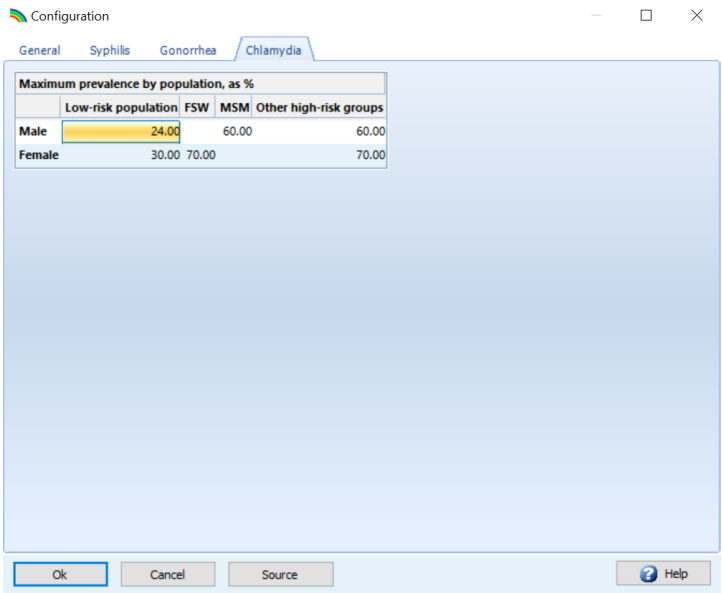


Maximum prevalence by population: The estimated point prevalence and the upper bound of the 95% CI for each population group are restricted. The default maximum values are based on empirical data from across low- and middle-income countries since 1990.

Dilution Factor: The default value of the dilution factor, used in moving average estimations, is 20%. The Configuration screen displays this as the complement i.e. 100% minus the dilution factor, i.e. 80%. The dilution factor for gonorrhea is also used for chlamydia.

Extrapolation period: For gonorrhea and chlamydia the estimate is fixed before and after the first and last data point, respectively.

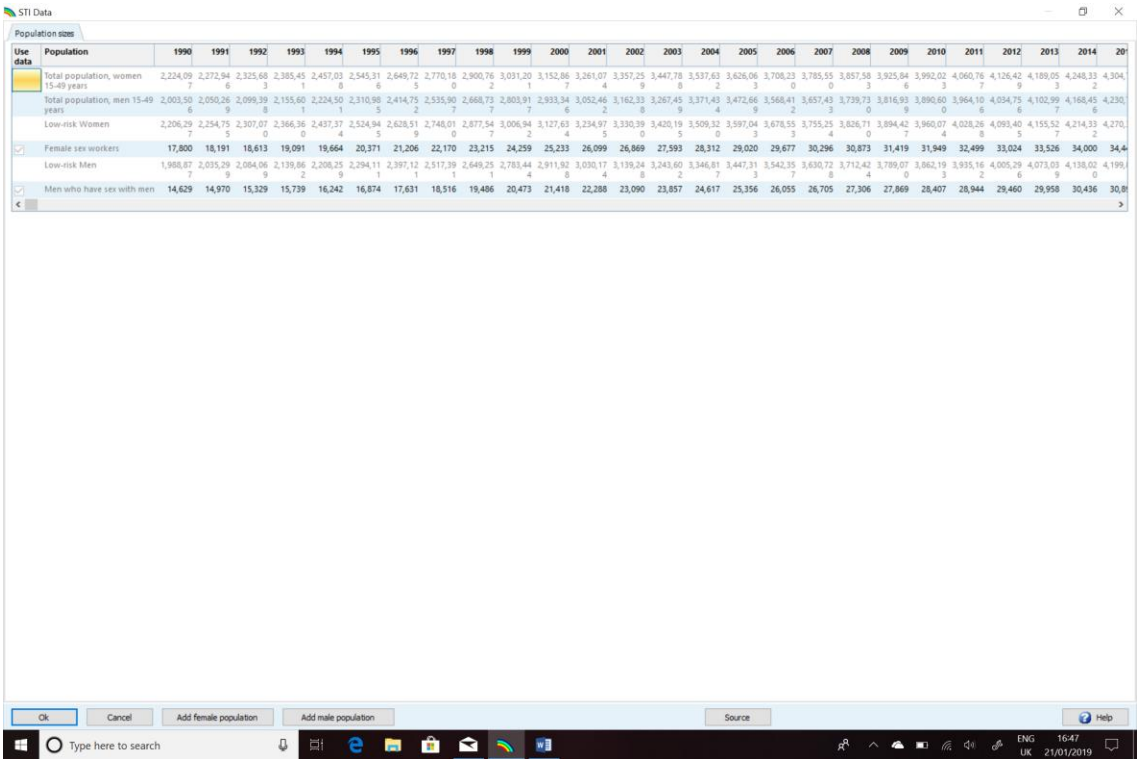
4.4 Chlamydia



Maximum prevalence by population: The estimated point prevalence and the upper bound of the 95% CI for each population group are restricted. The default maximum values are based on empirical data from across low- and middle-income countries since 1990.

5 STI Module: Population sizes

Spectrum-STI Version 5.75+ generates estimates for different population group and combines these to generate national estimates for adult men and women. The Spectrum-STI demographic database includes country estimates of adult population size and estimates of the size of the FSW and MSM populations.



5.1 Total population (15 to 49 years of age)

Spectrum-STI input data file includes national estimates and projections by year for each country of

- Total population, women 15-49 years
- Total population, men 15-49 years

These were drawn from the UN Population Division, World Population Prospects 2017 version [10].

5.2 Low-risk women and men

The number of low-risk adult women and men are generated by the program by subtracting the size of all the key groups (i.e., FSW, MSM) from the total population of women and men. The low-risk population estimates cannot be changed manually.

5.3 Female sex workers and Men who have sex with men

The Spectrum-STI input data file includes population size estimates for FSW and MSM based on:

1. Data reported by countries into the GAM system until May 2018. The GAM estimates are based on Integrated Bio-Behavioural Survey (IBBS) or other national Population Size Estimation studies.
2. For countries that did not report size estimates to GAM estimates were based on the estimates used in the country's HIV epidemic estimation when available, i.e. based on values used in their national (UNAIDS-supported) calibration to the Asian Epidemic Model or the Spectrum's AIM/EPP model.
3. When no national size estimates were available regional estimates were based on a literature review conducted by UNAIDS, GFATM and WHO (see Table 5.1, [11]).

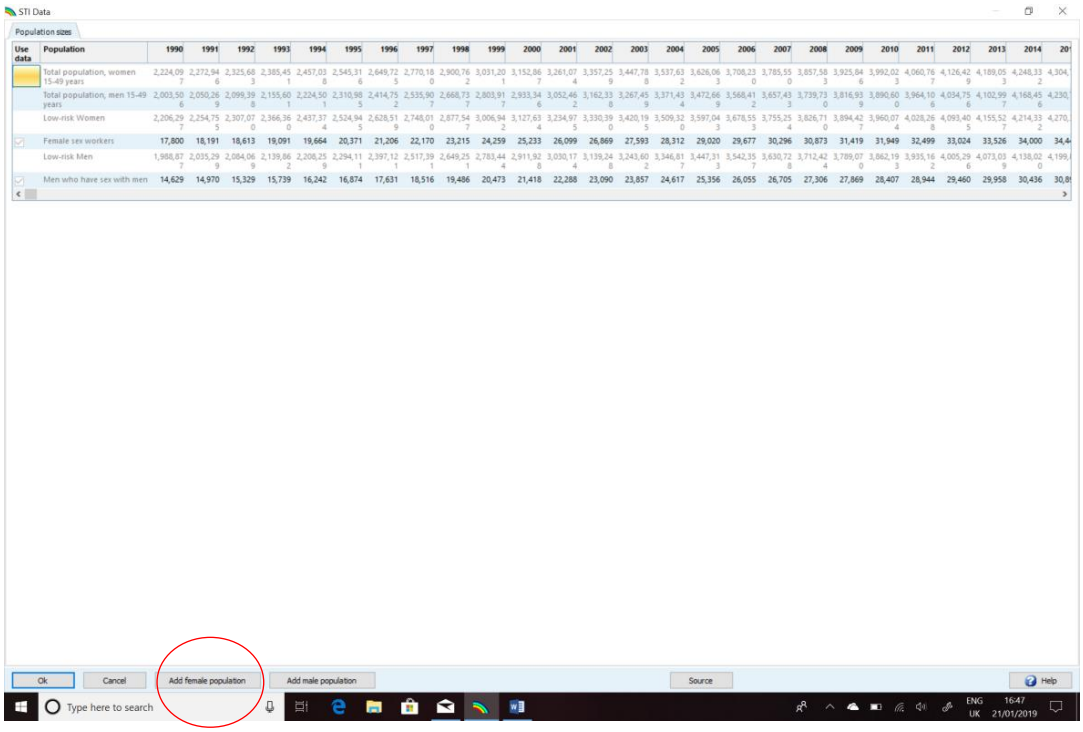
All of these population sizes can be modified. As size estimates for FSW and MSM are typically only available for a subset of years for any country, Spectrum-STI initially assumes that FSW and MSM are a fixed proportion of the total adult (15-49 years) population for those years without data. For example, if a country has 4,000 FSW in a population of 4 million women 15 to 49 years of age in 2012 then the FSW population is set at 1%, for all years throughout 2000-2025.

Table 5.1 Estimates of the population proportions of key populations in UNAIDS regions

% of 15-49 year-old women or men who are:	FSW	MSM
Asia and Pacific	0.35%	1.69%
Caribbean	0.49%	2.71%
Latin America	0.49%	1.49%
East and Southern Africa	0.58%	1.28%
East Europe and Central Asia	0.68%	1.39%
Western and Central Europe and North America	0.58%	1.28%
North Africa and Middle East	1.18%	0.90%
West and Central Africa	1.19%	0.72%

5.4 Other populations

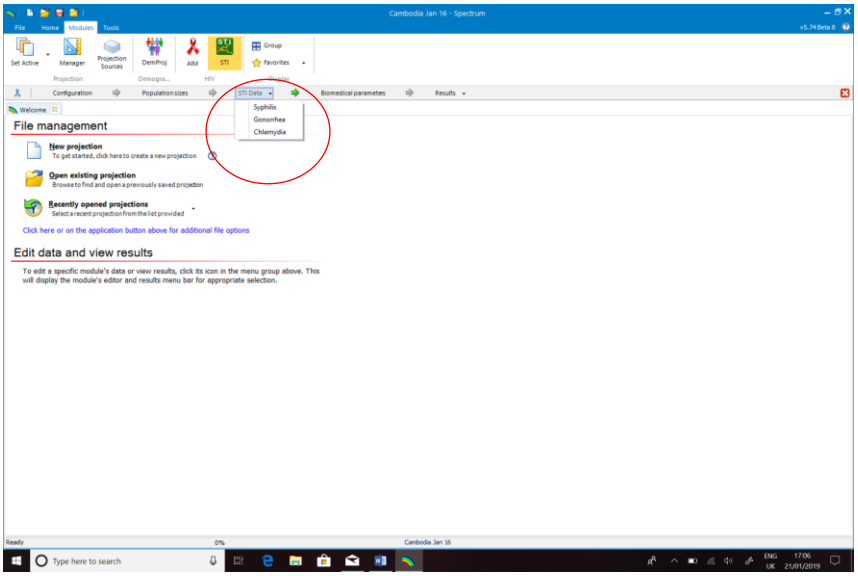
If prevalence data are available for other key population groups (e.g., PWID, or prisoners), then population size estimates will need to be entered for each group. This is done by using the "Add female population" or "Add male population" buttons at the bottom of the STI Data page.



6 STI Module: STI Data

6.1 STI prevalence data

There are three options under the STI Data menu: Syphilis; Gonorrhea; and Chlamydia. New projections are initially populated with data from the Spectrum-STI Global Prevalence Database (see Annex 1).



Most of the data elements, but not all, can be modified, deleted, or added to. The following columns cannot be modified, as they are calculated by the program based on the values (default or user entered) in the other columns.

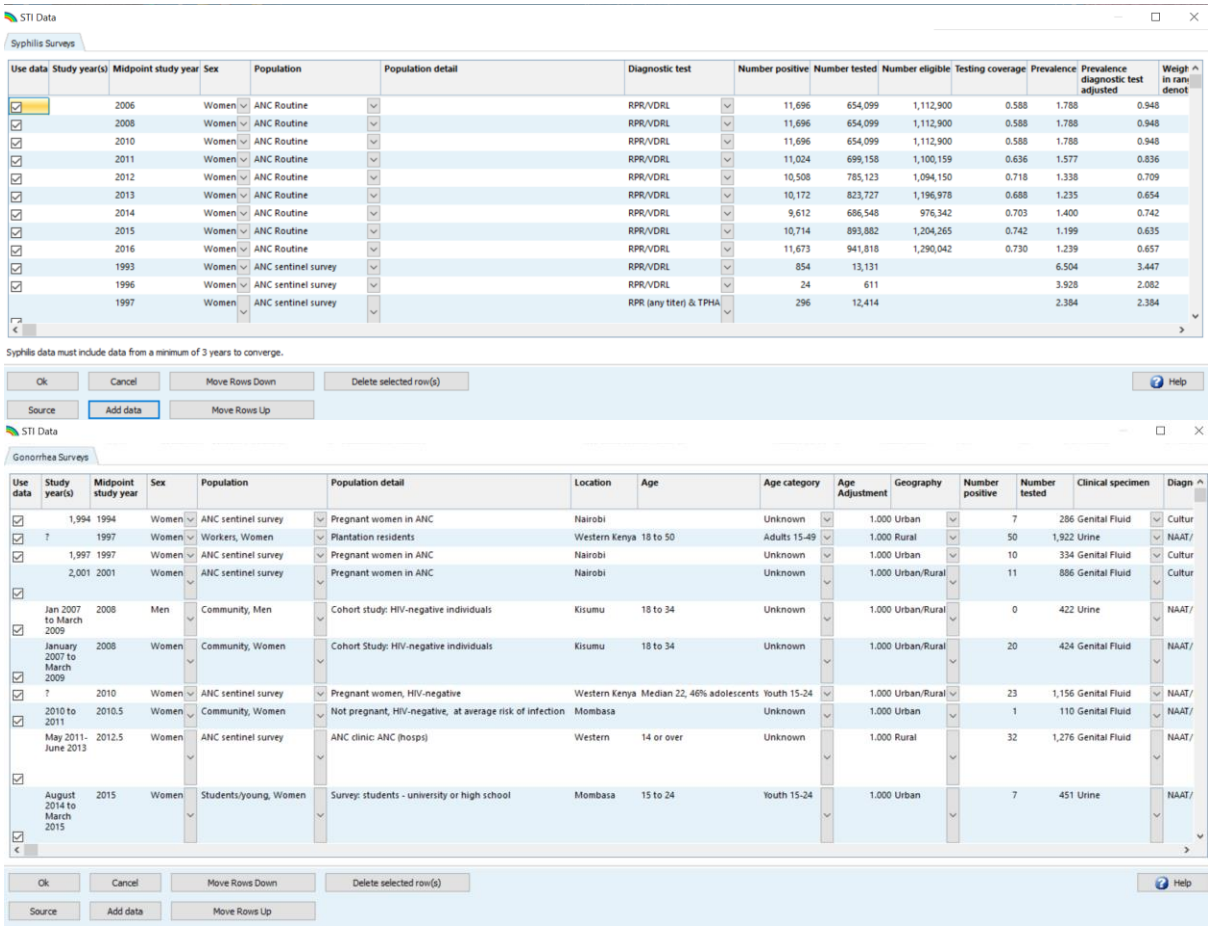
Syphilis:

- prevalence;
- prevalence, diagnostic test adjusted.

Gonorrhea & Chlamydia:

- prevalence;
- prevalence, diagnostic test adjusted
- urban prevalence test adjusted
- rural prevalence test adjusted
- national prevalence test and geography adjusted

Samples of the data entry tables are shown below for syphilis and gonorrhea. The chlamydia table has the same format as gonorrhea.



Tip:

- Only data that have a tick in the column "Use data", on the left, will be included in fitting of the model and will be shown in Results prevalence graphs.

To modify data: Select the cell you want to change, make the relevant change and press enter. Then to save the changes use the button "OK" at the bottom of the screen.

To delete prevalence data:

- Temporary: If you don't want to use a data row for a particular estimation, but may want to re-use it later again, uncheck the "Use data" button (first column).
- Permanent: If you want to permanently delete a data row, then use the "delete selected row(s)" button in at the bottom of the screen.

To add prevalence data that are not in the Spectrum-STI global database: Click on "Add data". A new line will be introduced at the bottom of the country data file, and the relevant details can be entered.

Prevalence data are entered as the number of people positive and the number tested, not as a percentage. If a study does not provide information on the number of people positive or tested, it is necessary to infer or estimate these based on the reported prevalence.

The column "Weight for Spectrum Fitting in range 0 to 100" is the weight assigned to each study in the statistical trend fitting. See Section 6.3 for more information about these weights.

Box: Reviewing and updating Spectrum-STI prevalence tables in Excel

Prevalence data tables can be imported into and out of Excel for reviewing and updating.

A. Copying a Spectrum-STI prevalence data table into Excel

- Put the cursor in the middle of the data table, right-click and then select "*Copy all".*
- Switch to Excel, select cell A1 and paste the data.

B. Modifying data in Excel

- Update or correct the relevant cells by typing in new values
  (Note: Do not edit the columns that are calculated by Spectrum-STI – these will be recalculated, and overwritten, by Spectrum-STI when the updated data are copied into Spectrum-STI).

C. Copying data from Excel into a Spectrum-STI prevalence data table

- Check that all of the cells in Excel are formatted as "*General*" (and not: Number, or Custom, etc.).
- Copy the cells starting from the column 'Study year(s)'. Do not try to copy the whole row.
- Switch to Spectrum-STI.
- If the data being input are modifications to an existing data row
  - Select the 'Study year(s)' column of the row being changed and paste the copied data.
- If the data are new:
  - Select 'Add data' from the Spectrum-STI data table
  - Paste the saved data into the newly entered rows at the bottom, starting with the 'Study year(s)'
  - Manually select, from the respective drop-down menus, for columns like Use data, sex, population, diagnostic test.
- Confirm your overall changes to the data editor by clicking 'OK'.
- Save the updated projection file, under File, 'Save' or 'Save as'.

6.2 Standardizing prevalence data across studies

The observed prevalence values are converted into true prevalence estimates by adjusting for the sensitivity and specificity of the diagnostic test, the age of the study population (for chlamydia only), and the geographic location of the study population.

6.2.1 Syphilis

The methods for standardizing data from prevalence studies are based on the methods and parameter values used in country Spectrum-STI estimations done over 2017-2018 [3-5]. A standardized prevalence data point was obtained by adjusting the reported prevalence to reflect the diagnostic test used.

Laboratory test adjustor:
The default laboratory test adjustors for syphilis are reported in Section 7.3. These adjustment factors are based on two global meta-analyses of prevalence ratios [12, 13] and consultations with international STI experts. They are assumed to remain constant over time.

6.2.2 Gonorrhea and chlamydia

The methods for standardizing data from prevalence studies were based on the methods and parameter values used to generate the WHO 2012 and 2016 estimates [8,9]. A standardized prevalence data point was obtained by adjusting the reported prevalence to reflect the sensitivity and specificity of the diagnostic test used, the age of the study population, and the geographic location of the study population using the following formulas:

$$SP = \frac{(RP + Specificity - 1)}{(Sensitivity + Specificity - 1)} \times \text{age adjustor} \times \text{geography adjustor}$$

where SP is the standardized prevalence, RP is the reported prevalence, specificity is the reported specificity of the lab test and sensitivity is the reported sensitivity of the lab test. The age and geography adjustors are described below.

Laboratory test adjustors: The performance characteristics of each laboratory test type are recorded in Section 7.3.

Age adjustor: Prevalence data for chlamydia in women and men were systematically adjusted for age (see Table 6.2). No adjustments were made for gonorrhea in women or men. The default values were assumed to remain constant over time

Table 6.2 Age adjustors

Sex	Age Group (years)	Value	Lower-bound	Upper-bound	Reference
Chlamydia					
Women	15-24	0.59	0.44	0.74	[5]
	25-49	1.39	1.04	1.74	[5]
	15-49	1.0	1.0	1.0	Reference category
	Unknown	1.0	1.0	1.0	Reference category
Men	15-24	0.8	0.60	1.00	Avenir Health (average between no adjustment in WHO global estimates [8,9], and strong adjustment for South Africa [5]
	25-49	1.2	1.00	1.50	
	15-49	1.0	1.0	1.0	Reference category
	Unknown	1.0	1.0	1.0	Reference category
Gonorrhea					
Women	All age groups	1.0	0.75	1.25	WHO 2012 global & regional estimates [8,9]
Men	All age groups	1.0	0.75	1.25	WHO 2012 global & regional estimates [8,9]

Geography adjustor: The geography adjustors are recorded in Table 6.3. The adjustors reflect both the proportion of the population living in urban areas and the ratio of the prevalence of infection in rural areas to urban areas (assumed to be 0.9).

Data from studies where information was available for both rural and urban areas suggest that the prevalence of non-ulcerative STIs is generally higher in urban areas than in rural areas. The number of studies with both urban and rural data for syphilis, chlamydia or gonorrhea, however, was small.

Spectrum-STI uses the urban-to-rural prevalence ratios to calculate for each study an urban prevalence, a rural prevalence and a corresponding 'urban + rural' prevalence. To calculate the latter, the country and group's urban and rural prevalences are aggregated, weighted by the country's national urban and rural population sizes, for the study year, using UN Population Division population estimates contained in the Spectrum DemProj module. No adjustment was made for studies that involved samples from different types of sites or where it was not clearly stated.

Table 6.3 Geography adjustors

Type of population	Adjustor
National	1
Urban	0.947
Rural	1.052
Unknown	1

Handling studies where the standardized prevalence was negative: When a negative number is generated for the standardized prevalence Spectrum-STI resets the standardized prevalence at 1 case divided by 100 times the sample size.

6.3 Weighting data from different studies

Each study is assigned a weight, reflecting its representativeness of the population group being estimated. In the Spectrum-STI global database, these weights were generated by the Spectrum-STI global team. These values, which appear as the default or starting point when a New projection is created in Spectrum-STI, need to be reviewed by users and adjusted to reflect representativeness and quality according to their expert opinion.

The default weights assigned to the **low-risk population data** in the Spectrum-STI global database were generated as follows:

Syphilis:

- Routine ANC screening data: weight is based on the national coverage of syphilis screening.
- ANC surveys: weight reflects the number of sites sampled or type of survey.
- Surveys in low-risk women (excluding ANC surveys): weight reflects the type of survey
- Surveys in low-risk men: weight reflects the type of survey
- Blood donor data from women: generally assigned a weight of 0.1
- Blood donor data from men: generally assigned a weight of 0.1
- Blood donor data and surveys that did not differentiate between men and women: assigned a weight of 0.

Gonorrhea and Chlamydia:

- Most studies were set at 100%. Some small studies, or studies of a specific age sub-group were assigned a lower weight.

For **FSWs** and **MSM** most studies were set at 100% for all three infections. In some countries when there were data from multiple years and where the number of sites tested varied by year, studies were weighted to reflect this.

7 STI Module: Biomedical parameters

There are three files under the Biomedical parameters menu: Population prevalence ratios; Duration of infection; Diagnostic test performance.

7.1 Population prevalence ratios

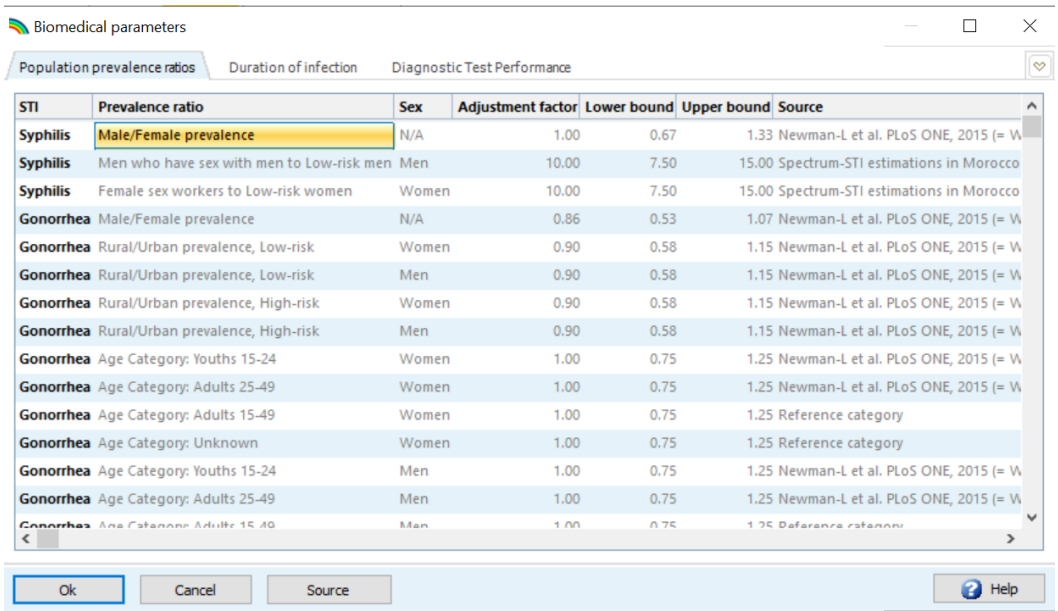
The population parameters are used to: (1) standardize and adjust the observed data from prevalence surveys before making a prevalence estimation within a group; (2) generate an estimate for a population group that has no data.

There are four types of population parameters.

1. Male-to-female prevalence ratio
2. Geographic adjustor or Rural / urban prevalence ratio
3. Age adjustor
4. Ratio of prevalence between high-risk groups and low-risk group

The values of the population parameters are based on expert opinion, consensus and agreed assumptions used in past global and regional STI estimates [8,9], and insights from recent Spectrum-STI country applications. For each population parameter there is a default/best value, as well as a Lower-bound and Upper-bound; the bounds are used to determine the uncertainty in a prevalence estimate that uses the parameter concerned.

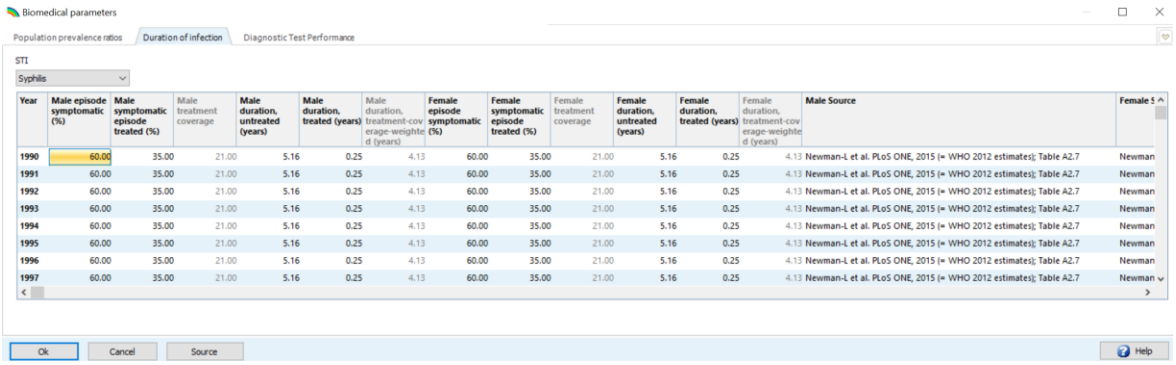
The population pattern parameters are all fixed and cannot be changed without going into the Spectrum Developer's mode (for advanced users). To change one or more of these parameters, please contact Eline Korenromp (EKorenromp@avenirhealth.org).



7.2 Duration of infection

The duration of an infection, or STI episode, is defined as the mean length of time that a person carries an infection. This in turn depends on a number of factors including the average duration of infection in the absence of treatment, the probability that a person with symptoms gets treated and how long, on average, it takes for a symptomatic person to get treated. In addition, people who are asymptomatic may receive treatment because of screening programmes, or partner notification, or inadvertent correct therapy while being treated for another health problem. The methods and parameters used to estimate the mean duration of infection are based on the methods used in the WHO 2012 and 2016 global and regional estimates [8,9].

All of the parameters that determine the duration of infection (Duration of untreated infection, duration of treated infection, proportion of episodes that is symptomatic and proportion of symptomatic episodes that are treated) can be changed for both men and women and over time to reflect, for example, historic time trends in health care seeking and/or treatment access. The final estimates for duration for each year for women and men are found in the circled columns, in grey font. These cannot be modified (and hence are in grey font); they are calculated from the preceding (left-hand) columns.



7.2.1 Chlamydia and Gonorrhea

For chlamydia and gonorrhea, the duration of infection (D) for a person of sex (k) in treatment area (r) is estimated using the following equation:

$$D(k,r) = S(k,r) \times [V^S(k,r) \times T^S(k,r) + (1 - V^S(k,r)) \times U^S(k,r)] + (1 - S(k,r)) \times [V^A(k,r) \times T^A(k,r) + (1 - V^A(k,r)) \times U^A(k,r)]$$

where:

$S(k,r)$ is the probability that an infected person is symptomatic (S).

$V^S(k,r)$ and $V^A(k,r)$ are the probabilities that infected people who are *symptomatic* (*S*) and *asymptomatic* (*A*) were treated, respectively.

$T^S(k,r)$ and $U^S(k,r)$ are the average durations of infections for symptomatic (*S*) people who are treated (*T*) and not treated (*U*), respectively.

$T^A(k,r)$ and $U^A(k,r)$ are the average durations of infections for asymptomatic (A) people who aree treated and not treated, respectively.

The estimates are based on the assumptions in Tables 7.1, 7.2 and 7.3.

Table 7.1 Probability of men and women developing symptoms

Infection	Men	Women
Chlamydia	0.54	0.17
Gonorrhea	0.64	0.34

Table 7.2 Average duration of infection

Infection	Asymptomatic and not treated		Symptomatic and treated	
	Men	Women	Men	Women
Chlamydia	15 months	15 months	4 weeks	8 weeks
Gonorrhea	5 months	6 months	2 weeks	4 weeks

Table 7.3 Probability that a symptomatic person is adequately treated, by treatment access group[†]

Treatment access group	Probability in men	Probability in women
A – good access	0.80	0.75
B – moderate access	0.65	0.50
C – poor access	0.35	0.225

[†]The probability that an asymptomatic person is treated is assumed to be 10% of the probability that a symptomatic person is treated.

For treatment coverage the default values are based on the values used in the WHO global and regional estimates [8, 9]. When generating the WHO countries were placed into one of 10 regions (see Table 7.4) and these regions were assigned into one of three treatment groups.

Table 7.4 Allocation of regions into one of three treatment groups according to probability of treatment

Treatment group	Regions
A	• Australasia and High Income Asia Pacific • High income North America • Western Europe
B	• Andean, Central, Southern, Tropical Latin America & Caribbean • North Africa & Middle East • Oceania • East Asia • Central & Eastern Europe & Central Asia
C	• Central, Eastern & Western Sub-Saharan Africa • Southern Sub-Saharan Africa • South Asia & South East Asia

7.2.2 Syphilis

A similar approach is followed for syphilis, after adjusting for the different stages of infection (primary, secondary, and latent). The probability of adequate treatment is assumed to be the same for men and women. It is also assumed that people with primary and secondary syphilis who do not develop symptoms are not treated.

The estimates are based on the assumptions in the Tables 7.5, 7.6 and 7.7. For all of the parameters it is assumed that there was no difference between men and women.

Table 7.5 Probability of developing symptoms by stage of infection.

% of episodes symptomatic	Primary stage	40%
	Secondary stage	60%

Table 7.6 Probability that a person is adequately treated for syphilis according to treatment group

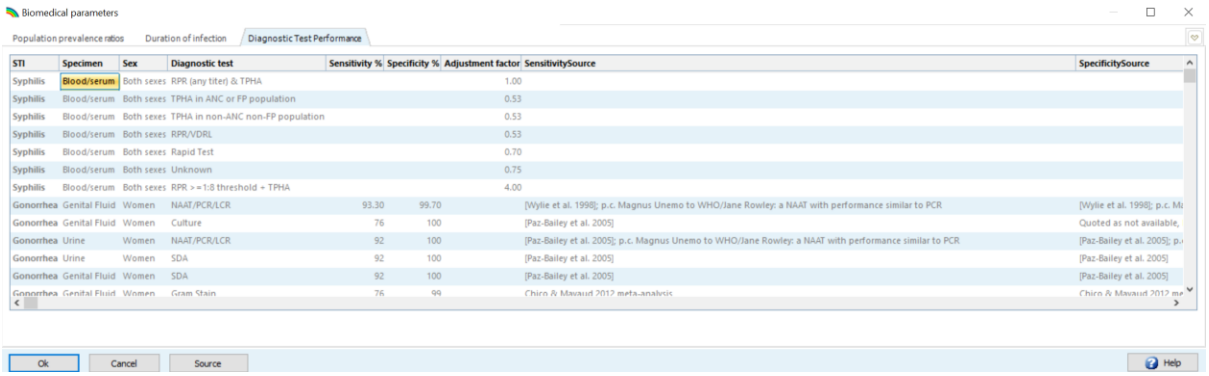
Treatment group	Symptomatic primary and secondary stages	Latent stages
A– good access	0.85	0.95
B– moderate access	0.60	0.85
C– poor access	0.35	0.75

Table 7.7 Average duration of infection in a person with syphilis, depending on stage at which they are treated

Stage of infection	time
Primary	1 month
Secondary	3 months
Latent	3 years
Tertiary	15 years

7.3 Diagnostic test performance

The defaults values of the performance characteristics of each laboratory test type are estimates based on reviews of the literature done for the WHO regional and global estimates and updated and expanded by Avenir Health for use in Spectrum-STI. These values are fixed and cannot be adjusted without going into the Spectrum Developer's mode. To change one or more of these parameters please contact Eline Korenromp (EKorenromp@avenirhealth.org).



8 STI Module: Results

Select the "Results" menu item and choose the infection you are interested in. For each infection there are four different outputs available: Prevalence; Incidence rate; Number of incident cases; and Summary. Results take the same format for all three infections.

Box: Exporting Spectrum-STI results into Excel

All of the Spectrum-STI result tables and line graphs can be exported into Excel, and then turned into additional charts using the various Excel features (see https://www.excel-easy.com/data-analysis/charts.html).
To export the results:

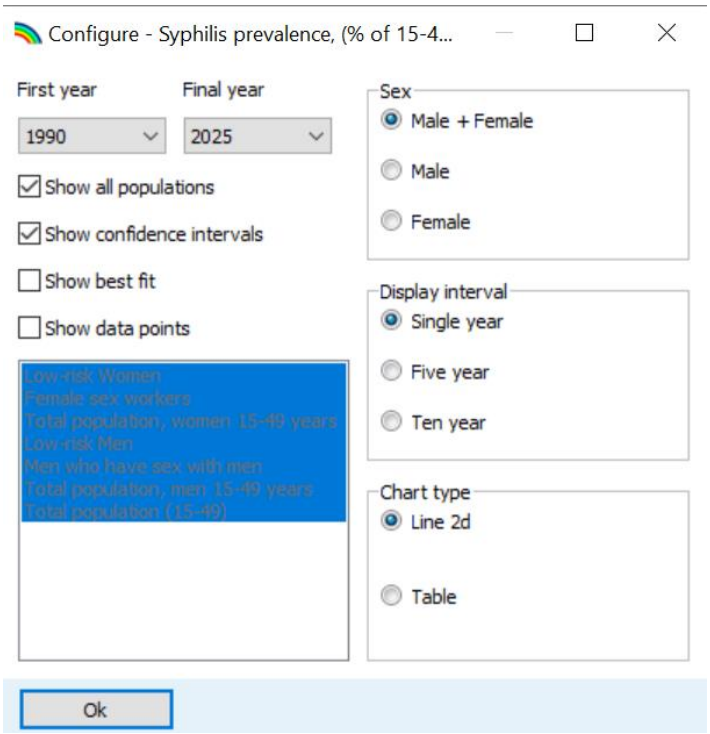
1. Put the mouse somewhere in the middle of one of the results tables or graphs and then right-click: *Copy all* if a table or right click: *Copy chart (Image)* to copy the graph or *Copy chart (data)* to copy the date in the figure.
2. Paste the Spectrum output table into Excel.

8.1 Prevalence

Users need to specify the desired configuration of the estimation output:

1. Sex: whether they want to view the results for males and females combined, males only or females only.
2. Display interval: single years or every five or ten years
3. Chart type: line graph or table
4. Time period: First and Final year of results shown.

And the results they would like to see. Users can select to view for one or more sub-populations in females, males, or females + males combined: the Spectrum-STI trend estimate, the corresponding 95% confidence interval, the statistical line of best fit and/ or the adjusted prevalence data points.

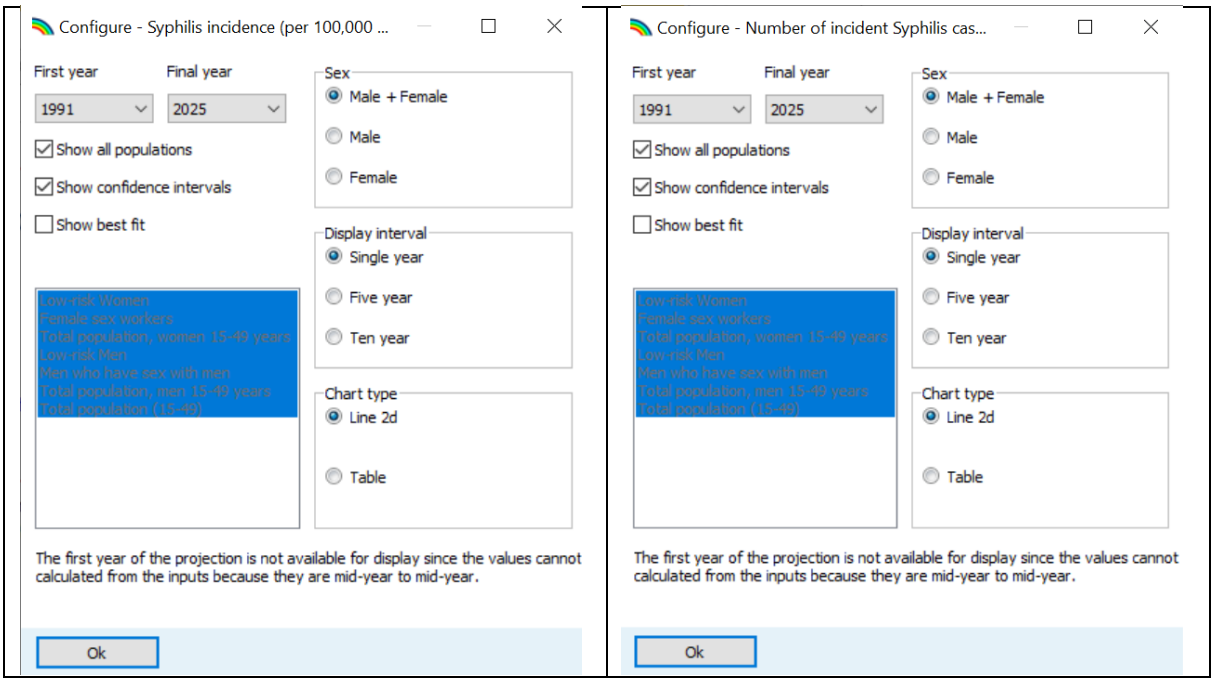


Tips:

- Graphs tend to get overcrowded if "Show confidence intervals" and "Show data points" are both selected. We would recommend selecting one *or* the other.
- The Median estimate is the most appropriate estimate to use when presenting Spectrum-STI results. It is the median within the estimated 95% confidence intervals.
- For populations groups estimated using one of the global default prevalence ratio (male to female *or* high-risk to low-risk), the estimation results do not necessarily reproduce the inputted/assumed global ratio. This is because Spectrum-STI samples and averages from the 95% CI for each parameter.

8.2 Incidence rate and incident cases

The incidence rate and number of incident cases estimates take the same form as the prevalence estimates. The only difference is that the incidence graphs to do not have the option of showing data points. As with the prevalence graphs, users need to select (1) First and Last year, (2) sex, (3) display interval, (4) chart type, and what they want to see in the chart (incidence for all populations, confidence intervals, best fit).



8.3 Summary

The summary table provides an overview of the results, for one particular year, broken down by population group for males and females, combined and separately. Besides the outputs also shown in prevalence and incidence graphs, this includes the share of each group in overall national prevalence and incidence, and the population size of each group.

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Annex 1: Spectrum-STI Global Prevalence Database

The Spectrum-STI global database has been populated with prevalence data from 1980 to 2018. The data included in the database come from studies using an internationally recognised diagnostic test with adequate performance characteristics on urine, urethral, serum or cervico-vaginal specimens conducted among:

- Populations considered representative of the general adult population. This includes: pregnant women, women at delivery, women attending family planning clinics, adults in household surveys, and military recruits;
- Men who have sex with men (MSM);
- Commercial female sex workers (FSW);
- In addition, for syphilis for countries with very few data points from populations considered representative of the general adult population routine national blood donor screening were included [1].

The data in the database come from a variety of sources including:

- WHO STI database of general population prevalence surveys in low-risk adult men and/or women compiled for the 2005, 2008, 2012 and 2016 global and regional STI estimates [2-4];
- Syphilis prevalence data reported to the Global AIDS Monitoring (GAM) system [5]. Prevalence data for ANC women are based on the GAM data set as of December 2017 and include data from sentinel surveys in pregnant women attending ANC care and routine programmatic screening in ANC. The data for MSM and FSW are based on the GAM data set as of August 2018 and are from surveys.
- WHO global status report on blood safety and availability which includes national blood donor screening results for syphilis [6];
- Institute of Health Metrics and Evaluation (IHME) syphilis prevalence database compiled for the 2015 Global Burden of Disease study [7];
- Systematic reviews of
    - STI prevalence among pregnant women in antenatal care in sub-Saharan Africa [8]
    - Curable STIs in pregnant women of low- and middle-income countries [Williams, in prep]
    - Gonorrhea prevalence in the Middle East and North Africa [Smolak, in prep]
    - Chlamydia prevalence in the Middle East and North Africa [9]
- Data compiled by the 10 countries that have used Spectrum-STI to generate national estimates as of September 2018 (Zimbabwe [10], Morocco [11, 12], Mongolia [13, 14], Colombia [15], Georgia [16], South Africa [17], China [18], Papua New Guinea, Fiji, Samoa and The Federal States of Micronesia [19]);
- Other data brought to the attention of the Avenir Health team (e.g., national HIV/syphilis household surveys conducted in 2016-2018 in Zimbabwe, Uganda and other African countries with support of the USA CDC and PEPFAR [20]).

The codes used in the database for the different population groups are summarized in Table A1.1

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Table A1.1 Population groups and codes for prevalence data

Population type	Pop. code
ANC Survey	1
ANC Routine screening	2
Survey LowRisk Women	3
Survey LowRisk Men	4
Survey LowRisk Men+Women	5
BloodDonor Screening Women	6
BloodDonor Screening Men	7
BloodDonor Screening Men + Women	8
FSW	9
PWID-Female	10
MSM	11
PWID-Male	12
Clinic attendees, Women	20
Community, Women	21
Community, sexually active, Women	22
Community, sexually active, HIV-negative, Women	23
Military, Women	24
Mixed groups / Unknown, Women	25
Ob/Gyn clinic attendees	26
Pregnant women, community (outside ANC)	27
Students/young, Women	28
Students/young, sexually active women	29
Workers, Women	30
Prisoners, Women	31
Wives of PWID	32
Clinic attendees, Men	40
Community, Men	41
Community, sexually active, Men	42
Community, sexually active, HIV-negative, Men	43
Military, Men	44
Mixed groups / Unknown, Men	45
Students/young, Men	46
Students/young, sexually active, Men	47
Workers, Men	48
Prisoners, Men	49
OtherHighRisk-Women1	
OtherHighRisk-Women2	
OtherHighRisk-Men1	
OtherHighRisk-Men2	

Annex 2: Technical Annex

A2.1 Prevalence: Statistical Methods

A2.1.1 Syphilis: Logistic regression

The prevalence (p_t) was assumed to vary as a function of time following the formula:

$$p_t = \frac{exp\ (\alpha + \beta t)}{1 + exp(\alpha + \beta t)}$$

The parameters α and β were estimated by minimizing the function:

$$L = \sum_j w_j \left(\tilde{p}_j \log p_{t_j} + \left(1 - \tilde{p}_j\right) \log\left(1 - p_{t_j}\right)\right) \qquad \text{Eq 1}$$

where $\tilde{p}_j$ is the observed prevalence at time t_j and w_j is the weight (typically the sample size) associated with the corresponding survey *j*.

A2.1.2 Syphilis: Polynomial segmented regression for incidence

This model is based on the relationship between incidence (i), prevalence and recovery rate (r):

$$\frac{dp}{dt} = i(1 - p) - rp \qquad \text{Eq 2}$$

and assumes that the incidence is a second order polynomial by intervals, i.e. there exists $k \geq 1$, $t_0 \ldots t_k$, $a_0, \ldots, a_k, b, \ldots, b_k$, and $c_0, \ldots, c_k$ such that $i(t) = a_l + b_l(t - t_l) + c_l(t - t_l)^2 \geq 0$ for all t in (t_l, t_{l+1}).

Parameters were estimated using Eq1 in which p_t is replaced with the solution of Eq2.

A2.1.3 Gonorrhea and Chlamydia: Moving average

Time trends in prevalence were fitted using the formula:

$$\hat{p}_t = \frac{\hat{e}_t}{\hat{E}_t} \qquad \text{Eq 3}$$

Where:

- $\hat{e}_t = \sum_{s=t_0}^{t_{max}} \sum_{j=1}^{J_S} \tilde{p}_{sj}\, w_{sj}\, v_{sj}$, $\hat{E}_t = \sum_{s=t_0}^{t_{max}} \sum_{j=1}^{J_S} w_{sj}\, v_{sj}$
  t_0 is the earliest year with available prevalence, t_{max} is the year with the latest prevalence survey, J_S is the number of surveys conducted during year s, $\tilde{p}_{sj}$ is the standardized prevalence, v_{sj} are the weights of the respective data points; and w_{sj} are temporal weights given by: $w_{sj} = \exp\left(|t - s| \log(d)\right)$.
- 'd' is an annual dilution factor that weighs the contribution of each data point to the estimation for other years than the study year (years before and after the study year, throughout the period from first to last data point). The dilution factor is assumed to be a fixed proportion for each additional year away from the estimated year (default value of the dilution factor is 20%).

A2.1.4 Uncertainty intervals

The 95% uncertainty or confidence intervals for each population group for all three infections account for (a) variability in prevalence observed in survey data, and (b) modelling error.

Prevalence trend estimation was applied to the bootstrapped data, using the same weights as in the initial analysis. The same seed was used for each bootstrapping iteration, so that prevalence estimates were correlated. This process was repeated 400 times (or an alternative, user-defined 'number of boot samples', specified under Configuration). The median bootstrapped prevalence was considered the best estimate and the 2.5% and 95% percentiles of bootstrapped prevalence were used as 95% confidence intervals (CI).

Variability in prevalence observed in survey data

For each study, the test-adjusted prevalence, *p* (in the range 0 to 1) was simulated using a beta distribution and adding an error term to the parameters of the beta distribution.

Specifically, we assumed that prevalence data from J surveys, $p_j, j = 1 \ldots J$ were available (. Let N_j and $n_j, j = 1 \ldots J$ denote the sample size and number of tested positive used to estimate p_j. For simplicity, let us assume that the test used to identify infected individuals is perfect. Let $\tilde{P}_j$ be the maximum likelihood estimation of $p_j, j = 1 \ldots J$. We have $\tilde{P}_j = \frac{n_j}{N_j}$ and $var\left(\tilde{P}_j\right) = \frac{\tilde{P}_j\left(1-\tilde{P}_j\right)}{N_j}$, and, asymptotically $\tilde{P}_j$ follows a Gaussian distribution.
This indicates that, for the purpose of estimating the uncertainty interval, the prevalence p_j can be simulated following a Gaussian distribution of mean $\tilde{P}_j$ and variance $var\left(\tilde{P}_j\right)$. Nevertheless, a Beta distribution was used rather than a Gaussian, as the sample sizes are typically not large in which case a Gaussian distribution can yield negative prevalence estimates. Because we have estimates of the expectation and of the variance of $\tilde{P}_j$, we can estimate the parameters of that beta distribution using the method of moments.

The test-adjusted prevalence of each data point p_j, was thus simulated following a beta distribution $P^* \sim \beta\left(a_j, b_j\right)$ with expectation $E(P^*) = p_j^*$ and variance $var(P^*) = \frac{p_j^*\left(1-p_j^*\right)}{N}$, where N is the sample size, the parameter r p_j^* is itself simulated using the relation $log\left(\frac{p_j^*}{1-p_j^*}\right) = log\left(\frac{\hat{p}_j}{1-\hat{p}_j}\right) + \varepsilon_j^*$, in which $\hat{p}_j$ is the fitted prevalence (from observed data set) and the error term ε_j^* sampled following a uniform distribution on the set of observed residuals (on the logit scale) with the same (unscaled) weight. Of note, we could have focused on $log\left(\tilde{P}_j\right)$ and derive its variance using the delta method. However, that technique also relies on the asymptotic theory.

A2.2 Incidence: Methods

For gonorrhea and chlamydia, and for syphilis when prevalence trends are estimated using logistic regression, incidence estimates for each population group are derived from the prevalence trend estimates. When syphilis estimates are generated using the segmented polynomials for incidence approach both prevalence and incidence estimates are generated directly.

A2.2.1 Estimating incidence: gonorrhea, chlamydia and syphilis (logistic regression)

Spectrum-STI assumes that the incidence hazard or density (among uninfected people) is constant in each consecutive interval of length 1 year, starting from the first projection year. If the incidence hazard or density, i, and the duration of the STI disease episode, D, are constant in the interval $(t_0, t_0 + 1)$, then for all t in that interval, the prevalence (p) satisfies the equation:

$$p(t) = \frac{i}{i+r} + \left(p(t_0) - \frac{i}{i+r}\right)\exp\left(-(i+r)(t-t_0)\right) \qquad \text{Eq 4}$$

where $r = 1/D$.

Spectrum-STI solves this equation for i piecewise every year, after setting $t = t_0 + 1$. From this incidence hazard, the corresponding incidence rate 'IR' *per capita* for each group is calculated as:

$$IR = i(1-p), \qquad \text{Eq 5}$$

where p is the prevalence.

A2.2.2 Uncertainty intervals

For incidence estimates the 95% CIs on incidence bounds reflect both the uncertainty (estimated by bootstrap) in prevalence, and an additional uncertainty on the duration of infection, set at ± 50%.