Spectrum

UNAIDS 2020

REFERENCE

Quick Start Guide for Spectrum

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Part I. Overview of estimates and projections tools

A. Purpose of estimation and projection models

A well-planned response to the HIV epidemic requires accurate information about the disease over time. Mathematical models are often the most appropriate way to describe the HIV epidemic and the impact of the response because it is impossible to count the exact number of people living with HIV, people who are newly infected with HIV or people who have died from AIDS-related causes in any country over time.

UNAIDS and partners have supported the development of the AIDS Impact Module in the Spectrum software to assist countries to monitor their HIV epidemic. The software uses HIV surveillance, survey and program data, combined with demographic data, to generate historical trends and short-term projections of key indicators. These indicators, including the number of people living with HIV, the number of new infections, the number of pregnant women infected with HIV, mortality due to AIDS and treatment coverage, are useful in assessing epidemic trends and the overall impact of the response and in planning for future health care service and pharmaceutical needs.

B. Technical oversight of Spectrum

The UNAIDS Reference Group on Estimates, Modelling and Projections oversees the development and revision of the Spectrum software. The group is composed of experts from multiple disciplines and institutions, including epidemiologists, demographers, clinicians, statisticians, modelers, and program implementers. The Reference Group meets twice a year to discuss revisions and updates the software routinely. For more information on the Reference Group go to www.epidem.org

C. Process of creating estimates and projections using Spectrum

Country teams are responsible for creating and updating annual Spectrum files. The country teams typically consist of individuals from the national programs who have a strong capacity for epidemiology and modeling. These teams also may include in-country development partners who work on HIV surveillance. The country teams work in groups to update the estimates with the country's most recent surveillance and program data. UNAIDS and partners support country teams to explain new features and review and validate program data and outputs.

Countries are expected to refine and share preliminary outputs with other interested parties in the country for their review. Once the results are finalized, UNAIDS uses these to inform the regional and global estimates of HIV. Countries are encouraged to publish estimates and to communicate the results to all relevant stakeholders.

D. What are the major changes in the 2021 software

Interface

Avenir Health has introduced a new web version of the AIM module of Spectrum. This can be accessed at the website https://aim.spectrumweb.org.

Adult ART and Child ART editors allow monthly input of numbers on ART for 2020 to allow for variation in monthly values due to COVID-19. Similarly these editors allow monthly input for lost to follow up for 2020.

New defaults have been employed in the trend in the sex ratio of new infections for generalized epidemics. This is found in the sex/age pattern tab.

In countries that have a viral suppression threshold other than 1000, a revised calculation is applied based on information from countries representing a wider set of regions than the calculation applied in the 2020 estimates.

At the bottom of the main Spectrum page a new flag will indicate to the user whether updates have occurred since Shiny90 was last run. The shiny90 model should always be run with the most recent Spectrum results.

CSAVR

A gamma distribution to estimate incidence from new diagnoses and AIDS death likelihood has replaced the previous Gaussian fitting method.

New estimates of AIDS-related deaths through 2019 are available from the Global Burden of Disease Study 2019 (GBD 2019) are also available for country use. UNAIDS recommends that countries use the latest GBD 2019 estimates of AIDS-related deaths, which are adjusted for incomplete reporting and garbage codes, to determine incidence. A new online Sankey diagram visualization tool is available at hivtools.unaids.org to depict the changes from the raw vital registration data into the adjusted estimate of AIDS-related deaths.

In addition, a new interface has been developed that allows the user to more easily see the input data and key results (incidence, prevalence, knowledge of status, AIDS-related mortality) by sex.

If the training run results do not show a good fit to the case notification and AIDS-related deaths, UNAIDS recommends refitting to the data while also fitting to the age and sex incidence rate ratios in Spectrum. A tick box with this option is included in the “Fit Incidence” option.

Advanced option

In the pediatrics transmission parameters the patterns of child mortality among children on ART have been updated based on data from the IeDEA network.

In addition, the model applies a new mapping that moves young children who are progressed using a CD4% to older children ages five and older who are progressed based on CD4 count.

As was done in the 2020 estimates, the modified assumptions about breastfeeding among women living with HIV were updated to include the latest survey data. Some of the PHIA surveys were removed from the calculation because of variations in how women were asked about breastfeeding patterns.

One of the most important updates to the model in 2021 is the update to the assumptions about how people not receiving ART progress (natural history patterns). This will have an important impact on mortality early in the epidemic and for countries with fairly low ART coverage.

In addition, a change was made on the allocation of people starting ART. Previously it was based a 50:50 split that weighed on whether people were eligible for treatment versus being close to death. Now the split is 80% is based on eligibility and 20% are based on being close to death. This is based on additional evidence from the IeDea network.

AIM calculations

Adults who drop off ART will be placed into a CD4 category one higher from the one they were in when they initiated ART to reflect the increase in CD4 counts while on ART.

One of the Tools available in Spectrum is to extract results in a format that can be imported into the PEPFAR Datapack. This import will now include new information from Naomi and the DMPPT 2 (voluntary medical male circumcision model).

Estimates and Projections Package

The assumption on the average reduction in HIV transmission per 1% increase in population ART coverage has been modified from 0.7 in the 2020 model to 0.8 in the 2021 model. This decision was based on evidence from Universal Test and Treat studies and other mathematical models. The assumption is less than standard assumptions about viral load suppressions impact on transmission (usually around 88-92%) because it also captures that people on ART are older, longer duration of infection and thus would contribute less to transmission.

E. Preparing to develop a Spectrum file

E1. Choosing a file structure

The Spectrum software is designed to produce estimates and projections for countries and sub-national regions with either generalized or concentrated epidemics. The epidemic typology and the amount and type of data available will determine how Spectrum files will be structured. The most common structures for each epidemic type are described below:

Generalized Epidemic

Historically, in countries with generalized epidemics, prevalence is usually higher in urban areas than in rural areas. Therefore, most countries with generalized epidemics have adopted a model structure that uses two distinct sub-populations (an urban population and a rural population).

Increasingly, countries with sufficient historical surveillance and program data may choose to produce estimates at the provincial level to better capture geospatial variations in the epidemic. In these cases, a country may either choose to create a single file with multiple geographic subdivisions or they may opt to create separate files for each geographic subdivision. If separate geographic files are developed, each file must contain surveillance, program and epidemiologic data specific to the geographic area.

Concentrated Epidemic

Countries with concentrated epidemics have historically modelled their epidemic by producing and then combining epidemic curves for key subpopulations most at risk (e.g., people who inject drugs, gay men and other men who have sex with men, female sex workers) and the general male and female populations at lower risk.

More recently, countries with strong case reporting and vital registration systems may use these data instead of serosurvey data to develop a single national set of estimates.

E2. Collating the required data inputs

The accuracy of the estimates and projections depend on the availability and quality of the data used as inputs to the model. For countries that have conducted routine surveillance on groups that are most important to the epidemic or that have robust historical HIV case reporting or vital registration data, they will be able to inform the model with substantial data and, in turn, produce high quality estimates and projections. In instances where data are scarce or of poorer quality, the estimates and projections may not fully describe the HIV epidemic in a country.

To produce a Spectrum model, countries must be able to supply historical program data about access to antiretroviral treatment among children and adults, the latter by sex. In addition,

trends in the number of pregnant women receiving ARVs for prophylaxis by regimen must be complete. Other demographic, epidemiological and clinical information to determine the impact of HIV are optional. Default values for much of the demographic and epidemiologic information are supplied within the software and can be updated by the country with local data if available.

Other data requirements or optional data depend on the type of epidemic being modelled. These data needs are described below.

Generalized Epidemic (high burden epidemics)

In high-burden epidemics, historical data from sentinel surveillance sites at antenatal clinics (ANC) are required. Beginning in 2017, routine HIV testing data among pregnant women attending all ANC sites or a subset of these sites also can be used as an input to the model. Data from population-based surveys continue to be an important input in calibrating prevalence and incidence levels and trends. Where sufficient data are available, the estimates can be produced for rural and urban areas as well as for different sub-national divisions.

Concentrated Epidemic (low level epidemics)

In low-level epidemics, the data that are required for the model depend on the type of surveillance that countries use to monitor their epidemic. For those countries that routinely conduct serosurveys among those populations most at risk, estimates of the population size and prevalence data for each group over time is required. For example, if a country identifies female sex workers and people who inject drugs as important at-risk populations, data for those two sub-populations and for the remaining general population, split into males and females, will be required. Beginning in 2017, routine HIV testing data among pregnant women attending all ANC sites or a subset of these sites also can be used as an input to the model.

Additionally, HIV outbreaks in hospitals or via medical procedures among paediatric patients are known in a number of countries. EPP allows for numbers of such cases to be entered in the Paediatric nosocomial infections window.

If surveillance data among key populations are sparse but case surveillance data are relatively complete and the quality of data on AIDS-related deaths from the vital registration system is relatively high, then incidence trends can be estimated from these data.

Part II. Using the Spectrum Software

This Quick Start Manual describes the detailed steps required to update your Spectrum file. A more concise, summary of these steps is available in the Basic Steps document or on the videos available at hivtools.unaids.org.

To create a new file as opposed to updating one, please see Annex 2.

Step 1. Install the most recent version of Spectrum

Spectrum can be downloaded from www.avenirhealth.org. Use the version listed under the AIM module. Spectrum will run on any computer running Windows Vista, 7, 8 or 10. It requires about 500MB of hard disk space.

Alternatively, there is a new web-based version of Spectrum available at: https://aim.spectrumweb.org. See the video on Spectrum on the web at hivtools.unaids.org.

Once Spectrum is downloaded from the internet, double click on the file named "SpecInstallAIM2021.exe". This will start the installation program. Follow the instructions on the screen to complete the installation.

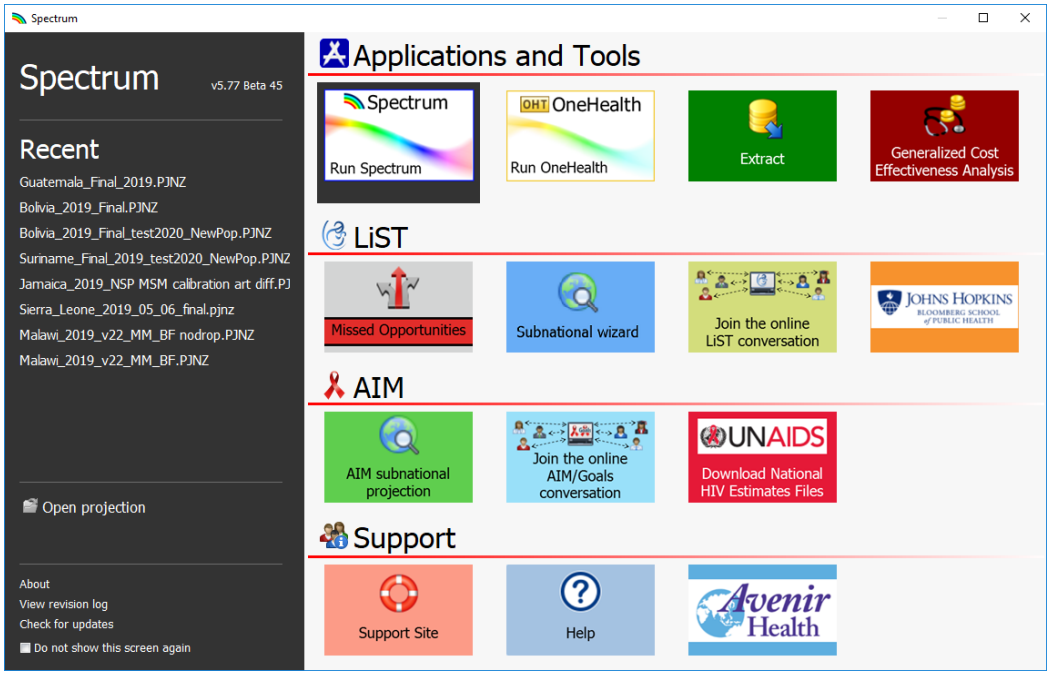
If you have trouble installing Spectrum you may not have permission to install programs on your computer. In that case, contact your IT office to install Spectrum for you.

After installing Spectrum, check your computer to make sure you have Java version 8 installed on your system. The easiest way to determine which version of Java you have is to click on the Windows start menu, select 'All Apps', click on Java and select 'About Java'. If you do not have version 8 (or do not have Java), please download or update the software at www.java.com.

Next make sure that Windows can find Java on your computer. To do this, start Spectrum and open your country file. Select **Modules** from the Spectrum menu and click the **AIM** icon to display the AIM menu. Select **Incidence** and **Configuration (EPP)**. If EPP starts after a few seconds, then you are ready to use EPP. If it does not start, then you need to tell Windows where to find Java. To do that select **File** and **Options.** Click the box next to **Use custom java.exe** to add a check mark. Then click the button **Select java.exe**. This will open Windows Explorer. You need to indicate the location of the java.exe file. To find it select the **C:** drive, then click **Program Files (x86)**, then **Java**, then click the folder for the most recent release of Java, then click **bin**, and, finally, click **java.exe.** This location will be saved so that Spectrum will always be able to find Java. If you update your version of Java, you will need to repeat this process to ensure Spectrum has the latest Java location.

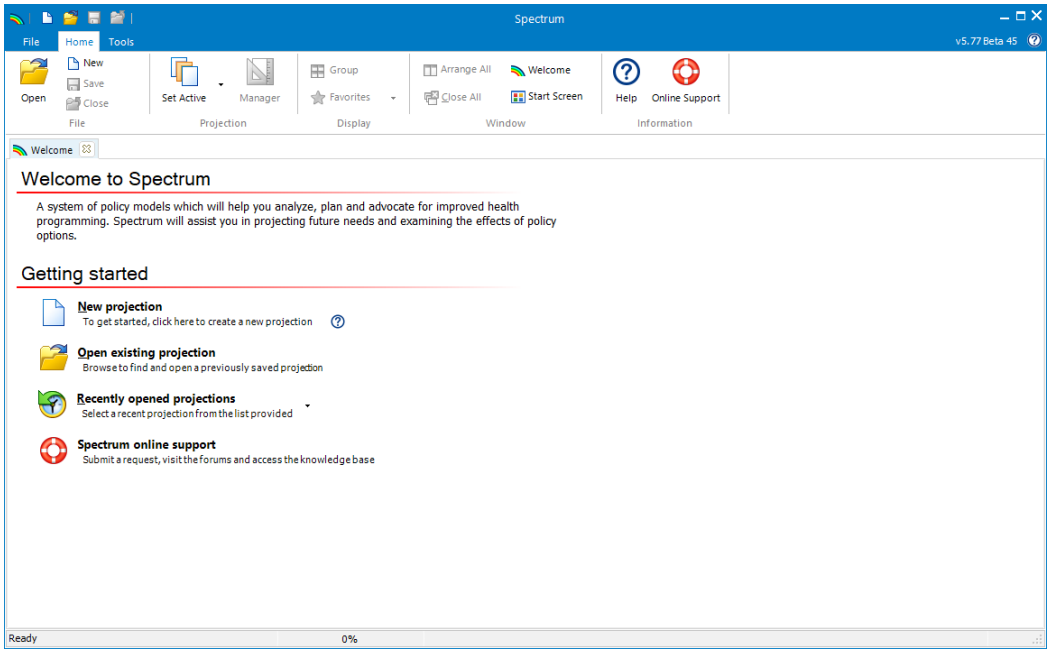
Step 2. Start Spectrum

Start the Spectrum program by selecting it from the **Start** menu on your computer (Windows 7 or earlier and Windows 10) or your **Start Screen** (Windows 8). When the program starts, you will see the welcome screen below.



From that screen you can run different applications including Spectrum. You can also open an existing Spectrum file directly.

If you run Spectrum by clicking on the icon, the main Spectrum module will appear.



From there, you will be able to select ‘New Projection’, ‘Open existing projection’, select a ‘Recently opened projection’ or use ‘Spectrum online support’ below the **Getting Started** header.

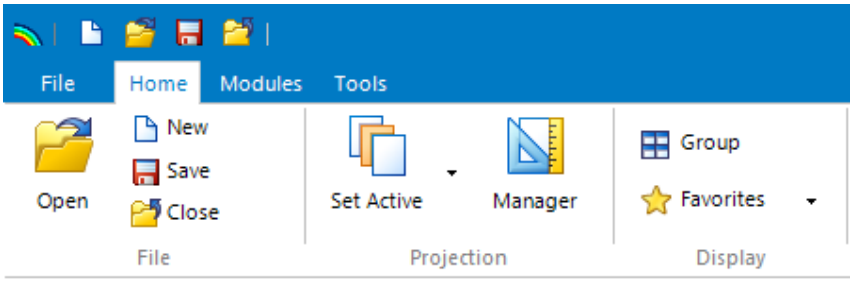
Choosing Spectrum’s default language

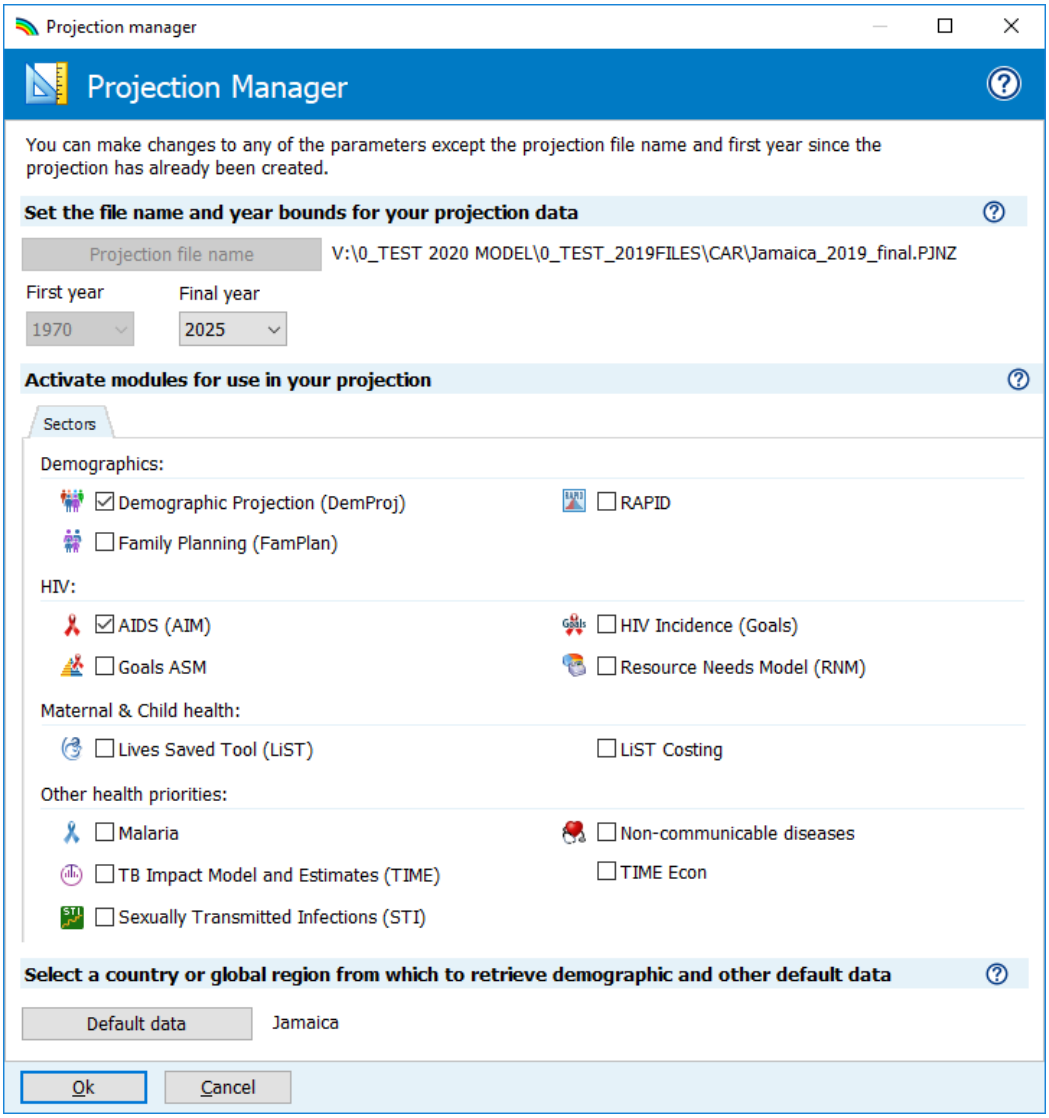
The first time you run Spectrum after installing it, the display will be in English. You can change to another language by selecting the Spectrum File tab, then Options, then selecting the language you want to use and finally clicking on Ok. If you select a language other than French, you must have the proper fonts or Windows version to display the language correctly.

If you have a Spectrum file from previous rounds of estimates, you should start by opening that file and following the instructions below.

Step 3. Update the population projection

When you open a projection you will select the “Manager” icon which will open the below dialogue box.





Caution: When to NOT update the demographic data in your projection

You should not update the demographic data in your projections if:

1. You have modified the default demographic data to incorporate country-specific census data
2. You have created a sub-national projection

If demographic data are updated you will lose the custom data.

Follow the three steps below to update the demographic or HIV data in your projection:

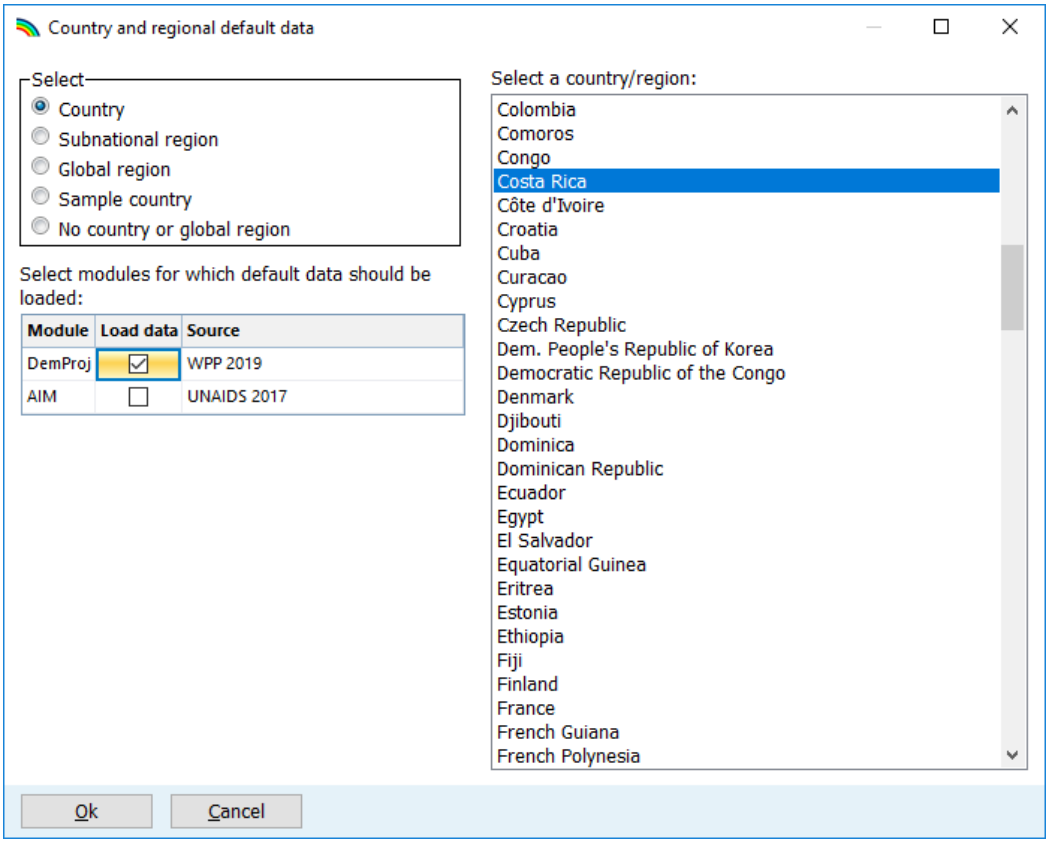
A. Change the final year to 2025, if this is not already the final year. The first year should be 1970 — before the start of the HIV epidemic.

For projections using AEM (AIDS Epidemic Model), the final year should be 2050.

Projections submitted to UNAIDS should use these settings.

B. Click the **Default Data** button.

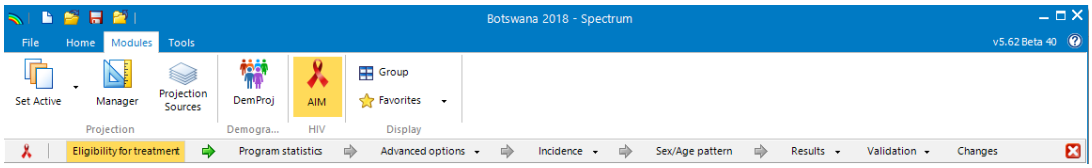
Select your country from the list. Also select the geographic level of the file (country, sub-national, global region, a sample country or none of the above). Also select the geographic level of the file (country, sub-national, global region, a sample country or none of the above).



C. Next, click the box next to DemProj to indicate that you want the demographic data to be updated to value from World Population Prospects 2019. *Do not update the AIM data as this will over-write your program data.* When you are done click the **OK** button.

Finally, save your file under a new name, such as Country_2021.

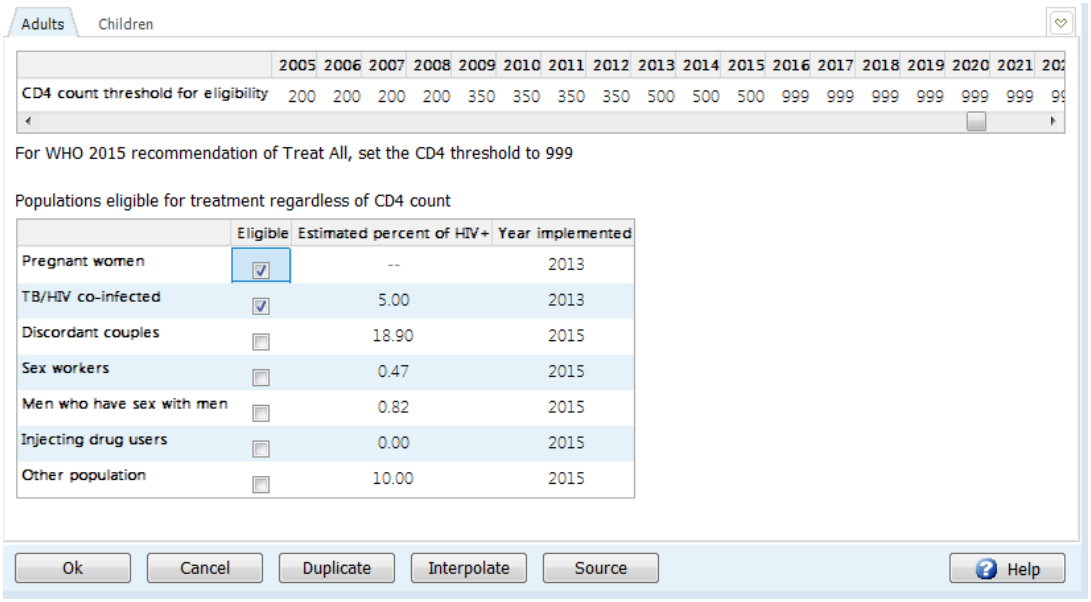
Now you can update the AIDS Impact Module within Spectrum. Select **Modules** from the Spectrum menu and click the **AIM** icon to display the AIM menu as shown below.



To produce the projection, you advance through the menus items one-at-a-time: **Eligibility for Treatment, Program statistics, Advanced options, Incidence, Sex/age pattern, Results, Validation, Changes.** The following sections explain each of these items in detail.

Step 4. Specify eligibility for treatment

Select the **Eligibility for treatment** menu item to see the editor shown below. Most countries will not need to adjust menu if the country has moved to Treat All.

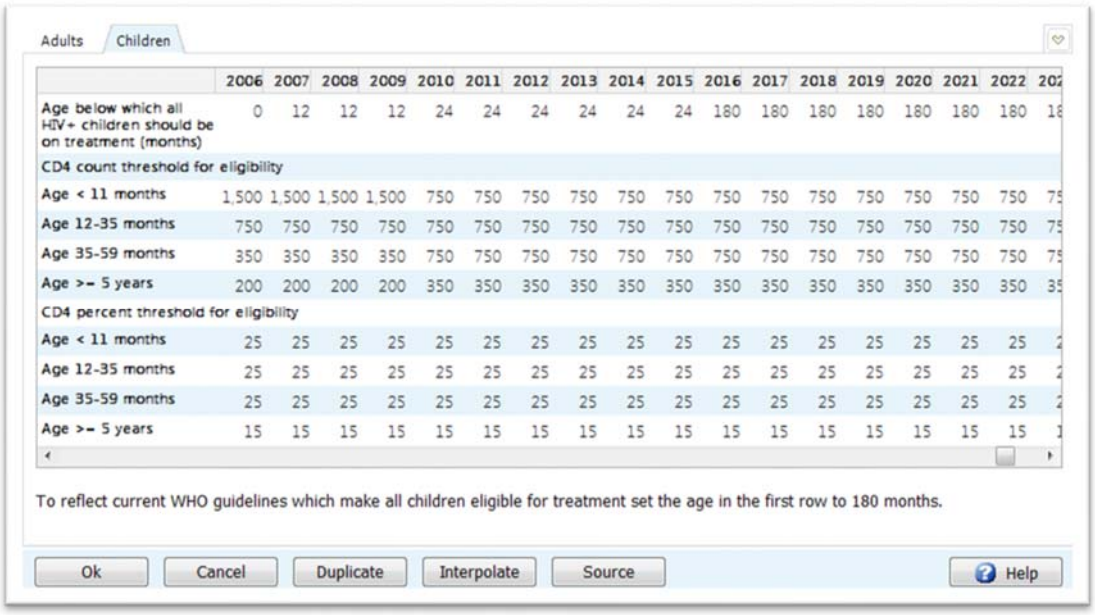


The first tab in this editor describes **eligibility for treatment for adults** (aged 15 years and older.)

In the first table, you should specify the eligibility for ART in terms of CD4 count. By default, eligibility is set to 200 cells/µl until 2009 and to 350 cells/µl for 2010, 500 for 2013 to 2015 and 999 (which corresponds to the 2015 recommendation to "treat all" people living HIV) from 2016. You should modify these inputs to match your country's guidelines.

The second table editor allows you to specify which population groups living with HIV are eligible for treatment regardless of CD4 count. To specify those populations, click the check box next to the name and enter the year in which the guidelines were changed to include that population group. As a final entry for the population, you should specify the estimated percent of PLHIV in this group as a proportion of all adult PLHIV. Spectrum supplies default estimates for most countries and will calculate this estimate for pregnant women directly from the model.

To modify **eligibility for treatment for children**, click on the **Children tab** at the top of the editor.



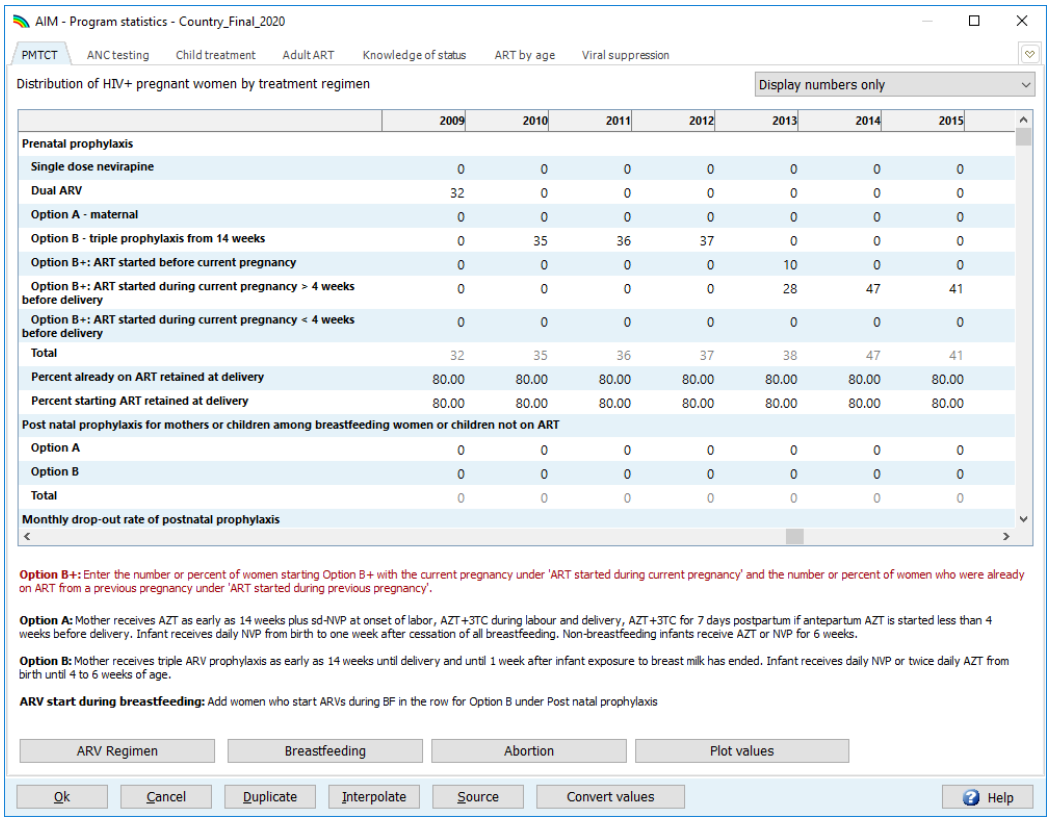
For children, eligibility has three different criteria:

- **By age**. Enter the age below which all HIV+ children are eligible or are started on treatment. By default this is set to 12 months from 2007 to 2009 and to 24 months from 2010 to 2012, 60 months from 2013 to 2015 and 180 months (to age 15) thereafter. For the Treat All scenario, set the first row to 180 months (15 years).
- **CD4 count**. The CD4 count for eligibility can be defined by four age groups and by year. The default values follow WHO guidelines for the corresponding years.
- **CD4 percent**. Eligibility may also be defined in terms of CD4 percent by age. The default values follow WHO guidelines.

Children are considered eligible for treatment if they meet any one of the three criteria.

Step 5. Enter program statistics

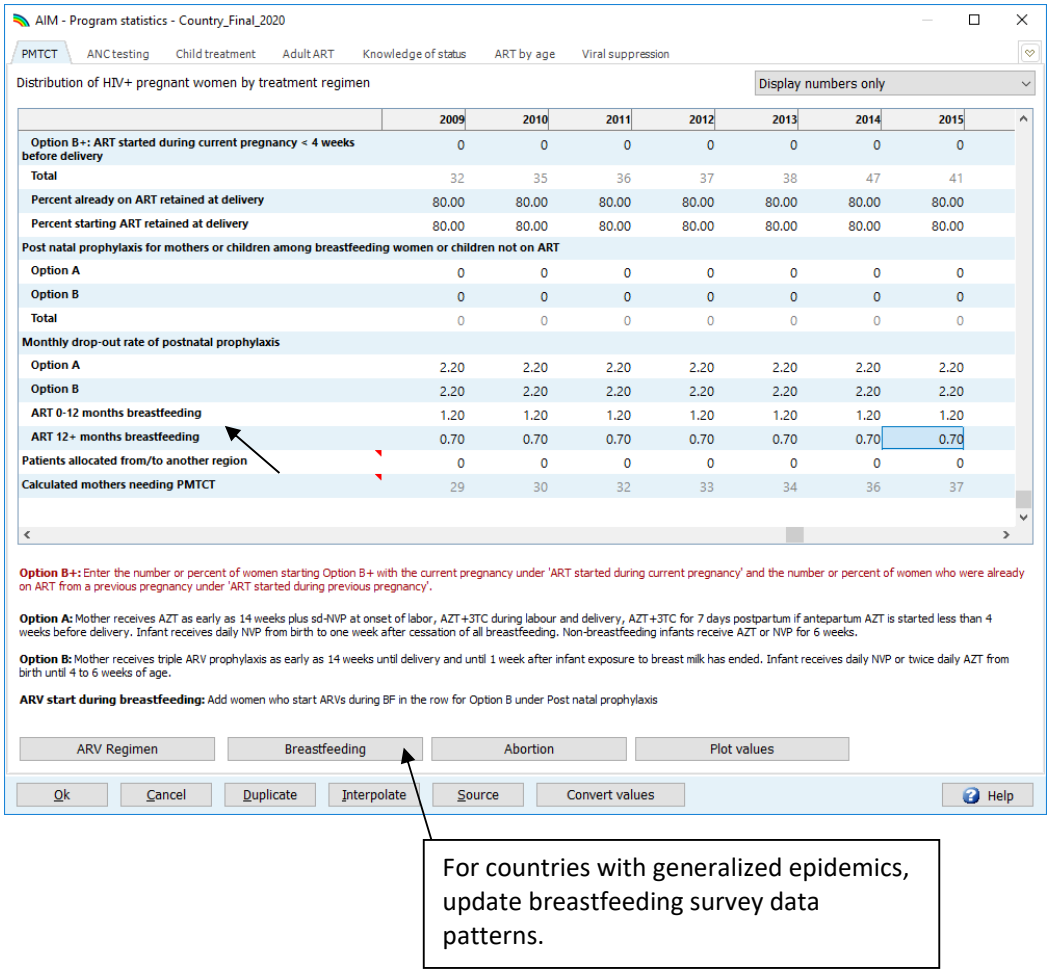
Click on the **Program statistics** menu item to see the program data editor. It will look like this:



In this editor, you will enter or revise PMTCT, ANC testing, treatment program, knowledge of status and viral suppression data for adults and children using the tabs at the top.

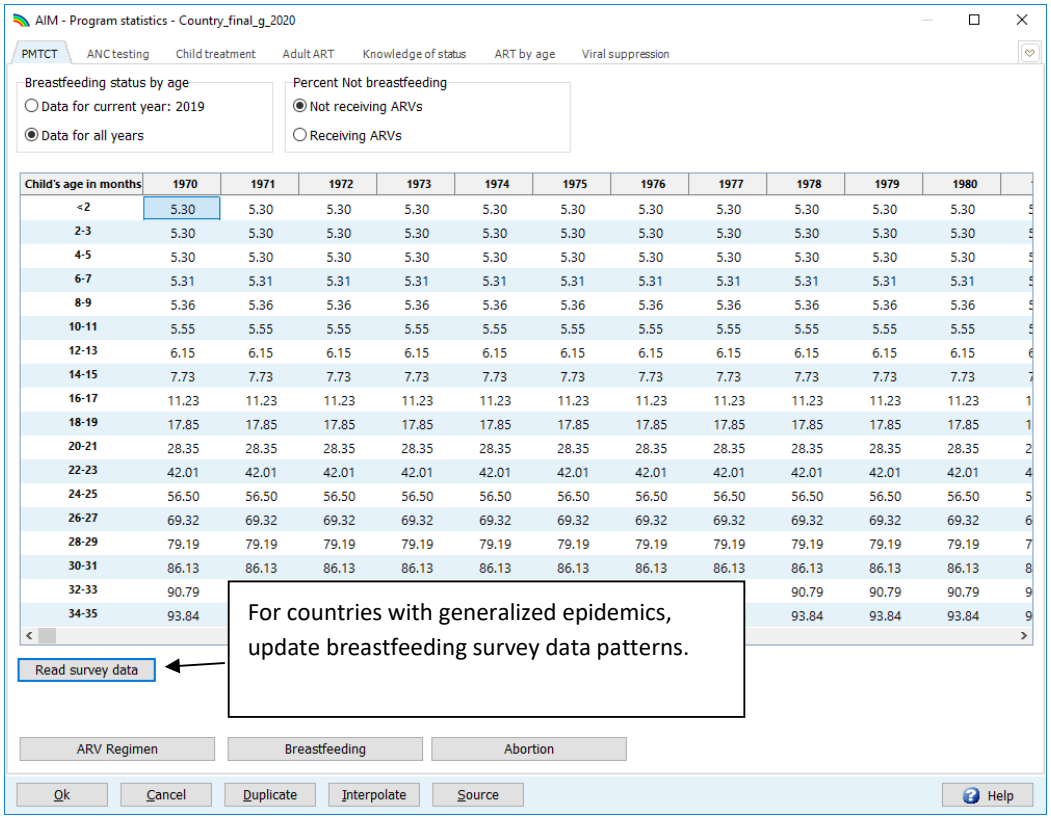
PMTCT, child and adult ART tabs: In the PMTCT, child treatment and Adult ART tabs you may enter any new data for 2020 as the *number* of people receiving the service or as *coverage*, the percentage of those in need of the service who receive it (for ART, this is defined as the proportion of all people living with HIV). Normally you will enter or update program statistics for all historical years (i.e., through 2020) using numbers. For future years (e.g., 2021 through 2025) you may enter either target numbers or percent coverage. Note that you can enter numbers for some years and coverage for other years but you cannot have a number and a percent in the same year.

On the PMTCT tab, update retention at delivery and the monthly drop-out rate of postnatal prophylaxis for all years. Default values (based on a review of published literature) for retention at delivery is 80% and 1.2% for those on ART between 0-12 months breastfeeding and 0.7% for those on ART 12+ months breastfeeding.



For countries with generalized epidemics only, please be sure to click on the **Breastfeeding** button and then the **Read survey data** button (see panel below) to update the breastfeeding patterns among women not receiving ARVs.

The **Abortion** button provides countries with the option of entering data on the percent of HIV-positive pregnant women terminating pregnancies, if this is known.

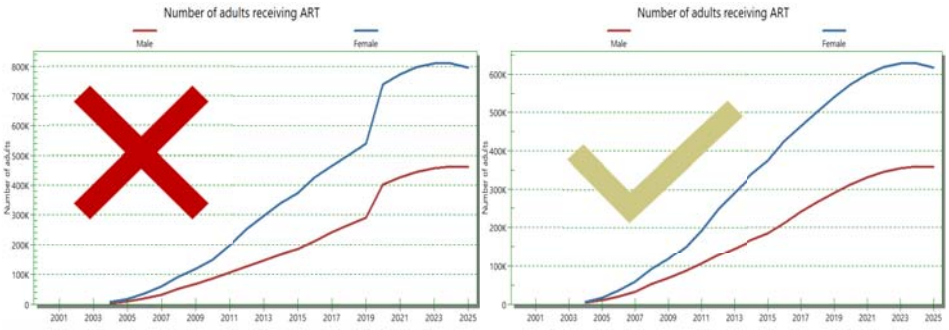


Once these patterns have been updated, you can return to review the ARV regimens or enter into another of the Programme Statistics tabs.

Clarification on the estimated numbers in need of PMTCT and ART in the Programme Statistics tabs: The grey numbers displaying the estimated number in need of PMTCT and ART services are based on the last time the projection was run. Substantial changes to the inputs (surveillance data, eligibility criteria or program data) will result in a change in these values. You should consider the needs in grey as indicative values and review them after the whole file has been updated.

Once you have entered the PMTCT and ART program data, you can use the “plot” feature in Spectrum to visualize these data over time. To access this feature, click on the **Plot Values** button on any of the PMTCT, Adult ART and Child Treatment tabs. For Adult ART and Children treatment plot, a check button in the upper left corner allows you to plot needs against eligibility.

Please review your assumptions regarding the scale-up of treatment coverage through 2025. The projected value should be achievable based on previously reported coverage achievements. If the projected 2021-2025 estimates are not consistent with current progress, the projected values should be revised.

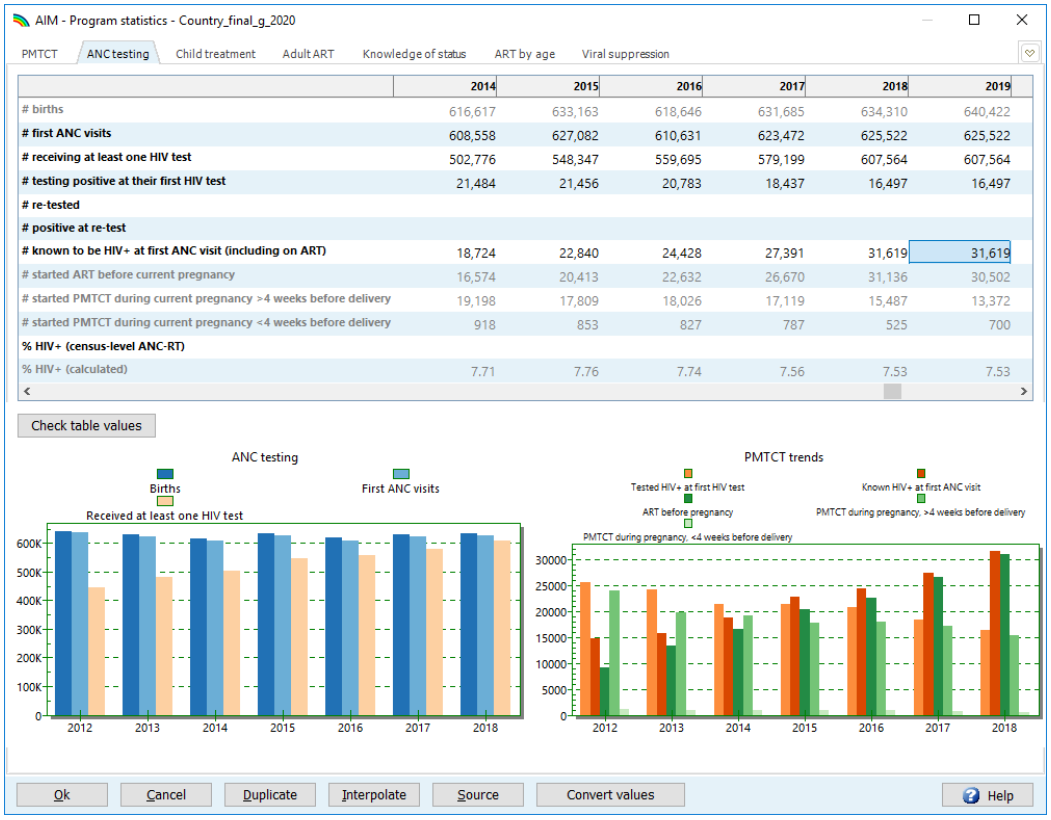


Important for 2020 ART data: Countries can enter data by month in the new software. This will allow for disruptions in treatment services due to COVID. Please also enter data on numbers of children and adults initiating treatment and the percent of people lost to follow up.

The data on lost to follow up should only include those people no longer retained in care. It should not include individuals who have died or transferred to another site. In addition, these data should be included for all years. If data are not available for some years, assume similar values to the years where data are available to avoid sharp changes in this value.

ANC testing tab: Reviewing data compiled around pregnant women found to be HIV positive during their routine antenatal care visits should be done before estimating prevalence using EPP and interpreting MTCT and child estimates. The purpose of this table is to let users check their ANC data inputs using clinic-based data and calculate an estimate of prevalence based on the direct ANC visit and testing data provided. This will be useful for identifying incorrect inputs, diagnosing regions where testing or reporting coverage is low, or looking for unexpected trends or patterns that indicate data quality issues.

To complete this tab you need to compile routine HIV testing data from all of the ANC sites in your country. Enter the data in the tab, use the graphs to look for discrepancies and use the "Check table values" button to verify that the data meet logical expectations of the ANC testing cascade.

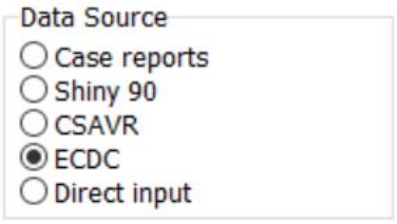


- **# first ANC visits**: the total number of women who have visited ANC clinics at least once in the area currently being modeled in EPP for the current pregnancy. Do NOT include repeat visits in this count.
- **# receiving at least one HIV test**: the total number of women who were tested at least once during their ANC visits. This includes both those testing positive and those testing negative.
- **# testing positive at their first HIV test**: the number who tested positive at their first HIV test during this pregnancy. This should not include women who received multiple tests and were positive only at the second or third test.
- **# re-tested**: the number who received a second or third test during their pregnancy.
- **# testing positive at re-test**: the number who tested positive at the second or third test.
- **# known to be HIV+ at first ANC visit (including on ART)**: This is the number of women who were already known to be positive before the ANC visit and, as a consequence, are recorded as positive, but did not receive an HIV test. This should include women who are already on ART.
- **% HIV+ (census level ANC-RT):** This should be calculated across regions to calculate a national value. The data should be weighted by the number of births to women living with HIV in each region.

Progress towards 90-90-90, Knowledge of Status, ART by detailed age group, and Viral suppression: Progress towards the first and third 90s are compiled in Spectrum alongside the numbers of adults and children on treatment by detailed age groups. These estimates or programme data are not used in Spectrum to derive prevalence or incidence estimates (i.e.,

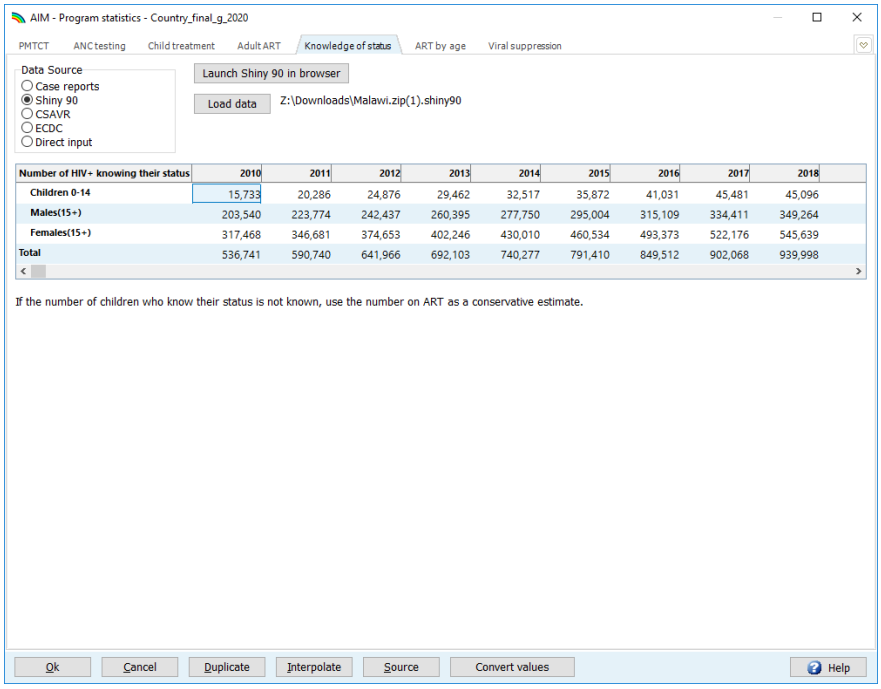
they do not affect the model outputs) so it is not necessary to complete data for years where high-quality data are not available or to enter projected estimates after 2020.

Knowledge of Status: On the Knowledge of Status tab, first select the source of the data to be entered. You will see several options for the source of these data:



For countries using case surveillance data, click on the radio button that says case reports and then enter in the number of children and adults, by sex, living with HIV who have been diagnosed (and were known to still be alive at the end of the year) for 2020. Please also enter and review historical data for the years going back to 2010 where these are available. You may wish to review GAM entries for 2015-2019 (Indicator 1.1) to see what numbers were previously reported. Numbers reported through Spectrum will replace historical estimates previously submitted in GAM, so they should be reviewed carefully for their accuracy.

For countries with population-based HIV surveys with or without serology testing, estimation of trends for the first 90 should be made using the Shiny 90 application. This app is accessed using a link directly from the tab or at: https://shiny90.unaids.org/.



Follow the instructions in the App to produce a file containing the estimates of the first 90 since 2010 for adults by sex. To import the estimates, click on the Shiny 90 radio button then click on Load Data. Estimates of the first 90 for adults by sex will appear in the table. Enter estimates of the number of children who know their status where these are available or,

otherwise, the numbers of children on treatment. Note: you should only load data from the Shiny 90 into the knowledge of status tab once the App has been run using your final Spectrum file.

For countries using CSAVR, there is an option to import sex-specific estimates of knowledge of status among adults by sex from a final Spectrum file. To import the estimates, click on the CSAVR radio button then click on Load Data. Estimates of the first 90 for adults by sex will appear in the table. Enter estimates of the number of children who know their status where these are available; otherwise, enter the number of children on treatment. Note: you should only load data from CSAVR in the knowledge of status tab once you have your final Spectrum file.

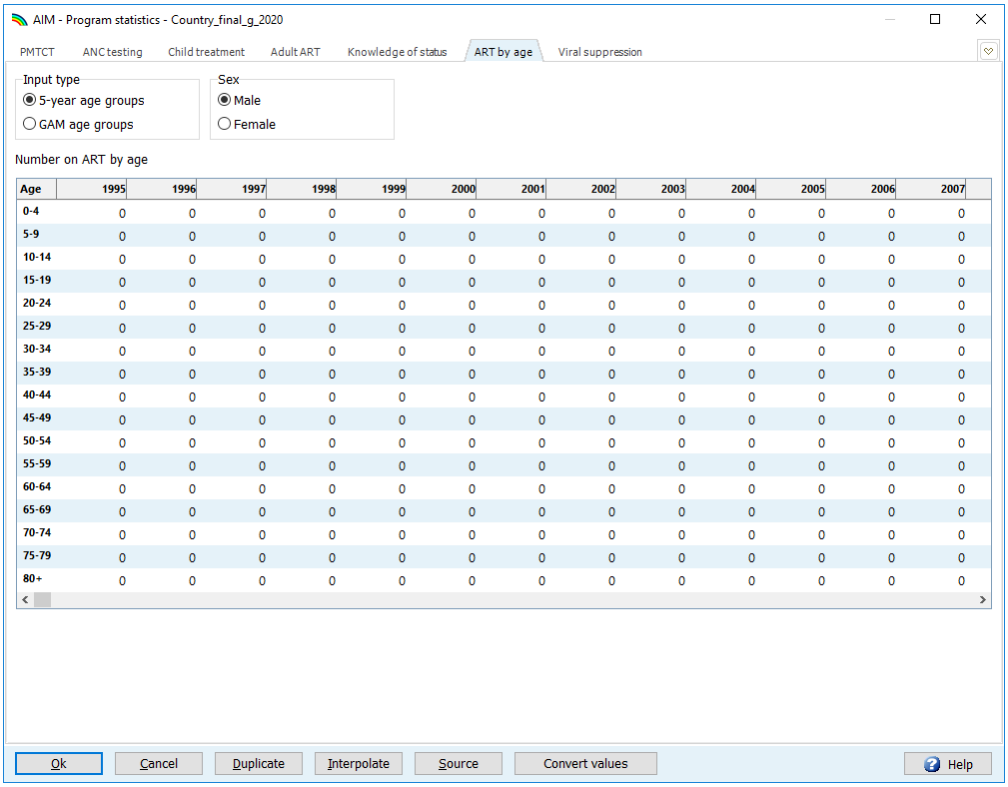
For countries with other model-based estimates (e.g., ECDC, other direct input), the source of the estimates should be selected in the radio button and then the number of people who know their HIV status by age and sex should be entered.

Note for all countries with first 90 estimates: If data on knowledge of status among children are not available in a given year, you should conservatively enter the number of children on treatment at each year end. If you do not enter estimates of knowledge of status for children, it will not be possible to estimate the first 90 for all ages.

ART by age tab:

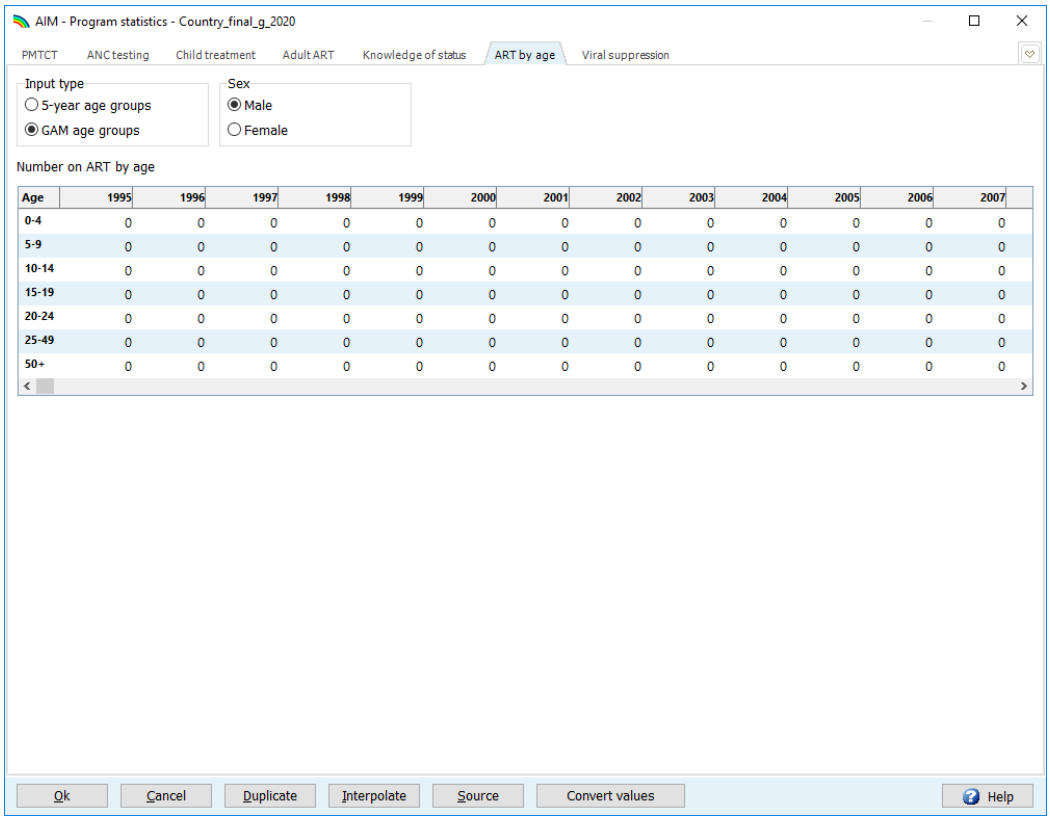
On the ART by age tab, enter in data for all people currently on treatment, disaggregated by 5 year age groups and sex or GAM age groups if the further refined age groups are not available. These totals should add up to the child treatment and adult ART totals, respectively.

Screen for 5-year age group ART data:



Age	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
0-4	0	0	0	0	0	0	0	0	0	0	0	0	0
5-9	0	0	0	0	0	0	0	0	0	0	0	0	0
10-14	0	0	0	0	0	0	0	0	0	0	0	0	0
15-19	0	0	0	0	0	0	0	0	0	0	0	0	0
20-24	0	0	0	0	0	0	0	0	0	0	0	0	0
25-29	0	0	0	0	0	0	0	0	0	0	0	0	0
30-34	0	0	0	0	0	0	0	0	0	0	0	0	0
35-39	0	0	0	0	0	0	0	0	0	0	0	0	0
40-44	0	0	0	0	0	0	0	0	0	0	0	0	0
45-49	0	0	0	0	0	0	0	0	0	0	0	0	0
50-54	0	0	0	0	0	0	0	0	0	0	0	0	0
55-59	0	0	0	0	0	0	0	0	0	0	0	0	0
60-64	0	0	0	0	0	0	0	0	0	0	0	0	0
65-69	0	0	0	0	0	0	0	0	0	0	0	0	0
70-74	0	0	0	0	0	0	0	0	0	0	0	0	0
75-79	0	0	0	0	0	0	0	0	0	0	0	0	0
80+	0	0	0	0	0	0	0	0	0	0	0	0	0

Screen for detailed GAM age group ART data:



Viral load suppression tab: On the viral load suppression tab, please select the radio button describing the data source for 2020.

For countries using laboratory, programme or case surveillance data, the number of people reported annually to have received a viral load test should be entered first. At the bottom of the table, a percentage will be calculated showing testing coverage among people on treatment.

If testing coverage is greater than 50%, viral load suppression is calculated as the proportion suppressed among those tested multiplied by the number of people on treatment.

If testing coverage is below 50%, data on the numbers of people virally suppressed should not be entered unless access to testing is believed to be unbiased with regard to geographic location or facility level.

If sex and age disaggregated data are not available, it is possible to assume some distribution to obtain the known overall total. Assumptions used to inform the age and sex disaggregated data should be included in the source notes.

Note that the above approach assumes that suppression levels are the same among the untested and tested populations. If there is evidence that this is not true, please discuss this with the Estimates team at UNAIDS.

For countries using survey data to report, please remember to extrapolate the results to the total number of people living with HIV in the country. Also, enter in the numbers of people with an annual viral load test, even if the results from these tests are not used to estimate suppression.

For countries that report suppression using an assay with a detection threshold below 1000 copies/mL, you can adjust the results to reflect the numbers expected to be suppressed at the recommended 1000 copies/mL. The detection threshold can be entered for each year and the adjustment will be made automatically made and visible as a separate category in Results in the disaggregated HIV testing and treatment cascade. This will ensure the data reported by countries with different thresholds are comparable.

Additional tips on entering adult ART data

Most countries should use the default option to enter the number or percent of people accessing ART. Additional data should be entered on the percent of people lost to follow up each year (e.g., those who drop out as opposed to die on ART or transfer to another facility) and the number initiating ART by sex, and among those the number reinitiating after dropping out. These data are used in the detailed treatment cascade under the Results.

Countries with more detailed information about the CD4 count profile of people initiating ART may choose to enter ART data as either a percent coverage or a number.

Additional tips on entering pediatric ART data

The child ART data entry tab provides two options for entering the number of children on ART: (1) ART for all children and (2) ART by 5-year age group. Option 1 works as in previous versions. You enter the total number of children aged 0-14 on ART. The second option allows you to enter the number of children on ART by five-year age group. If you have this information, you should use it here to inform the allocation of ART by age. The choice of entering for all children or by 5-year age group can vary by year, so if these data are only available in recent years, they can be entered for the years available.

When you are finished entering the PMTCT, ANC testing, child treatment data, and testing and treatment cascade data click the **Ok** button.

Step 6. Restore default values in Advanced options

The **Advanced options** menu item allows you to see the default adult and child parameter values used in the projection. These parameter values are informed by special studies and surveys from many sites around the world. **In most cases the default values should be used and you should update these every round of estimates by selecting Restore Defaults**. You should only change them if you have conclusive evidence for alternative values. The parameter groupings are as follows:

- **Pediatric transition parameters:** These tabs include assumptions around progression rates to lower CD4 levels, the distribution of new infections by CD4 percent, HIV-related mortality for children with and without ART and the probability of initiating ART by age. Assumptions about the effectiveness of cotrimoxazole on reducing mortality over time are also included.
- **Adult transition parameters**. These include the amount of time an average adult spends in each CD4 category, the distribution of new infections by CD4 category, HIV-related mortality by CD4 category without ART, HIV-related mortality on ART by CD4 count at the initiation of treatment, including the option of a scaling factor to adjust annual mortality rates relative to 2012, and the effects of HIV infection on fertility. Different parameters exist by region for HIV-related mortality. By selecting the tab for HIV-related mortality you can select the country's region to improve the mortality estimates. The total fertility rate adjustment is also included in this tab. This describes the assumed difference in fertility among HIV+ women not on ART and HIV- women.

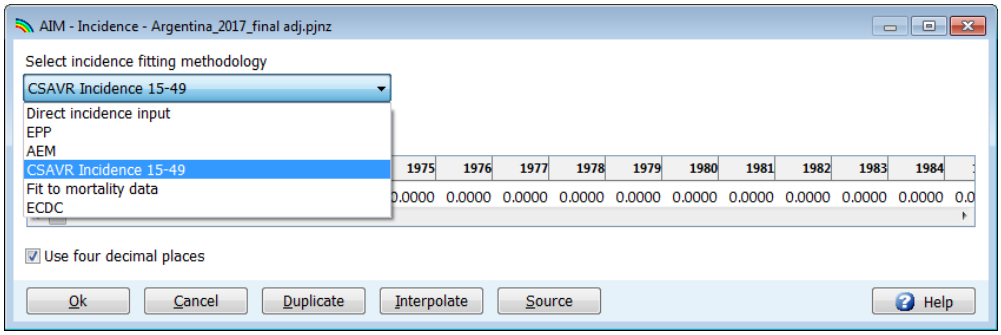
- **HIV-related fertility reductions.** The HIV-related fertility tab contains the parameters for estimating births to women living with HIV. Reductions in fertility by age and CD4 count that allow the model to best fit HIV prevalence among pregnant women are displayed. Select **Calculate 15-19-year old** to estimate the fertility adjustment for the first age group based on the most recent surveys. Further adjustment based on local data by selecting Fit Local Adjustment Factor. If available Read the ANC-RT census data from EPP. This will copy the aggregated prevalence from pregnant woman. Click on 'Fit Fertility Rates' to fit to those routine data. If the Read ANC-RT data button is not active, that means that no data are available on HIV prevalence among pregnant women. If new routine ANC data are being entered into EPP this step should be repeated after those data have been entered.
- **MTCT transmission probabilities:** these are the assumptions around the transmission from mother to children based on the mother's CD4 level and different ARV regimens. These probabilities are taken from the literature and should only be changed in countries with strong evidence for alternative values. If the values in this table are red, it implies that the values do not match the current default values.
- **DALYs and Orphans:** these pages provide the assumptions around the calculation of disability adjusted life years and orphans.
- **Allocation method for new ART patients:** this allows you to change how ART is allocated to new patients by CD4 category. In Spectrum, ART is allocated to the eligible population according to their CD4 count and the expected mortality of those who have not yet started ART. By default, these are weighed as 83% to the eligible population and 17% based on their mortality among those not on ART. You can test the effects of different allocations on mortality by changing one of these weights. The other will automatically update so that both sum to one. You can also choose to assign ART proportion to the mortality rate, to the number eligible or to those with the lowest CD4 counts first.

How can I update to the default values for some parameters without losing my custom values for others?

Custom values are identifiable by their red font (although the red font may also indicate an out-of-date value). To update all parameters but not lose those that are customized, the custom values should be saved in a separate excel file first. Following that, you can press the restore default value and then re-enter the customized parameters.

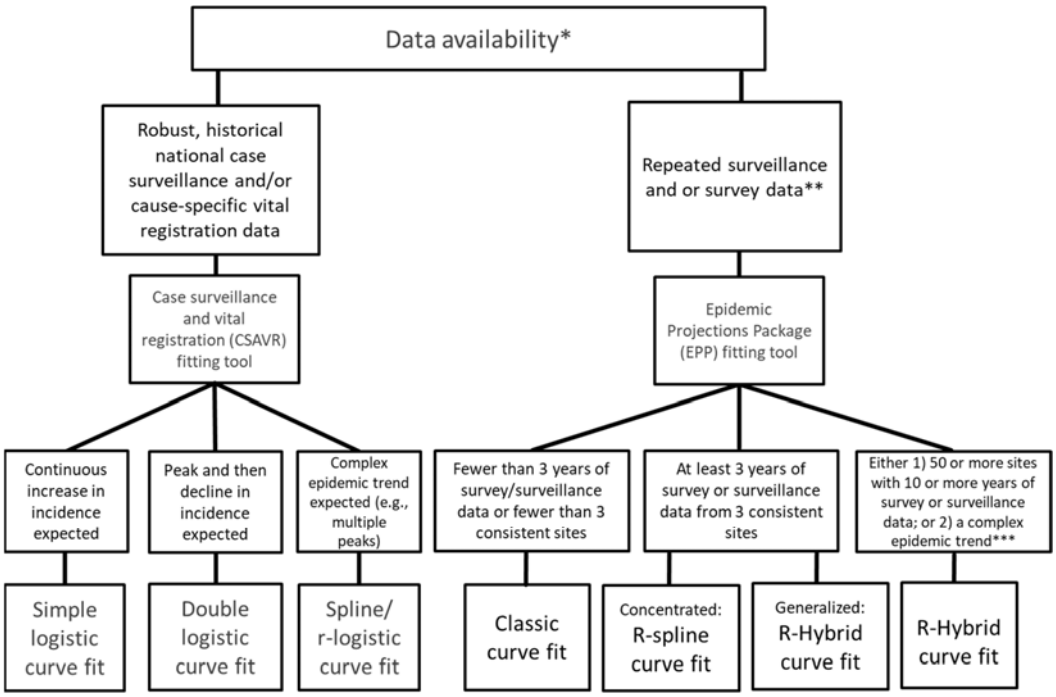
Step 7. Deriving Incidence

When you select **Incidence option** from the incidence menu you will see a drop-down menu with six different fitting methodology options. The method that was used in the previous year will be selected by default.



You should review the decision tree below and the quality and quantity of surveillance data available for your country to make sure you are choosing the best model for deriving incidence in Spectrum.

Figure 1: Decision tree on use of estimates tools

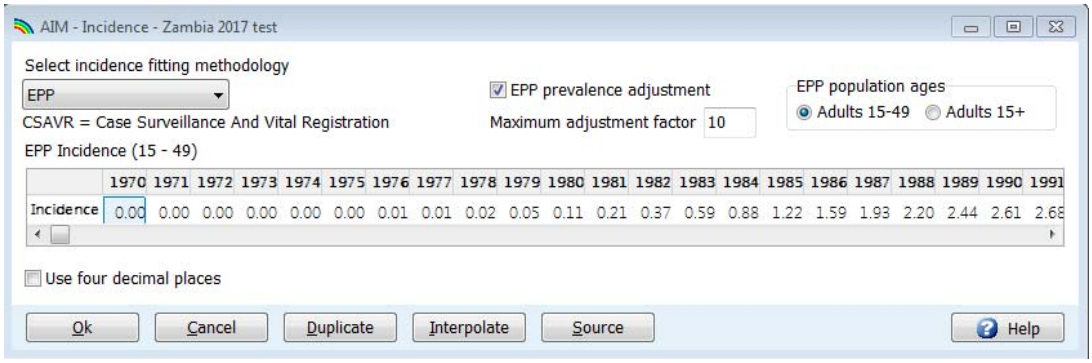


* Some countries may use alternative tools (e.g., AEM, ECDC) to estimate incidence. These rates can be directly entered into Spectrum.
** The most appropriate curve fitting tool should be selected for each sub-population modelled in a country's national file; Countries may have a national incidence and prevalence curve comprised of different fitting methods.
*** Countries with sufficient data may construct sub-national Spectrum file(s)

For countries that are producing subnational estimates, a decision on which tool to use should be made for each geographical area.

If you are directly entering annual incidence obtained from another tool, then select the 'Direct incidence input' options and then simply enter the incidence estimates and click Ok.

For countries that are using EPP, ensure EPP is selected in the drop-down menu, then choose the age group that best reflects your surveillance data. For most countries with ANC surveillance or population survey data, this should be adults' ages 15-49 years. Also, for most countries, the box for EPP prevalence adjustment should be checked, which allows AIM to adjust for small differences in the prevalence trend fitted by EPP as compared to the trend fitted by AIM. The maximum adjustment factor of 10 will allow the resulting prevalence trend to closely match the prevalence curve from EPP. A lower value of the maximum adjustment factor will produce a smoother incidence curve but the prevalence trend may differ from the curve fit in EPP.



The other options are:

- AEM. This option allows you to use AEM to determine the incidence trend. Generally, it is used by only a few countries that already have AEM applications.
- CSAVR (Case surveillance and vital registration) fitting tool. This option estimates incidence by fitting to program estimates of the AIDS deaths, new HIV case reports and mean CD4 count. This option may be best for countries without good surveillance data but with good case surveillance on case reports and AIDS deaths from vital registration systems.
- ECDC model – This option uses the number of new HIV infections estimated from the ECDC HIV model to calculate incidence. For more information on the ECDC model, please access: https://ecdc.europa.eu/en/publications-data/hiv-modelling-tool.

  Note: For countries using ECDC model results, to pull in the incidence data, you should click the 'Read from database' button, then select the ECDC output file. This will have a name such as COUNTRY_Result_main.csv. This file is produced automatically when you complete a run of the ECDC model. Once you select the file the number of new infections will be read into Spectrum and displayed in the editor. Incidence will be calculated and displayed in the second row. You can edit these numbers if necessary, but normally they would remain as they are read from the file. Then click the Ok button. The incidence from the ECDC model will then be used in the Spectrum projections.

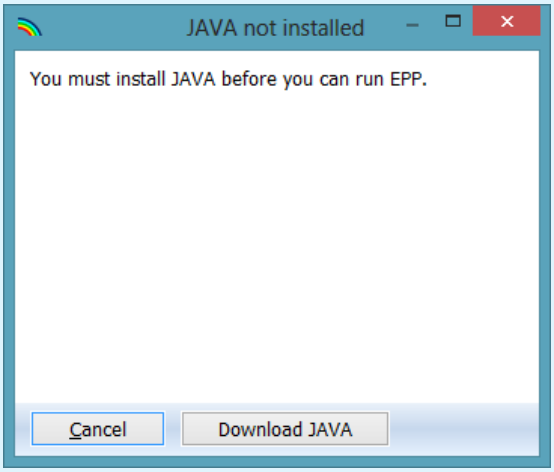
Once you have made your selections, click OK and then click on Incidence in the menu to see the access to the various fitting steps.

For EPP these are **Configuration, Surveillance, Curve fitting, Restore values, and Review** required to derive an incidence curve in EPP. Each of these items is discussed in more detail in steps 9 through 11. For the CSAVR fitting tool, the menu option **Fit Incidence to CSAVR** data

should be visible. If you are using CSAVR, you should skip to step 12. If you are using EPP, you should complete steps 9 to 11 and skip step 12.

I've selected one of the menu items in EPP – why can't I see the program?

If you do not have the Java Runtime installed on your system, the first time you go to run an incidence calculation, you will see the following prompt within Spectrum to download and install Java before proceeding:



Click on "Download JAVA" and you will be taken to the Java site, where you can click on "Free Java Download" followed by "Agree and Start Free Download" to begin the install. When asked if you want to "run or save this file?", click on "Run" and follow the prompts to install the software.

As an alternative, you can visit the site java.com and install the Java software directly from there prior to running Spectrum. To install Java, you must have administrative rights to your computer. If you cannot successfully add this program, please contact your IT department.

If you do not see this error message but EPP still does not run, it may be because you have two versions of Java on your computer, for example Java 7 and Java 8. EPP will not run if both versions are present. The two options to fix this issue are the following:

(i) in Spectrum, go to file -> options, check the "Use custom java.exe file" box and then click on "Select java.exe". Browse to your Java 8 executable that can be found in your C:\Program Files (x86)\jreYYY\bin where YYY is the Java version number. Please note that in Spectrum 2021, you must be using Java 8 or EPP will not run.

(ii). You should go to Control Panel, and use Uninstall Programs to uninstall the older version of Java unless your institution has installed software requiring an older version of Java.

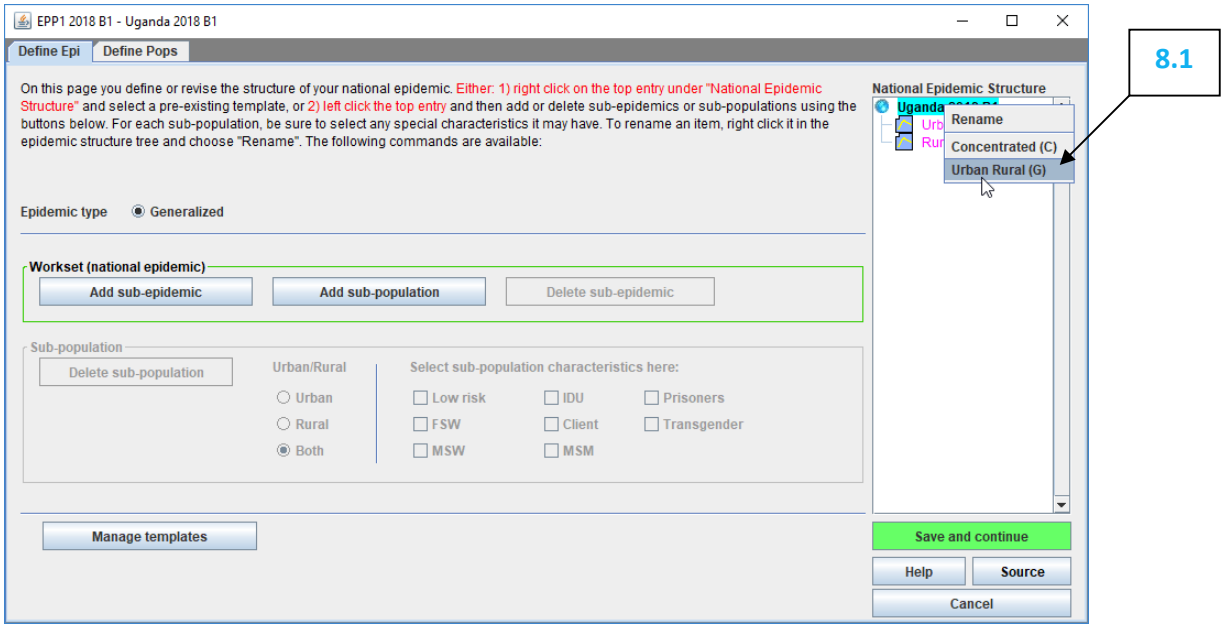
Step 8. EPP Incidence: Configuration

If EPP is your incidence fitting methodology the following steps should be taken to update your file. The first step is to review the epidemic structure. Normally, if you are updating an existing Spectrum file, you will not need to change the epidemic structure or the sub-population characteristics. If you do change it, be sure you have both population size data and epidemiological data for any sub-populations you add.

To change the epidemic structure:

8.1 Right click on the top entry under National epidemic structure. Select the appropriate template. There are two template options: Concentrated (C) and Urban/rural (G). For most countries with generalized epidemics use the Urban/Rural template. For most other countries, use the Concentrated template. See additional information on this topic in Annex 1.

Tip: In countries with well-documented epidemics in which HIV in the general population has increased beyond 1% (such as, Russia, Ukraine, Myanmar, Thailand) but a significant portion of new infections are also occurring in key population groups, the concentrated epidemic template should continue to be used.



Alternatively, create a custom template by left clicking on the top entry and then add or delete sub-epidemics or sub-populations using the buttons to the left, as shown below. For each sub-population, be sure to select any special characteristics it may have. To rename an item, right click it in the epidemic structure tree and choose "Rename".

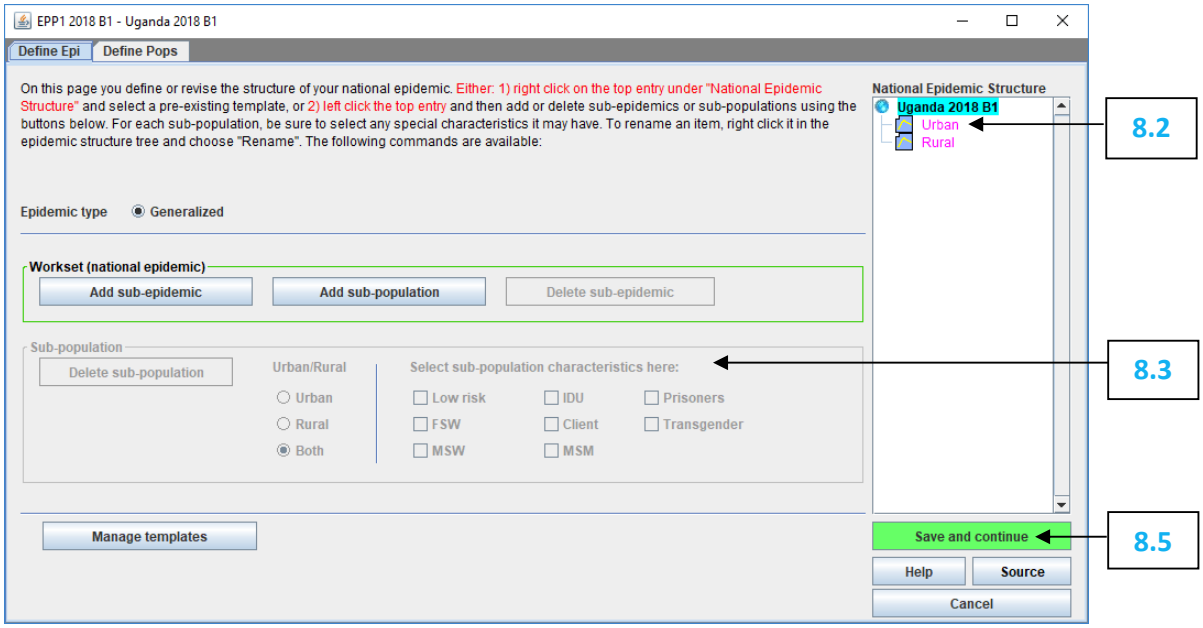
Review the sub-population characteristics:

8.2 Highlight the sub-population in the epidemic structure.

8.3 Click on the characteristic of that sub-population (for examples sex workers should be “FSW” and the “General pop women” should be “low risk”).

8.4 Repeat this for each sub-population

8.5 Click on “Save and continue”



Generalized epidemics:

For many countries with generalized epidemics, one urban and one rural sub-population are sufficient to describe the epidemic. Alternatively, you could create sub-epidemics by region if there are significant differences in regions of the country.

Producing estimates for sub-national regions other than rural and urban

In some setting it might be necessary to create estimates based on sub-national regions to provide more specific estimates. A number of options are available to help countries create sub-national estimates. Two options are described here.

Option 1. Create a national Spectrum file using sub-regions (instead of urban/rural) to fit curves and display a regional summary table within Spectrum

Option 2. Create separate regional Spectrum files

Option 1

Create an epidemic structure in the configuration page using regions. Assign the sites to each region and produce sub-epidemic curves for each region. Produce national curve in Spectrum. Use Spectrum’s Regional Table output to see regional estimates. Use this option when many surveillance sites are available in each region. This option captures the different epidemics for each region. However, the indicators are only allocated based on prevalence or incidence.

Option 2

Create one separate Spectrum file and curve fit for each region. Use the Spectrum Aggregate tool to produce a national estimate. Use this option when there are many surveillance sites in each region and you have full epidemic information for each region (program data, size estimates, non-AIDS population data). This option produces full epidemic information (all variables) for each region. However, it requires that all the demographic projection information is available by region. More information on this option is available from your UNAIDS strategic information advisor.

Option 3

A new tool has been added to Spectrum that allows you to disaggregate the estimates created through Spectrum to lower national levels. More information will be provided in the January release of the software.

Concentrated epidemics:

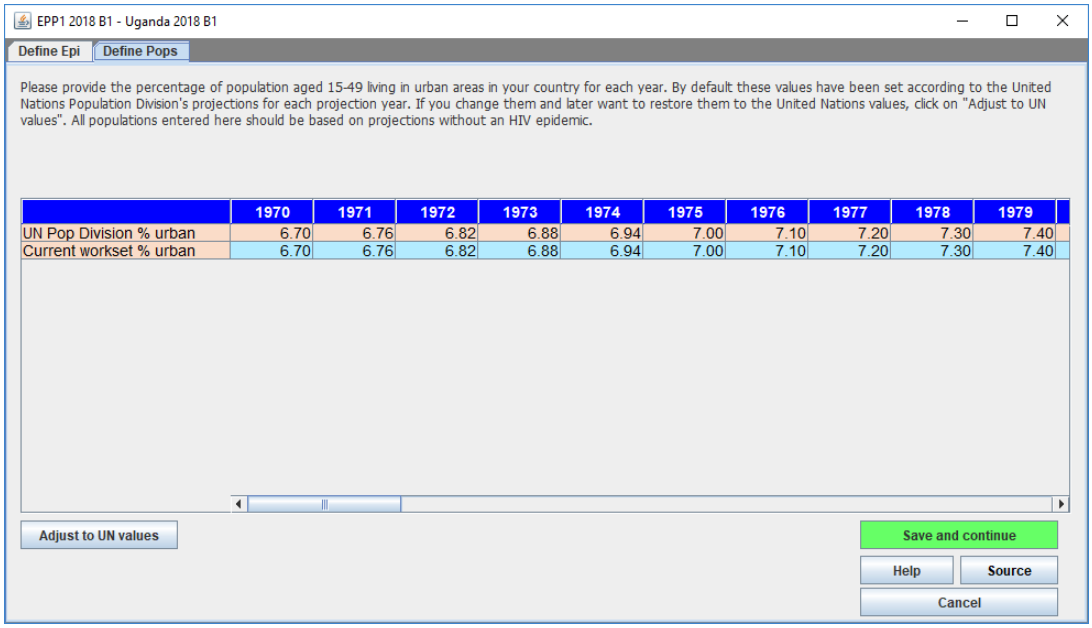
For concentrated epidemics each sub-population created will require the following data: HIV prevalence data, estimates of the number of persons in the sub-population, average time spent with the risk behavior for those sub-populations of persons with high risk behavior. Do not create sub-populations for which no data are available.

Define the populations

The **Define Pops** page allows you to define the size of each sub-population.

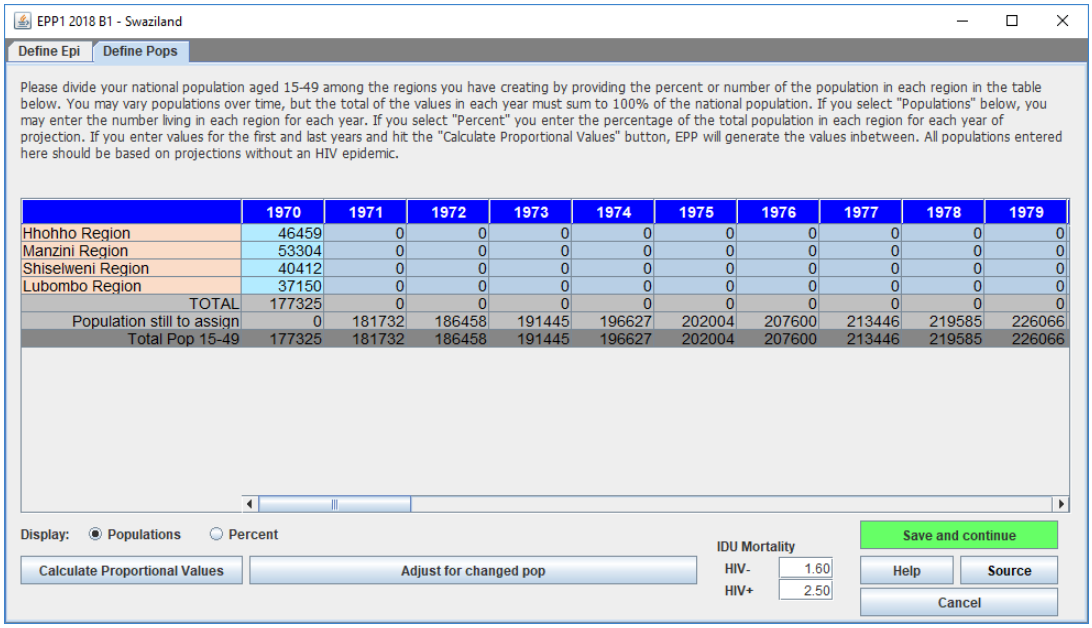
Generalized epidemic (urban/rural template):

In a generalized epidemic, when using the urban/rural structure, you define the number of the adult population in urban and rural areas by specifying the percentage of the population living in urban areas. If using the urban/rural structure, this is all you need to enter. The software already contains the United Nations Population Division values for each country and these are displayed when you first open this page. In Spectrum 2018 these were updated to the latest United Nations Population Division urbanization projections available, which you can change to by clicking on “Adjust to UN values” in the lower left-hand corner of the interface. If you wish to change the urban percentages, you can by filling in the cells marked in blue. When done, click on “Save and continue” to store your results.



Generalized epidemic (user defined regions):

If, instead, you have created your national epidemic using a set of regional sub-populations, you will need to provide the population for each of those regions. The table will appear as shown below. At the bottom of the table is the total number of people aged 15-49 years in the population (based on the UN Population Division Non-AIDS estimates). You must assign all this population to different groups within the epidemic structure.



8.6 For each region, enter the population for each year from 1970 to the end of the projection. Make sure the numbers for each year sum to the national total populations and that “Population still to assign” is zero for each column.

Tip: When you return to an existing Spectrum file and update the file with new demographic data, including overall population size, the population still to assign will no longer equal 0. To automatically adjust the population to the updated population figure select **Adjust for changed pop** and EPP will apply the same annual regional distribution to the new population.

8.7 When done entering all population data, click on “Save and continue”.

If you do not have populations for each year, but do know the percentages of the total population in each region in the starting and ending year, it is possible to have the software fill in the table for you. To do this:

8.8 Change to percentages by selecting “Percent” next to the word “Display:” at the bottom left-hand side of the page.

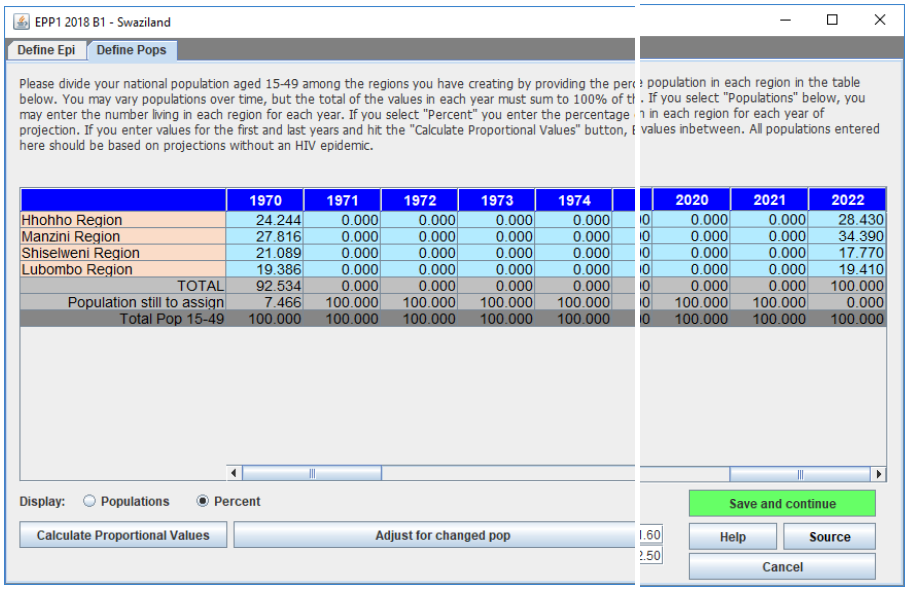
8.9 Fill in the percentages of the population in each region for the first year, 1970, in the table. Make sure that the percentages sum to 100% so that “Population still to assign” is zero.

8.10 Fill in the percentages for the final year in the final column in the table. These need not be the same percentages, as the software will assume they grow or decrease according to the values you enter. Again, make sure that the percentages sum to 100% so that “Population still to assign” is zero.

8.11 Click on the button “Calculate Proportional Values” and the software will fill in the additional entries for the entire table.

8.12 Hit “Save and continue” to store your results and return to the AIM interface.

You can also use “Calculate Proportional Values” for the actual populations (instead of the percentages) if you have the total population in each region for the first year and final year. The procedure is the same: fill in the table for the first and last years, making sure that “Population still to assign” is zero for both years. Then click on “Calculate Proportional Values”.



Concentrated epidemics:

For concentrated epidemics this page requires more detailed information supplied in two additional tabs. On the first tab the user should provide the estimates of the number of persons in each sub-population. Alternatively, the percent of the adult population in each sub-population can be provided. These values can be changed over time if data permit. This is done exactly as previously described for generalized epidemics using user-defined regions.

8.6 Enter the estimated population size or the proportion of the **adult (15-49) population** in each sub-population by year (see previous section for a description of the procedure).

Key population size estimates at increased risk to HIV (in low or concentrated epidemics)

The estimates of the size of key populations should be based on studies from the country. (Guidelines on how to estimate the sizes of most at risk populations are available at the UNAIDS website.) For clients of sex workers, consider using higher size estimates than those available from Demographic and Health Surveys or other population-based surveys. The West African Modes of Transmission project suggests that estimates of client of sex workers are higher than the estimates from these surveys, when calculated based on estimates of number of sex workers combined with data on number of clients reported by sex workers.

Consider applying the percent of the population with increased risk to HIV (for example MSM or PWID) to only the urban population if these behaviours are relatively rare in the rural populations. Similarly, consider using a smaller percent when applying percent of rural population that are sex workers and clients of sex workers.

Some estimates of population sizes by region
Table 1: Population Proportions of Key Populations in UNAIDS regions

Data are based on a literature review conducted by UNAIDS, GFATM, and WHO with assistance from other agencies. Other findings from the review were published in PLoS One (2016; 11(5): e0155150.) Data reflect population size estimates conducted between 2010 and 2015 in low and middle-income countries. The data are consistent with findings from similar exercises published in 2006 in Sexually Transmitted Infections (2006 Jun; 82(Suppl 3).)

Table 1: Population Proportions of Key Populations in UNAIDS regions, based on nationally adequate estimates only

		Asia and the Pacific	Caribbean	East and southern Africa	Eastern Europe and Central Asia	Latin America	Middle East and North Africa	West and central Africa	Western and central Europe and North America
Female sex workers	# countries	13	3	1	7	4	1	1	1
	Median (%)	0.59	3.14	1.1	0.81	0.75*	0.8*	3*	1.1*
	Range								
	25-75th percentiles	0.60-0.76	--	--	0.81-1.09		--		
Men who have sex with men	# countries	12	4	2	6	3	3	8	3
	Median (%)	1.63	2.71	1.45*	2.11	3.37	1.02	1.28	4.5*
	Range								-
	25-75th percentiles	0.26-3.10	--	--	1.75 -2.49	--	--	0.45-1.50	-
People who inject drugs	# countries	12	0	0	7	2	2	2	6
	Median (%)	0.35	-	-	2.99	0.32*	0.4*	.18*	1.5
	Range		-	-					
	25-75th percentiles	0.07-0.73	-	-	2.50-4.41	-	-		1.06-1.94
Transgender women	# countries	9	4	0	0	5	0	1	1
	Median (%)	0.24	0.36*	-	-	0.18	-	0.18*	1.31*
	Range			-	-		-		
	25-75th percentiles	0.05-0.66		-	-	0.11-0.21	-	-	1

*Not technically a median given too few data
For description of nationally adequate estimates see:
https://journals.plos.org/plosone/article/authors?id=10.1371/journal.pone.0155150

For concentrated epidemics, additional information is required on the proportion of the sub-population that is male and the average duration an individual stays in the sub-population. These are used to calculate female/male ratios and to calculate the rate of turnover in the sub-population. This is provided on the second tab of the define populations page titled "% Male and Turnover" if you are using a concentrated epidemic template.

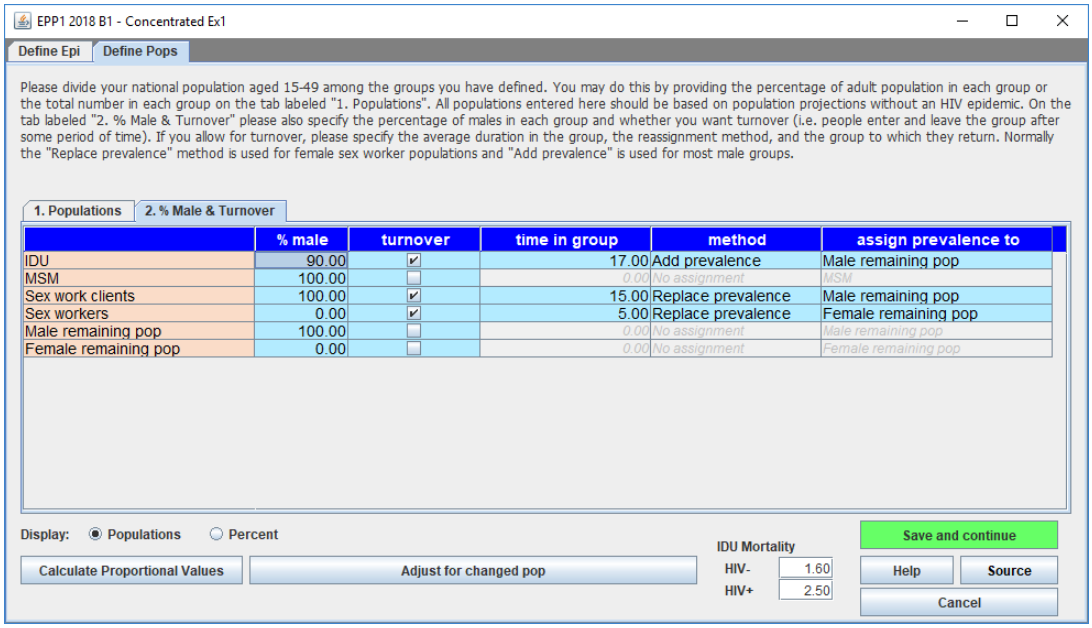
8.7 Indicate whether people are likely to move in and out of this sub-population. If you have evidence that there is a turnover in these groups (i.e. that sex workers move in and out of the sex work occupation) you should select the "on" button. Populations that are static such as the remaining populations will have no turnover.

8.8 Enter the estimated time (in years) that a person spends in that sub-population. This is used to determine the rate at which new members enter and old members leave the population. For example, if it is set to 5 years, then 1/5 of the population must change every year, i.e., 20% of older members are replaced by newer ones. Sex workers in most countries are known to have a short average duration (few years).

8.9 If turnover has been selected you will need to specify where the population will go after "turnover", or after they have left the most at-risk population. Under "assign prevalence to" select the sub-population they will enter, normally the male or female remaining population.

8.10 You also need to determine whether to add the prevalence of each sub-population to the overall prevalence or to replace it. You should choose "add prevalence" if those who are HIV positive from the former at-risk group members are added to the HIV positive members of the target population. This means they have NOT been captured in

surveillance. You will need to “replace prevalence” if some of the people who are HIV positive in the target population are assumed to come from the former at-risk populations. The remaining infections that occurred “within group” are calculated. Identify the population to which the prevalence from the most-at-risk group should be added.



Examples of adding or replacing prevalence in concentrated epidemics

Replacing prevalence: Suppose we have former sex workers who are detected in antenatal testing. If we fit the data to ANC prevalence, then some of the prevalence here is due to former sex workers and some is due to other sources of infection, e.g., husband-to-wife or boyfriend-girlfriend heterosexual transmission. Thus, the HIV infections among ex-sex workers replace some of the detected prevalence in ANC women. They do not increase the overall prevalence rate among ANC women, but they do mean that less transmission occurred through the other routes of transmission.

Adding prevalence: On the other hand, men who injected drugs while young and then stopped are unlikely to be detected since we do not have routine surveillance in male populations. We do not detect these infections in our surveillance, but the infections are definitely still out there. We need to add these undetected infections into our total prevalence picture. For former male clients or people who inject drugs then, we would want to add these additional infections into the overall prevalence in the male population.

Estimates of time in most at risk populations by region

Average duration of female sex work, by region

Region	Duration of behaviour in years
Africa	5.5 (4 studies)
Asia/Oceania	2.9 (12 studies)
North America	10.2 to 11.0 (3 studies)
Europe	8.4 to 10.0 (10 studies)
Latin America	11.2 to 12.0 (6 studies)

Average duration of injecting drug use, by region

Region	Duration of behaviour in years
Africa	5.6 (1 study)
Asia	8.7 (6 studies)
Oceania	17 (1 study)
Europe	13.9 (1 study)
North America	9.5 (1 study)
South America	21 or 19.6 (9 studies)

Source: Fazito E, Cuchi P, Mahy M, Brown T. Analysis of duration of risk behavior for key populations: a literature review Sex Transm Infec 2012;88:i24-I32. doi:10.1136/sextrans-2012-050647.

Step 9. Incidence: Entering surveillance and survey data

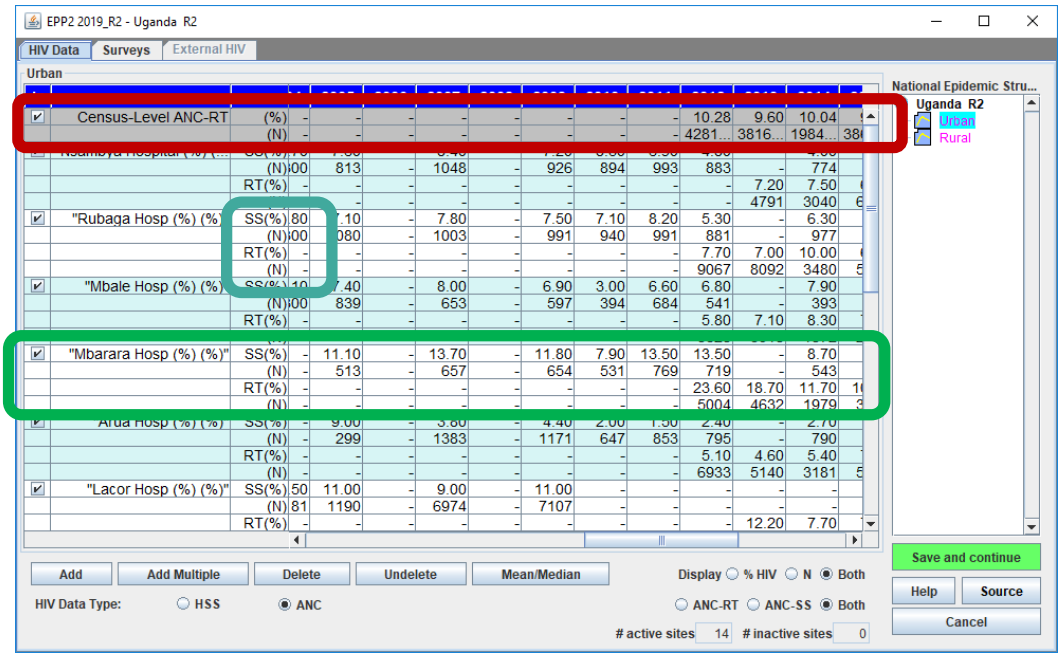
Once the epidemic structure and populations have been defined it is time to enter the available HIV prevalence and incidence data. From the AIM menu choose: Incidence and Surveillance Data (EPP). This will take you to the Surveillance Data page. There is a separate data entry spreadsheet for each sub-population.

9.1 The first step on this page is to identify what sort of data are being entered.

- The "HIV Data Type" selection radio buttons on the lower left specify whether the data presented on this page is for ANC based samples ("ANC") or from HIV sentinel surveillance ("HSS"), such as surveys among key populations. If "ANC" is selected, it becomes possible to enter both ANC sentinel surveillance (ANC-SS) data and ANC routine testing (ANC-RT) data for sites. The changes this makes to the interface are described further below. If ONLY routine data for ANC are available (e.g.., the summed value of all ANC routine testing in the country as in some Eastern European countries) then the HSS setting MUST be used with the data entered as a single site, otherwise EPP may not be able to fit the data.
- The "ANC-RT, ANC-SS, Both" selection radio buttons are on the right. If the "HIV Data Type" button on the left is set to "ANC", this controls whether ANC-RT data, ANC-SS data or both types of data are displayed in the table (see below for an example). If the "HIV Data Type" is "HSS", then these are grayed out and there will only be one type of HIV data displayed in the table.

  Any previously generated Spectrum/EPP files will have the type set to "HSS" by default upon loading. This is because those files contain no ANC-RT data, which could not be entered in previous versions. If you have no ANC-RT data to enter or do not wish to use it in the fitting, then do not change this and the data entry here will be exactly as in previous versions of EPP, i.e., for each site enter a prevalence value (%) and a sample size (N), creating as many sites as needed.

If there is ANC-RT data to be entered, then change the "HIV Data Type" to "ANC". The table on the page will now change to the following format:



If you select ANC data each site (green box in the figure) now has four lines (SS % and N, and RT % and N), instead of two (% and N). The first two lines (label “SS”) are where you can enter your ANC sentinel surveillance data (prevalence and samples size for that site). The next two lines (label “RT”) are where you enter your ANC routine testing data (prevalence and sample size) for that specific site.

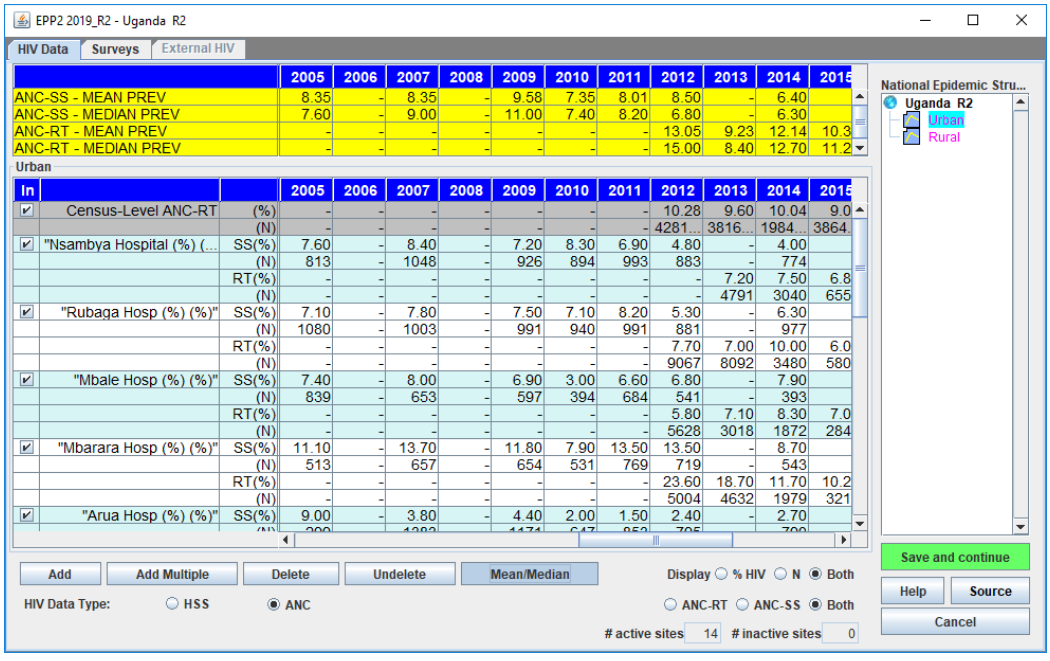
The line at the top (“Census level”) is for entry of the entire routine testing sample prevalence and total sample size for the region being modeled. This can be entered with or without site-specific ANC routine testing data. If the box in the first column is checked, the census level data will be used in the fitting. If the box is not ticked any data in the census-level row will be ignored.

The figure above shows that the same site can have both ANC-SS and ANC-RT data. While this example shows ANC-SS up to 2015 and ANC-RT after 2012, it is also possible for these to overlap with some years having both types of data, e.g., 2012 and 2014.

To simplify data entry or to allow the user to focus on either the ANC-SS or ANC-RT data, it is possible to change the radio buttons on the right hand side. Note that in the above figure, “Both” is selected. If instead one changes it to “ANC-RT” on the right hand side, the display will only show the ANC-RT data and hide the ANC-SS data. On the other hand, if one selects only the ANC-RT data, the interface will show only the ANC-SS data.

As before, these values can be cut and paste into the revised HIV Data Page from Excel using standard copy and paste procedures, e.g.., CTRL-C and CTRL-V.

The “Mean/Median” button at the bottom of the page controls the display of rows containing the means and the medians. If clicked once, the screen will appear as below with the means and medians (for active sites only) displayed at the top of the page. Click it again and those rows are hidden again.



NOTE: if you are using ANC routine testing (ANC-RT) data for the first time, there are many considerations to keep in mind when entering this data:

- For both ANC-RT site data and ANC census data, the denominators (N) entered should be based on the number of women attending the clinics for antenatal care. Should all women not be tested (e.g., if some women are known to be positive already and therefore are not retested), the prevalence entered should be based on the sum of women newly diagnosed and those known to be positive divided by the number of women attending for antenatal care.
- It is possible to enter ANC-SS, ANC-RT or both ANC-SS and ANC-RT for any given site in any year. If there is overlap, it will be useful for establishing the relationship between ANC-RT and ANC-SS in the fitting.
- It is important to remember that in the first few years, the number of routine testing samples may be expanding quickly as testing is scaled up and the system expands to reach women in areas not previously covered by testing. The quality of the data may also be improving as the reporting system is strengthening. These factors may influence the prevalence measured, e.g., as the system expands into lower prevalence areas or the testing algorithms improve to better exclude false positives. To best inform the fit, it is important not to enter trends for this data into EPP until the routine testing system has stabilized and sample sizes are fairly consistent from year to year. Using data during the rapid scale-up period may produce spurious trends in the prevalence data. See the ANC testing review page under Program data to check this.
- In assessing the quality of data and whether or not to use it in fitting, it is also important to review: any data quality assessments of the ANC-RT in the last few years, weaknesses in test results (e.g., false positives), the testing algorithm and how it may have changed in recent years, whether the reporting is timely and complete, whether there have been testing stock-outs that may have led to incomplete testing or preferential testing of higher risk women, refusal rates and proportions of attendees not tested for any reason, and the timing of testing (ideally results used in this analysis should be from the first ANC visit only).

The specific steps for entering surveillance and survey data are:

9.1 Count the number of sites with data for the sub-population. Add rows on the data entry page by clicking on “Add sites” so that there is one set of rows per site. (For each site there is a row for the prevalence and a row for the sample size.) You can also add many sites at a time using “Add Multiple” and entering the number of sites to be added.

9.2 Enter the surveillance data: If the data are already available in a spreadsheet format it is easy to copy and paste the data into the worksheet. Copy and paste the site names into the far-left column. Copy and paste the data into the page for that sub-population (e.g. for urban sites or for sex workers). When pasting the data, be sure that the years align correctly.

9.3 Press “Save and continue”. If you forget this step you will lose the data that you have pasted into the page! Enter the data for all of the remaining sub-populations using the same steps as above. After you have saved the data for the last sub-population, you will be automatically taken to the Surveys tab.

Tip: If the sample sizes for each site are not available change the “Display” variable to be “% HIV”. This will allow you to copy and paste just the prevalence information by site into the worksheet. A default size of 300 will be assigned to each site in this case.

Tip: Prevalence estimates should be entered as whole numbers not as percentages (e.g., a prevalence of 12% should be entered as 12, not as 0.12).

Tip: Be sure the boxes on the left corner are ticked. If they are not ticked the site will not be included in the fitting of the model.

Tip: if you do not enter sample sizes, you will receive a message when you click “Save and continue” that will inform you that all samples sizes are being set to a default of 300.

Tip: If the prevalence for a site is 0% and this is an actual measured value (not one created to anchor the early prevalence), then leave it in the data set along with its sample size.

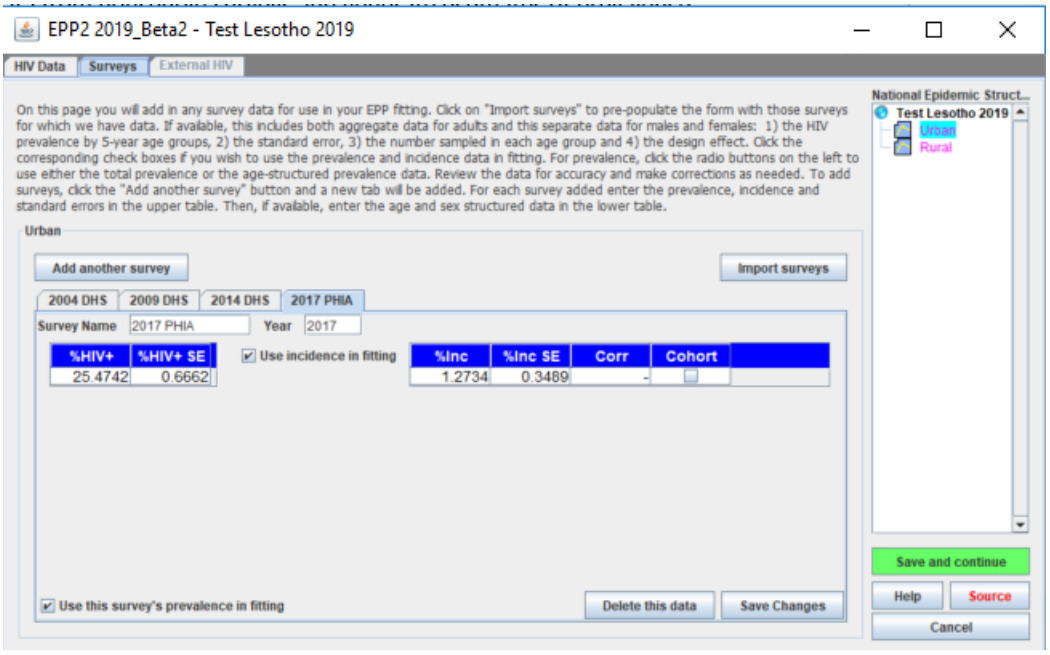
Tip: if you get a warning that the prevalence is too low for the sample size, you have entered a prevalence value that could not be determined from a set of measurements with the sample size you provided. Please use a larger sample size that reflects the actual origin of the prevalence value. For example, one could not determine a prevalence of 0.5% with a sample of 100 as this would imply that only one-half a person was living with HIV.

9.4 **Enter survey data for prevalence and incidence.** If your country has collected HIV prevalence and/or incidence in a national population-based survey or incidence through incidence assays or cohort studies, you can add those data on the Surveys page to inform your curve. In the current version of EPP prevalence and incidence data, if available, are entered on separate tabs. Most surveys will be automatically filled in by selecting the “Import surveys” button. If you do not have a standardized survey, or if the survey is not available to the general public you might need to enter these data by clicking on “Add another survey”.

If the same survey measures both prevalence and incidence, enter the values on the same line and provide the correlation between the prevalence and incidence estimates.

Prevalence and incidence estimates collected from the same survey are correlated because (1) the formula for estimating incidence from recent infection relies on prevalence as one of the inputs, and (2) correlation may arise from the clustered sampling structure of the household survey. The incidence calculator available at https://incidence.shinyapps.io/incidence_calculator/ provides a tool to input summary data from household surveys and generate estimates of prevalence, incidence and the correlation. If it is not possible to generate an estimate of the correlation to input to EPP, leave the **Corr** field empty, and EPP will supply an estimate for the correlation under the assumption that the prevalence and proportion recent are uncorrelated, as would be the case for data generated from simple random sampling. If the incidence estimate arises from a prospective cohort and the **Corr** field is blank, the assumed correlation is 0.

If the survey collects only incidence or prevalence, enter the measured value and the standard error. If the incidence comes from a prospective cohort instead of a recent infection testing algorithm ("incidence assay") in a cross-sectional survey, check the box in the final column. In this case the input year should correspond to the year of the baseline survey for the cohort measure.

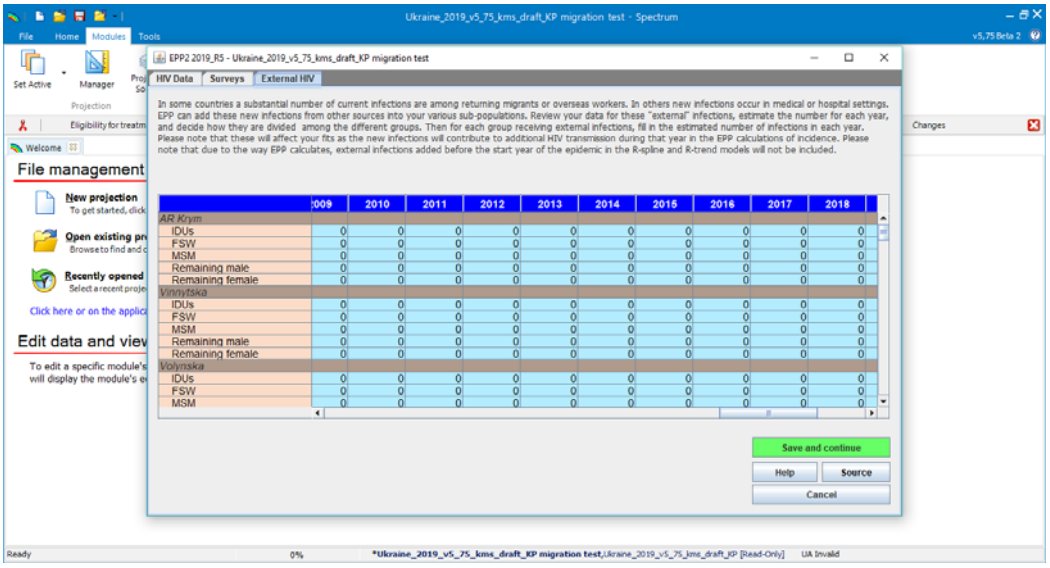


If you do not wish to use the incidence or prevalence from any particular survey, uncheck the boxes labeled “Use this survey’s prevalence in fitting” and “Use incidence in fitting”.

If your country does not have HIV prevalence or incidence data that is representative of the population being modeled, just do not add any surveys for that population.

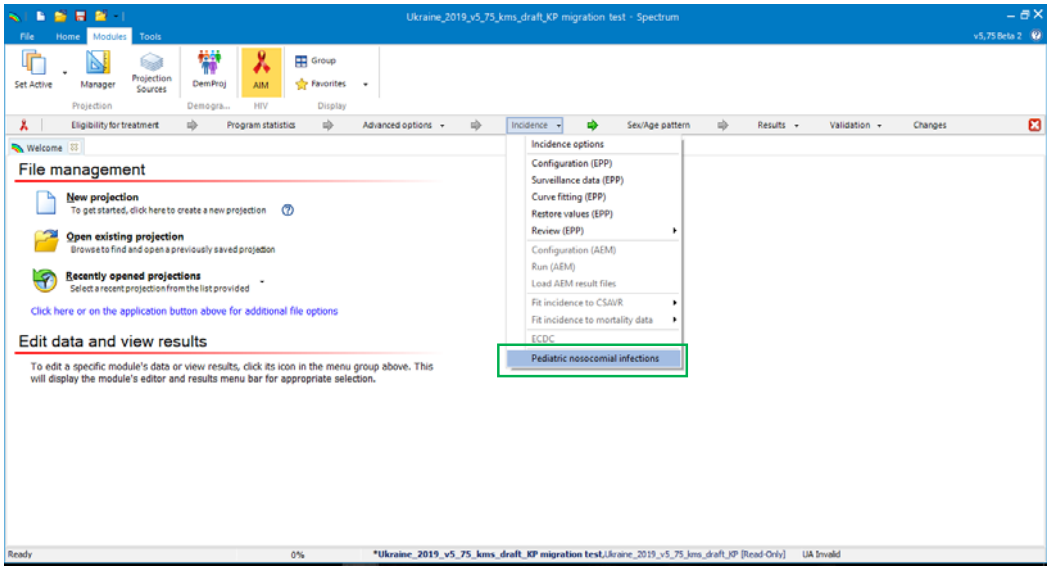
External HIV

HIV infections among people who migrate into a population are common in some settings. For example, in some regions it is common for women and men to travel to neighboring countries to participate in sex work. Some will return home having contracted HIV while abroad. If such data are available, by subpopulation, this window provides a way in which to account for these infections contracted abroad. See text in the window for more information.



Nosocomial paediatric infections

In countries where nosocomial or iatrogenic outbreak transmission of HIV to children has occurred, this window allows for paediatric infections to be added to the paediatric HIV burden, which are added to those estimated via mother to child transmission. Example: there are reports of “shot doctors” giving injections with contaminated syringes to entire villages, transmitting HIV and other bloodborne pathogens to a large number of people.



Step 10. Incidence: Curve fitting

On this page the data entered in the previous pages are used to create an HIV epidemic curve and to analyze the uncertainty around that curve. There are four models that can be used for the curve fitting:

- R-Hybrid: This will be the best model for most geographic areas and includes a more structured model from the start of the epidemic until the early 2000s when data are sparse, and then allows the rate of infection to fluctuate as increasing data are available from 2005 or so until recent years.
- R-Spline: This model allows considerable fluctuation but forces the recent prevalence to be flat.
- R-Trend: This model is useful for geographic areas with many years (8+) of surveillance data and many (7+) surveillance sites.
- EPP Classic. This model should be used for geographic areas with few data points.

Within a country, if there are areas with five or more years of surveillance data (high-data-quality), and other areas with less than five years of surveillance data (low-data-quality), then we recommend running a hierarchical model to help inform the low data quality area to improve the accuracy. See Annex 3.

10.1 Select the model you wish to use in the upper left portion of the screen, using the decision tree in Figure 1 to help you select the correct model.

10.2 If you are running the model as an exercise, click the "Training" button under "Purpose of run" a smaller number of curves will be calculated (400). If you are running the model as your final country estimation, click "For national projection" under "Purpose of run" which will increase the number of curves to 1,900 for R-Trend and R-Spline and 1000 for R-Hybrid. This number of curves will take much longer to run. To interpret any results this should be run as a "National projection"; training fits may fluctuate greatly and may not yet have settled into the best fit to available data.

10.3 To produce the HIV incidence curve, click the green 'Fit' button. This will fit a curve for the sub-population selected. To run the curves for all sub-populations together, click 'Fit all' *after* selecting each sub-population in the list of sub-populations on the right and choosing the model to be used for each one.

10.4 Review the curve. The median curve will be shown as a red line and the 95% confidence intervals will be shown as blue dashed lines. Make sure the start year of the epidemic reflects the best understanding of the HIV epidemic in your country. This is especially important if you are using EPP classic or R-Trend.

Note: If ANC-routine testing data are entered, it will appear on the Project Page as purple sites, while the ANC-SS data will appear in green. The ANC census data will show up as a dark purple series. After selecting the "Fit" or "Fit All" buttons, the ANC-RT data will be used in the fitting. The ANC-RT data will also appear on the Fitting Results page, as a series of connected data points, if you have chosen to display "Surveillance data":

10.5 If you are satisfied with the fit choose "Save and continue" and move on to fitting a curve for the next sub-population. If you used 'Fit all', you may wish to click 'Save all' once all the fits are complete and EPP will step through the fitted projections, saving each one as it goes. Alternatively, you can click 'Save and continue' for each one, but be sure to do so for all fitted projections or you may lose some of your fits.

10.6 If you are not satisfied with the curve you can use the model parameters tab in the lower left of the interface to constrain the curves (see the box titled "**Setting restrictions on prevalence curves**"). For example, if there is little data for early in the epidemic, the model will often allow the curves to grow very quickly at the start of the epidemic. This can be constrained by limiting the prevalence in 1980 to <1% (or some appropriate value).

Setting restrictions on prevalence curves

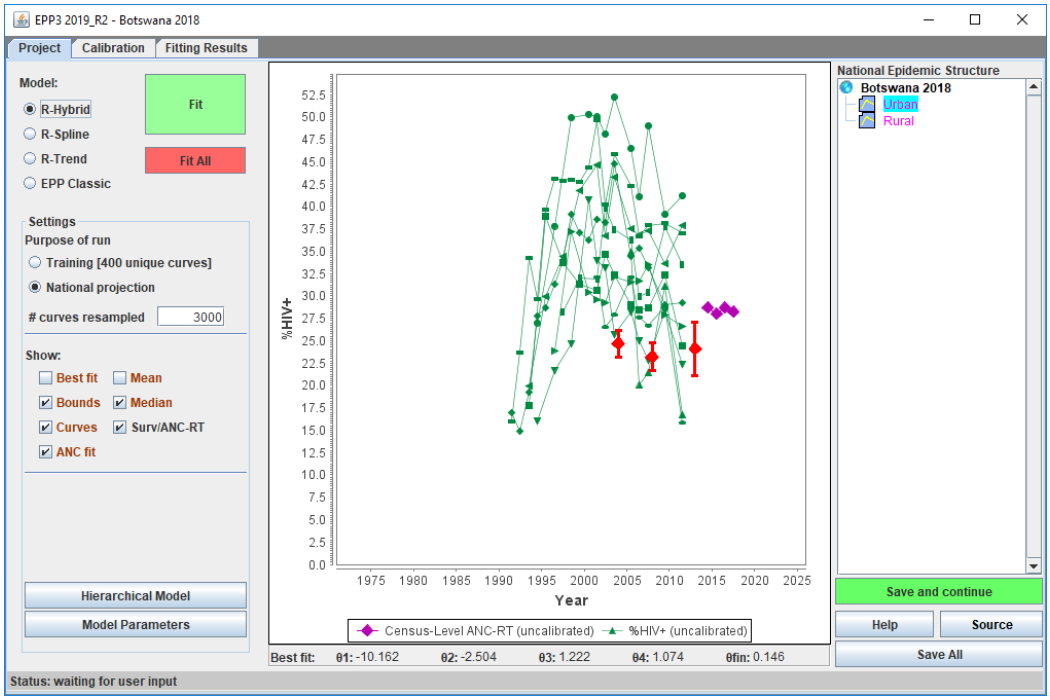
In some instances, where there is limited data, the models will find curves that are not realistic given what is known about the epidemic in your country. If the model produces curves that are not realistic, constraints should be placed on the curves using the **Model parameters** tab. Under this tab, you can: a) alter the range of possible start years to be more realistic for your country; and 2) apply conditions on prevalence that allow you to eliminate epidemiologically unrealistic sets of curves. These constraints on start years and prevalence should be used sparingly and with careful consideration of the following guidance:

1. **Before making prevalence conditions make sure the start year covers the full range of possible start years** (a range of about 15-20 years). Normally, they should start up to 5 years before the first detection of local transmission of HIV or AIDS in your country and run until about 5 years after the first non-zero data point. This will give the models the flexibility they need to consider all possibilities. NOTE: this applies to R-Trend and EPP Classic, but does not apply to R-Hybrid and R-Spline where the start year is already set in a country-specific way.
2. **Also before applying any prevalence conditions run the model without any constraints.** Then carefully examine the results to determine if there are curves which are absolutely outside the realm of possibilities given your data.
3. **Limit the number of prevalence conditions to the minimum number needed** to eliminate unrealistic curves. If you apply too many constraints you may eliminate curves that are legitimate fits to the data given its statistical uncertainties.
4. **Do not set lower constraints and higher constraints in the same year.** This will artificially restrict the uncertainty in your curves and they will not reflect the true uncertainty in your data.
5. **Avoid setting restraints close to years in which data are available** (within 3-5 years) if possible. If you must apply them in the available data range use them to reflect knowledge of allowable prevalence in the early stages of the epidemic when data was less available or to eliminate unrealistically high curves, e.g., 80-90% prevalence or 5 to 10 times the peak prevalence in the EPP fit during the data years.
6. **Look at the resulting fit (red line with crosses) relative to the data in terms of deciding if the fit is reasonable** and not necessarily the full range of possible curves (gray) some of which may be very high or low in future years. These high or low future values may reflect the true uncertainty in your epidemic's future when data is sparse.

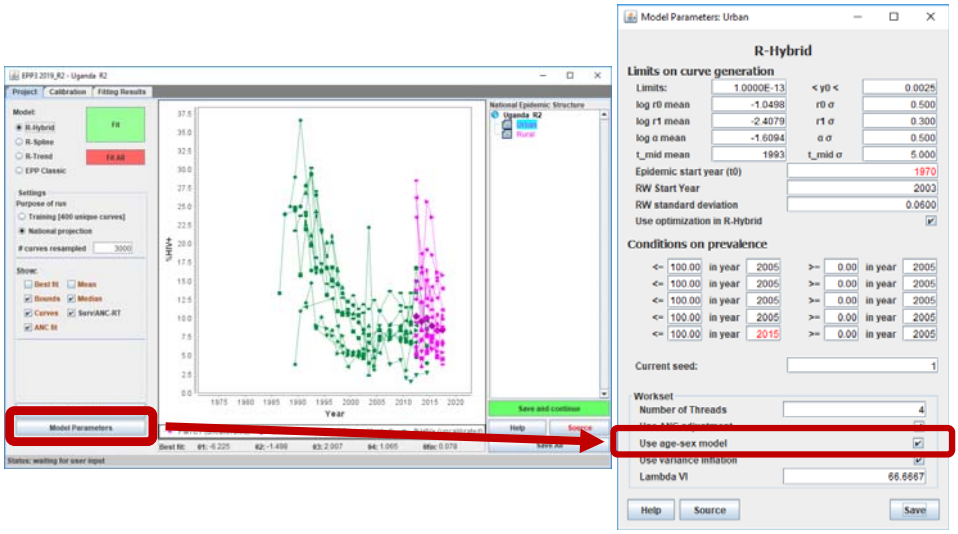
10.1

10.2

10.6



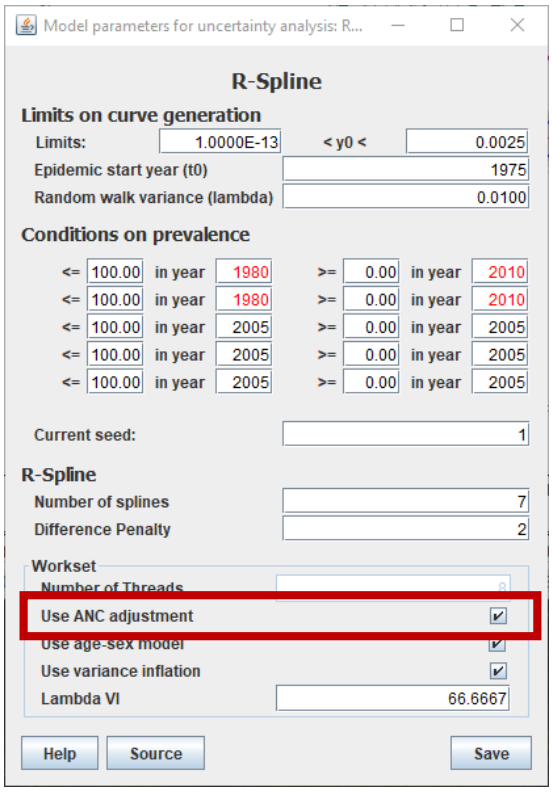
For generalized epidemic countries which have used the Urban/Rural template or are using the same sub-national structure as in the previous round of projections, an age-structured version of EPP is now available. This takes the age-sex structure from Spectrum and applies it in the EPP calculations to produce calculations aligned with the age-sex structure of the country.



The user controls the use of the age-structured model by clicking on the “Model Parameters” button on the Project Page, and then checking the box near the bottom of the panel labeled “Use age-sex model”. If the current EPP workset is not a generalized epidemic or not based on the Urban/Rural template or an existing sub-national region, this button will be grayed out and the age-sex structured model will not be available. If this checkbox is selected, then an age-sex-structured version of the R-Hybrid, R-Spline or R-Trend models is fit. By default, if R-Hybrid is selected the age-sex structured model will be used, but it must be explicitly selected for the other two models.

In reviewing ANC data for many countries with generalized epidemics, the UNAIDS Reference Group identified a number of issues, including changing age structures, sub-fertility in HIV-positive women, and varying ART levels, that changed the biases in using ANC women as a proxy for the population as a whole over time. If not using the age-sex structured model, which adjusts for these factors automatically, EPP has an adjustment for these changes in countries with generalized epidemics. This will result in some small changes in the fitted curve, generally making them flatter and with somewhat slower incidence declines. If the impact of these adjustments is not acceptable, they can be turned off by unchecking the box at the bottom of the 'Model Parameters' page labeled "Use ANC adjustment" (see figure below) and refitting. If this entry is greyed out, then the country was not eligible for this adjustment and its fits are not affected by it.

If using the age-sex model, then the "Use ANC adjustment" checkbox on the Model Parameters panel determines if prevalence among pregnant women from the model is used in fitting against ANC sources of data, while national adult prevalence from the model is fit against national survey results. If you turn it off, then all sources of data will be fit against national HIV prevalence.



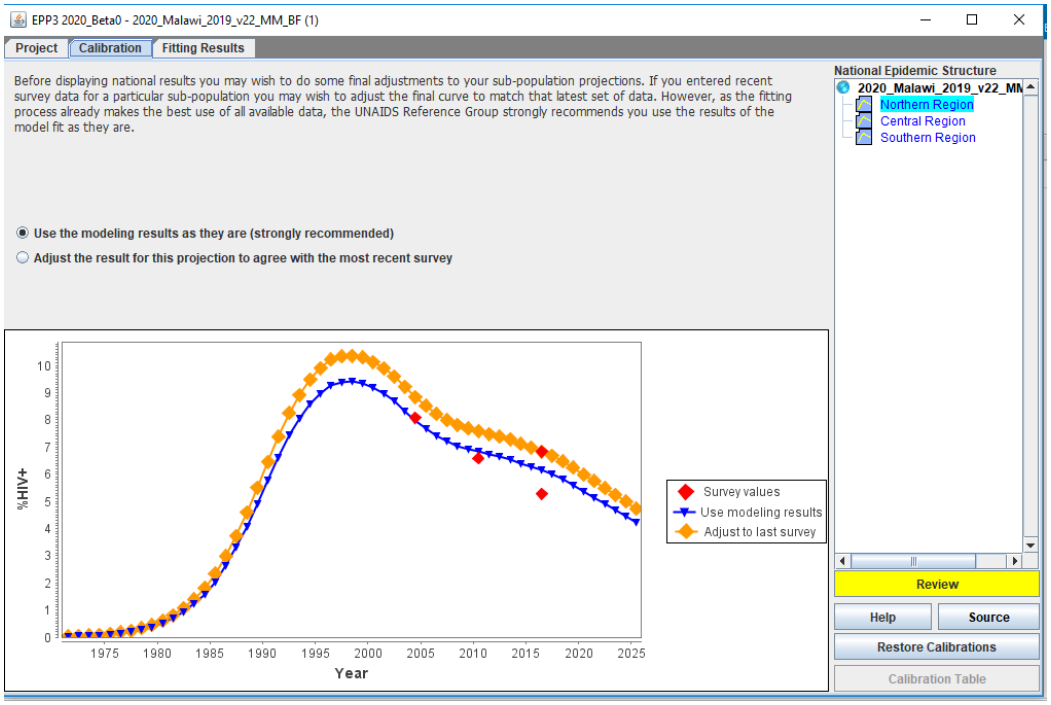
It is important to know that some calibration is normally done during the fitting procedure. If you have entered surveys in either a generalized or concentrated epidemic, they are used in the fitting calculation and the result will normally be a fit which is a good balance between the various surveys entered and the observed surveillance data. It should be noted that this curve will not always pass exactly through the survey point(s) itself – this is normal, do not be concerned by it. You can change it on the next page, the Calibration Page.

On the Calibration tab you can calibrate to the survey specifically or for concentrated epidemic countries you can calibrate to other data sources.

Generalized epidemics:

On this page you can adjust the curves based on the most recent national population based survey data that you have entered.

If you have not had a national population based survey, then leave the default setting on “Use the modeling results as they are”. This has already shifted urban and rural prevalence based on regional averages from numerous countries with surveys.



10.7

10.8

Concentrated epidemics:

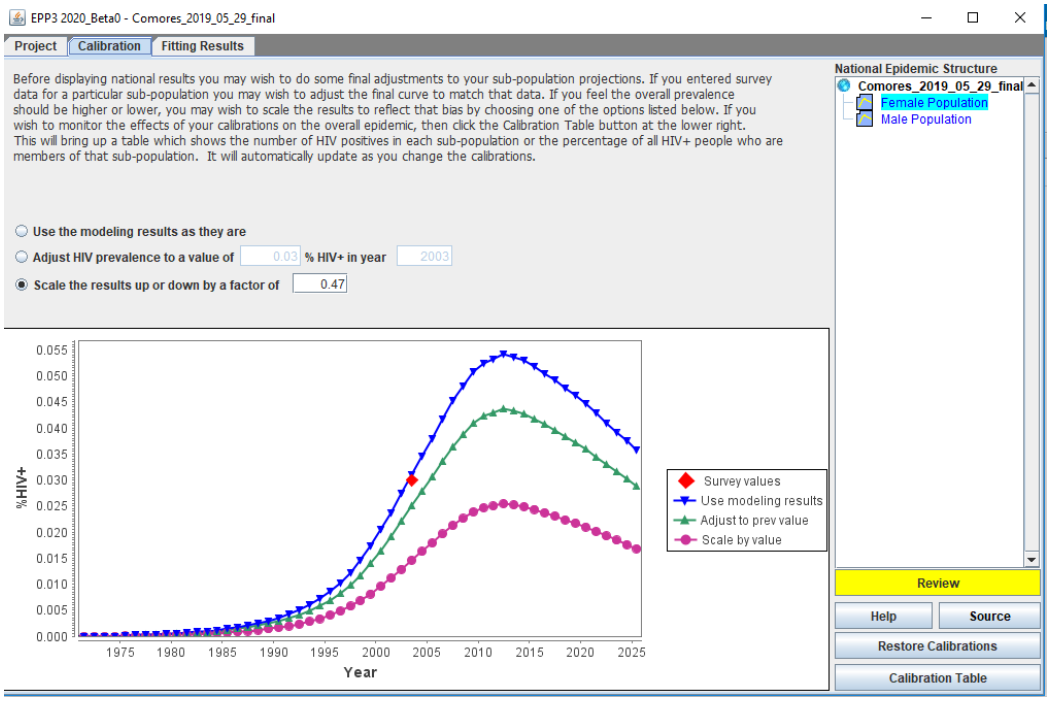
The calibration page gives you the option of specifying either an expected prevalence in each year or a scale factor for each individual sub-population.

To use the calibration section:

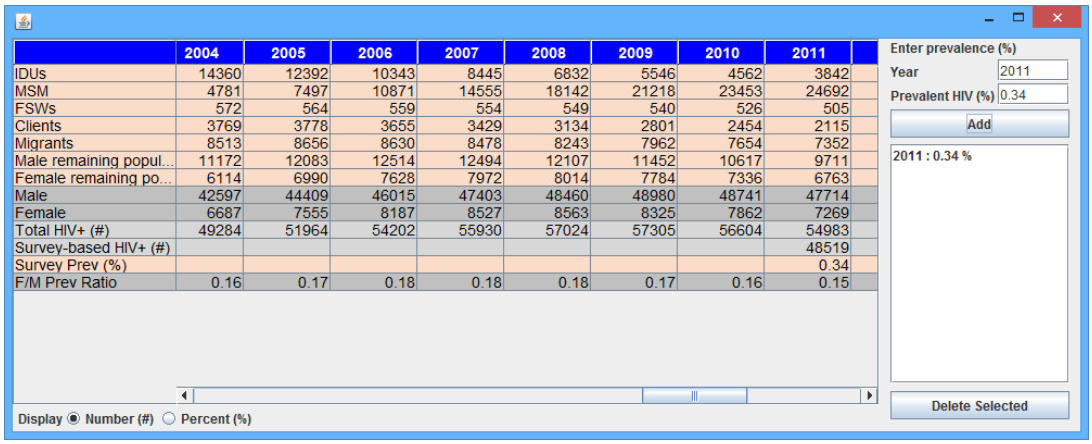
10.7 Select the sub-population you wish to scale in the list of sub-populations shown

10.8 Select one of the options

- *Use the modeling results are they are.* This option keeps the calibration that was established during the fitting.
- *Adjust HIV prevalence to a user specified value.* This calibrates the best fit curve by multiplying all prevalence values by a constant number which ensures that the adjusted best fit curve goes through a user-specified prevalence value in a user-specified year. This might be the value from a more representative sample of the specific surveillance population, e.g., an IBBS study of female sex workers.
- *Scale the results up and down by a factor.* Choosing this option scales all prevalence by the user-provided provided number. For example, if you enter 0.5, it gives a prevalence curve with each value cut in half.



For concentrated epidemics, a Calibration Table is available by clicking the 'Calibration Table' button in the lower right-hand side of the Calibration page. This will bring up a table, which shows the number of people living with HIV in each of the sub-populations *with* the calibrations applied. You can also enter national estimates of prevalence among those 15 to 49 years old on the right-hand side of the page for different years and the corresponding number of people living with HIV in that year will be shown in the 3rd line from the bottom labeled 'Survey-based HIV+ (#)'. You can compare this against the numbers of people living with HIV after your calibrations are applied. The final row of the table also shows the female-to-male prevalence ratio, so you can ensure that your calibrations are producing an appropriate proportion of female and male infections that matches data on this ratio from your country. This table is dynamic, so as you change the calibrations on the Calibration page, the table will adjust.



	2004	2005	2006	2007	2008	2009	2010	2011
IDUs	14360	12392	10343	8445	6832	5546	4562	3842
MSM	4781	7497	10871	14555	18142	21218	23453	24692
FSWs	572	564	559	554	549	540	526	505
Clients	3769	3778	3655	3429	3134	2801	2454	2115
Migrants	8513	8656	8630	8478	8243	7962	7654	7352
Male remaining popul...	11172	12083	12514	12494	12107	11452	10617	9711
Female remaining po...	6114	6990	7628	7972	8014	7784	7336	6763
Male	42597	44409	46015	47403	48460	48980	48741	47714
Female	6687	7555	8187	8527	8563	8325	7862	7269
Total HIV+ (#)	49284	51964	54202	55930	57024	57305	56604	54983
Survey-based HIV+ (#)								48519
Survey Prev (%)								0.34
F/M Prev Ratio	0.16	0.17	0.18	0.18	0.18	0.17	0.16	0.15

Adjusting prevalence for the "remaining male or female populations" (low risk populations)

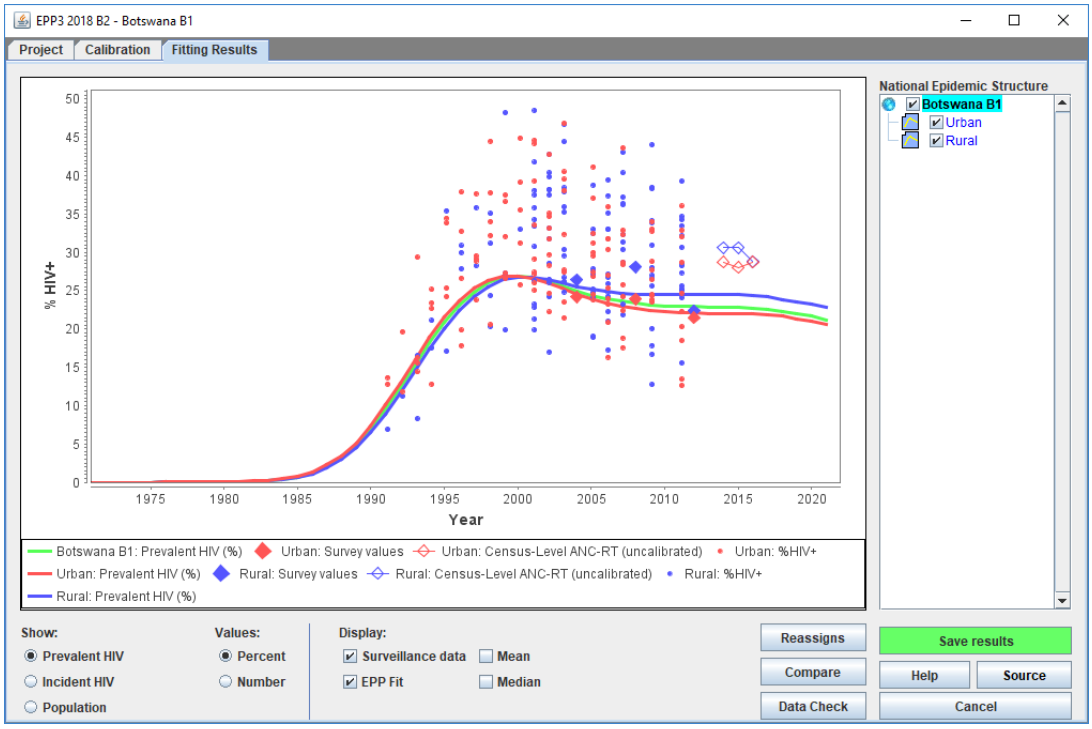
ANC prevalence can represent the remaining female population. However, when using surveillance data from ANC to describe the remaining female population the ANC estimate needs to be adjusted because women attending ANC are likely to have higher HIV prevalence because of biases in the geographic selection of antenatal clinics in the sentinel surveillance as well as a bias in the age of women attending ANC versus women in the general population. Comparing data available from ANC against HIV prevalence coming from population based surveys in a number of low-level epidemic countries (or states), show that on average, HIV prevalence among all women was 47 percent of that measured in ANC prevalence. Thus, a proposed adjustment value for women in the remaining population of 0.47 is required when assigning the ANC data to the remaining female population. The option "Scale HIV by factor of" should be chosen and 0.47should be entered into the cell.

For men a similar analysis showed that the scale of HIV prevalence in the remaining male population is approximately 56 percent of ANC prevalence. As a result, the adjustment from ANC data to men in the general population should be 0.56. (Note that these adjustments are based on a small number of countries.) If countries have data on sex ratios of HIV prevalence among the general population over time, these ratios rather than the proposed 0.56 scaling factor should be used to adjust the estimates from the remaining male population. To do this, the ANC surveillance data for the remaining male population first should be adjusted using the sex ratio data prior to fitting the incidence and prevalence curves. Then, the post-hoc calibration adjustment for females should be applied using the "Scale HIV by factor of" with 0.47.

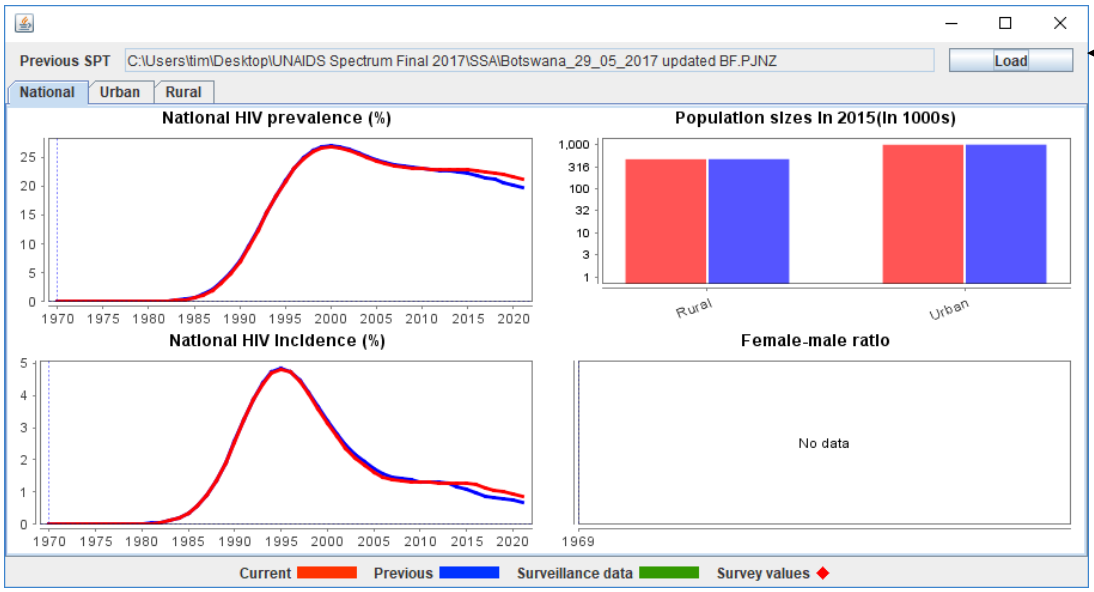
If prevalence is available from a population-based survey (e.g. India, Cambodia, Dominican Republic, Senegal, or Mali) use the survey results to calibrate the general population prevalence.

Where universal PMTCT is standard practice (as in Russian Federation, Thailand, among others) it is possible to use these data to also inform the prevalence among the female remaining population. However, it is important to standardize the data coming from the PMTCT system to the age structure of the general female population. Similarly, if there are data on men from a universal service, such as mandatory military service, (which is not restricted to a specific age group and does not increase their risk to HIV) these data can also be used to inform prevalence among the male remaining population.

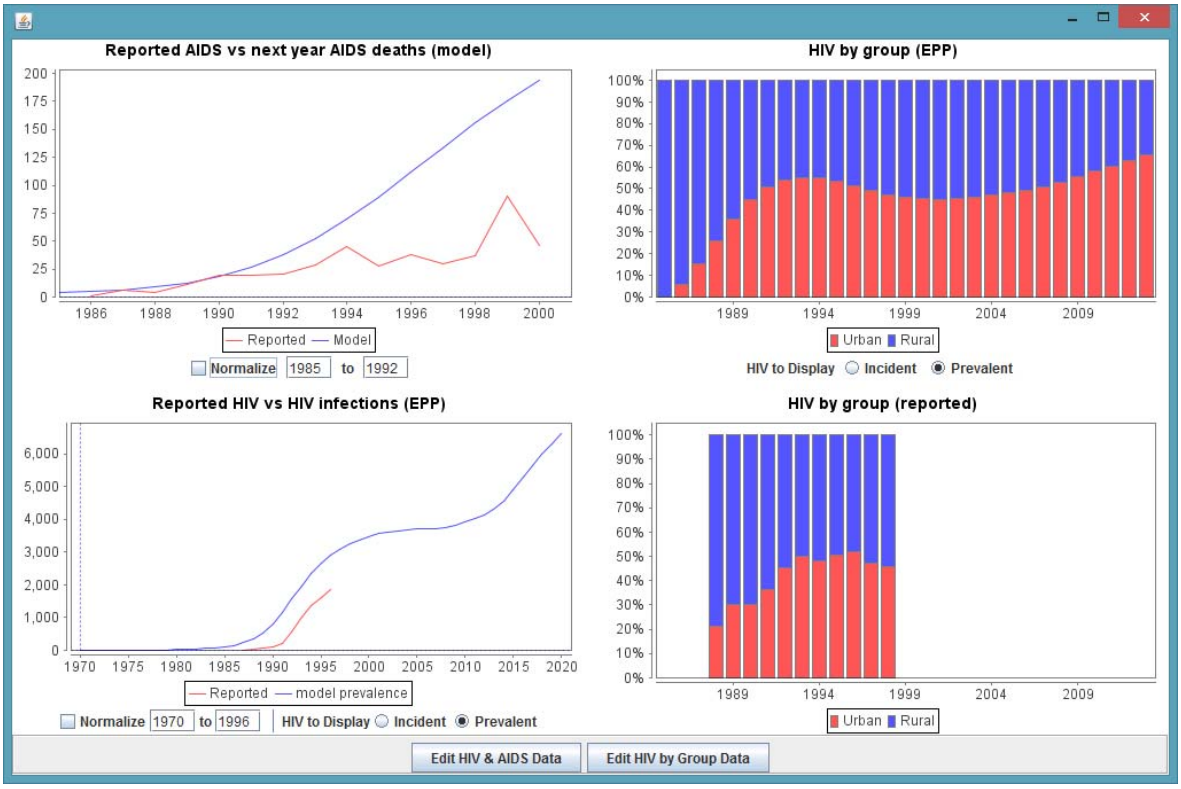
Once completed you should click on 'Save and continue' to move to the **Fitting Results** page. Here you can review the resulting prevalence trends by population type and see the national trend that is produced by combining the trends for all the sub-populations. Just select the population you want to examine from the list at the top right of the page [A].



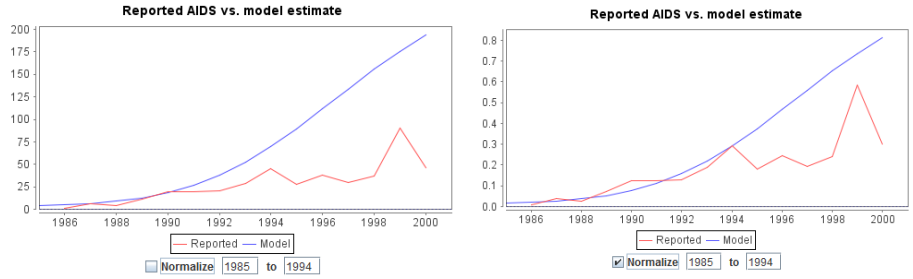
You may also compare your new results with the prevalence trends from a previous projection by clicking the 'Compare' button [B]. That will display a screen like the one shown below. You need to click the 'Load' button [A, figure on next page] and select the comparison projection's Spectrum (*.SPT) file or the previous projection file (*.PJNZ) which contains the previous projection. Then the charts will compare your new projection (red) with the previous projection (blue) for prevalence, incidence, population size and female to male ratio (for concentrated epidemics only, this will remain blank for generalized epidemics where female to male ratio is calculated within Spectrum). When you have finished viewing this page, close it by clicking the 'X' in the top right of the window.



For some countries you will also be able to check the estimated number of AIDS cases or HIV infections (prevalent or incident) from the new trend with program data on the reported number of AIDS and HIV cases. Select this option by clicking the 'Data Check' button. This will bring up the display shown.



If you enter start and end years below the graph and check the box marked "Normalize", the reported and model data for those years will be adjusted to the same scale as can be seen by comparing the graphs below.



Once you have finished viewing the results click 'Save and continue' to move to the next step.

Additional fitting tool for countries with strong vital registration systems: Fit to mortality data

For countries with strong vital registration systems, typically in low-level epidemic, and good surveillance data, it may be useful to compare, and if necessary, adjust the HIV mortality curve from AIM based on incidence derived in EPP to more closely match mortality data in the country. The Fit Mortality option at the bottom of the Incidence menu can help countries make this adjustment once the EPP curve fitting procedure is complete.

To do this fitting, you need to enter annual estimates of mortality, bounds if available, as well the percent estimate of under-reporting or misclassification by year. If estimates of under-reporting are available for only selected years, you should enter an estimate for all years where AIDS-related mortality data are available.

Once completed, click OK and then return to the Fit Mortality menu and select Fit Incidence. You can then adjust the mortality curve (and related outputs) to match country vital registration data using the Annual adjustment or Trend adjustment buttons. You may need to click these buttons several times to find a curve that provides the best fit to your data.

When you are done, click on the Close button to save and exit the tool.

Reassigns

The Reassigns window was added in 2018. It provides a means to examine the effect of Turnover (from the Configuration window) on the distribution of PLHIV to subpopulations. This is an important tool for analysing the true estimated source of HIV infections. That is, all "Remaining males" and "Remaining females" should not be assumed to have contracted HIV through ostensibly low risk heterosexual intercourse.

In the figure below, in 2013, there are 3780 PLHIV among the "Remaining male" population. In that year, 2542 former PWID living with HIV were reassigned, added, to "Remaining males" because they had spent the full time allotted, for example, 10 years, in the PWID population. It is assumed that those people who injected drugs who are still alive after 10 years will cease injecting drugs and become part of the "Remaining male" population within Spectrum. Another 1239 men in the "Remaining male" population became infected via another route, presumably heterosexually.

Similarly, female sex workers who retire from sex work after their "turnover time" are reassigned to the "Remaining female" population (502 women in 2013.) These women effectively replace women living with HIV in the "Remaining female" population who may have been identified through antenatal clinic surveys, to assure that double counting is minimized. Women infected with HIV via other routes, estimated from antenatal clinic surveys, number 1271 in the example below.

	008	2009	2010	2011	2012	2013
Remaining male						
HIV+ after reassignment	3767	3868	3906	3894	3840	3780
IDUs (Add HIV+)	2632	2699	2710	2675	2609	2542
HIV+ from within group	1135	1169	1197	1218	1231	1239
Original HIV+ in group	1135	1169	1197	1218	1231	1239
Remaining female						
HIV+ after reassignment	1632	1678	1717	1746	1765	1773
FSW (Replace HIV+)	474	505	520	522	514	502
HIV+ from within group	1159	1173	1197	1224	1250	1271
Original HIV+ in group	1632	1678	1717	1746	1765	1773

Step 11. Case surveillance and vital registration (CSAVR) fitting tool

Note: Prior to fitting incidence in CSAVR for the first time, open the Sex/Age pattern menu item and click the **Restore default value buttons** for both the Sex and Agee patterns. See Step 12 for more detailed instructions. The Sex/Age incidence pattern tab does not need to be reviewed again, unless further changes to these distributions are required. If changes are made to the Sex/Age pattern tabs and the option to include IRRs in the fitting is selected, incidence should be fit again in CSAVR.

For countries with strong vital registration and HIV case reporting systems and sparse or inconsistent surveillance data, fitting incidence curves to a combination of HIV case surveillance and vital registration data may produce more accurate outputs for monitoring the epidemic.

Possible CSAVR inputs are:

- **The number of new HIV diagnoses (i.e., the first report of infection to the surveillance system, whether HIV or AIDS) among adults ages 15 years and older (disaggregated by age and sex where available);**
- **The number of estimated AIDS-related deaths disaggregated by age and sex based on data from vital registration systems for adults ages 15 years and older.** AIDS-related deaths should be adjusted for incomplete reporting and misclassification in cause of death (e.g., garbage codes). Country specific estimates of AIDS-related deaths disaggregated by age and sex and based on raw vital registration data since 1990 are available in a standard .csv Excel file from UNAIDS or from IHME (http://ghdx.healthdata.org/gbd-results-tool)

To access the CSAVR fitting tool, you first select **Incidence** options from the **Incidence** menu. Next, select **CSAVR** from the drop-down incidence fitting methodology menu and then the **Fit Incidence to CSAVR** data option.

The first step in fitting incidence within the CSAVR tool is to select the **enter/edit data** menu item.

Next, import the new diagnoses data and age and sex specific mortality data using the button **Read data from CSV file**. Imported case surveillance data come either from the previous year's Spectrum CSAVR file or the TESSy data if countries (primarily in Europe) report to this system. Estimates of AIDS-related mortality by age and sex are abstracted and imported from IHME 2019 Global Burden of Disease. Caution: Reading data from the CSV file will overwrite the new diagnosis data and estimates of AIDS-related mortality data from the previous year's CSAVR data input screen. Starting in 2021, you can select if you want to import only case diagnoses

data, AIDS-related mortality estimates from the latest round of IHME, or all data. Note that when you import IHME estimates, these will be for the latest as well as the historical period.

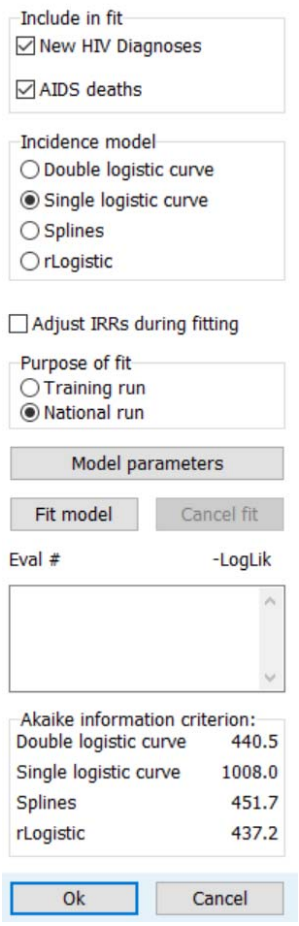
After reading in the data, enter in new diagnoses data for 2020 where available. Next, click on the **Data by sex** and **Data by sex and age** tabs to review and/or enter any further disaggregation of the new diagnoses data on the Data, Both sexes tab. Sex and/or age specific data can be entered for the years in which they are reasonably complete, even if they are not available for every year or for all diagnoses. If data are not reasonably complete or known to be biased (e.g, age data only available for women), do not enter the data.

In 2021, UNAIDS recommends that infections that are known to have occurred outside of the country but reported upon a person's arrival into the country be excluded from the reported counts. For countries using case notification data from TESSy, cases with an HIV status of "previous positive" have been removed from the new diagnoses in the .csv files.

When entering or revising new diagnoses, please include as needed any additional diagnoses as a result of delays in notifications or missing reports from a specific region or facility. If complete diagnosis data are not available or cannot be estimated for a year, the data for that year should be left blank rather than 0. The 2021 model will assume that cells with 0s have no diagnoses or deaths.

After entering, updating and reviewing the CSAVR inputs, click **Ok**.

The second step in fitting incidence within the CSAVR tool is to select the **Fit Incidence** menu item within the **Fit Incidence to CSAVR menu.**



On this panel, first review the new HIV diagnoses and AIDS-related death data you have entered in the panel graphs. These data will be visible as red diamonds. Any outliers should be examined carefully to understand whether these reflect true changes in the data or are anomalies of the reporting or vital registration system for those years. You can click on the Model validation tab to see the HIV diagnoses and AIDS-related death data by sex. It is not possible to see these data by age group unfortunately.

Next, select the data (new HIV diagnoses and AIDS deaths) that will be included in the fitting process in the left-hand panel.

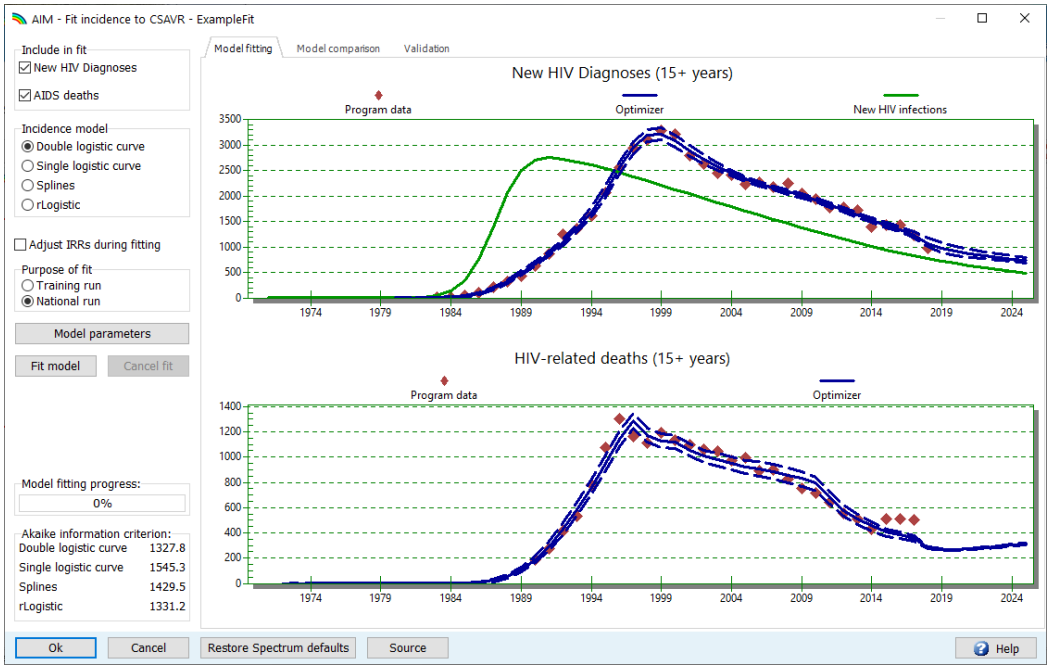
It is recommended that the model first be run using all available data that are of high quality. Other fits using all data could be done if the initial fit is not satisfactory.

Next, select the type of fit to be used:

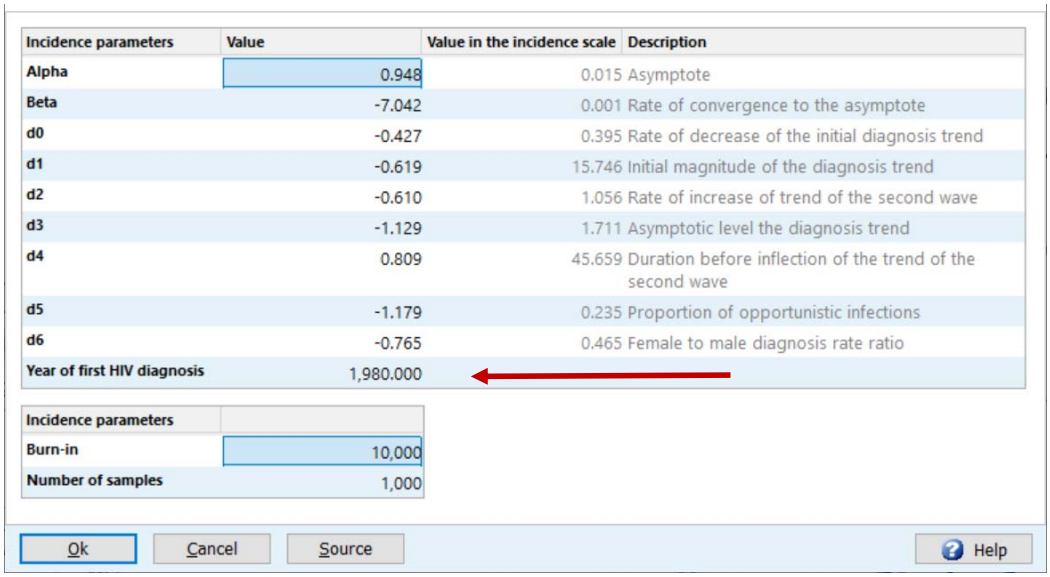
- Double logistic curve
- Single logistic curve
- Splines
- rLogistic

The type of curve fitting approach used will depend on the shape of expected incidence trend. For countries where there is evidence that incidence has already peaked and is now declining, the **Double Logistic fit** option should be selected. For countries where there is evidence for ongoing increases in incidence, the **Simple Logistic fit** option is more appropriate. The **Spline** and the **rLogistic** options are for epidemic patterns that are too complex to describe incidence with either the simple or double logistics curves. The most appropriate approach to fitting the epidemic in your country is selected as the default, although you may wish to explore other approaches. If you do not have accurate data on the number of people on treatment over time, UNAIDS does not recommend the use of rLogistic.

Once the type of fit has been selected, next choose the fitting method – **training run** or **national run**. The Training run option will give you a similar result to the national run option but the time for the model to converge will be shorter in the training run because uncertainty around incidence estimates are only generated in the national run. Training runs can be done to explore initial fits to different data sources included in the fit or the type of fitting method. *However, your file will not be final until you fit incidence using the National Run to generate uncertainty around the fits (the dashed blue lines).*



In general, clicking on the model parameters button and changing the incidence parameters should not be required. However, if CSAVR results of the proportion who know their HIV status are being used from the model, the correct year of the first HIV diagnoses should be specified in this box. The year of first HIV diagnoses is defined as the period when diagnostic testing was first made available to the public on a routine basis. Once this screen has been reviewed, click “Ok” to exit.



Incidence parameters	Value	Value in the incidence scale	Description
Alpha	0.948	0.015	Asymptote
Beta	-7.042	0.001	Rate of convergence to the asymptote
d0	-0.427	0.395	Rate of decrease of the initial diagnosis trend
d1	-0.619	15.746	Initial magnitude of the diagnosis trend
d2	-0.610	1.056	Rate of increase of trend of the second wave
d3	-1.129	1.711	Asymptotic level the diagnosis trend
d4	0.809	45.659	Duration before inflection of the trend of the second wave
d5	-1.179	0.235	Proportion of opportunistic infections
d6	-0.765	0.465	Female to male diagnosis rate ratio
Year of first HIV diagnosis	1,980.000		

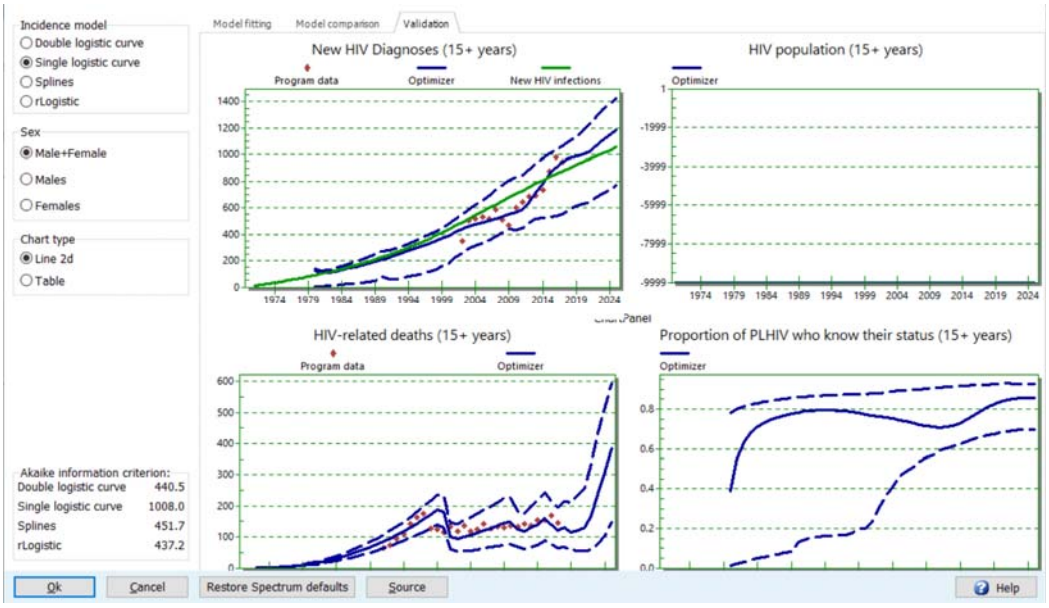
Incidence parameters	
Burn-in	10,000
Number of samples	1,000

Finally, the **Fit incidence** button can be clicked. The blue lines will show the model's best fit to the CSAVR programme data.

The model fitting progress bar will show 100% when the model fitting is complete. Below that, the Akaike information criterion (AIC) value will be provided. This value can be used to compare and select the best model. Typically, the best model will have the lowest value. AIC values from different types of fit (e.g., single and double logistic) can only be compared when fitting to the same data (e.g, new HIV diagnoses and AIDS deaths). Also, Model AIC values that are within 10 points of each other suggest equally plausible fits. If the AIC values are similar, countries should select the model that best appears to represent their understanding of the epidemic in their setting.

Starting in 2021, results from different incidence models are available for comparison on the Model Comparison tab. Indicators that can be displayed include new HIV diagnoses, HIV related deaths, Knowledge of Status, Mean CD4 count at diagnosis, estimates of the number of adults living with HIV and the number of new HIV infections among adults.

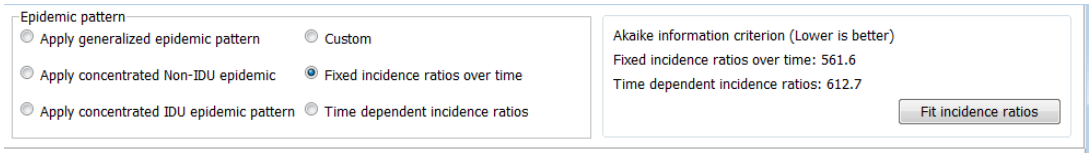
On the Validation tab, results are available by sex for selected key indicators.



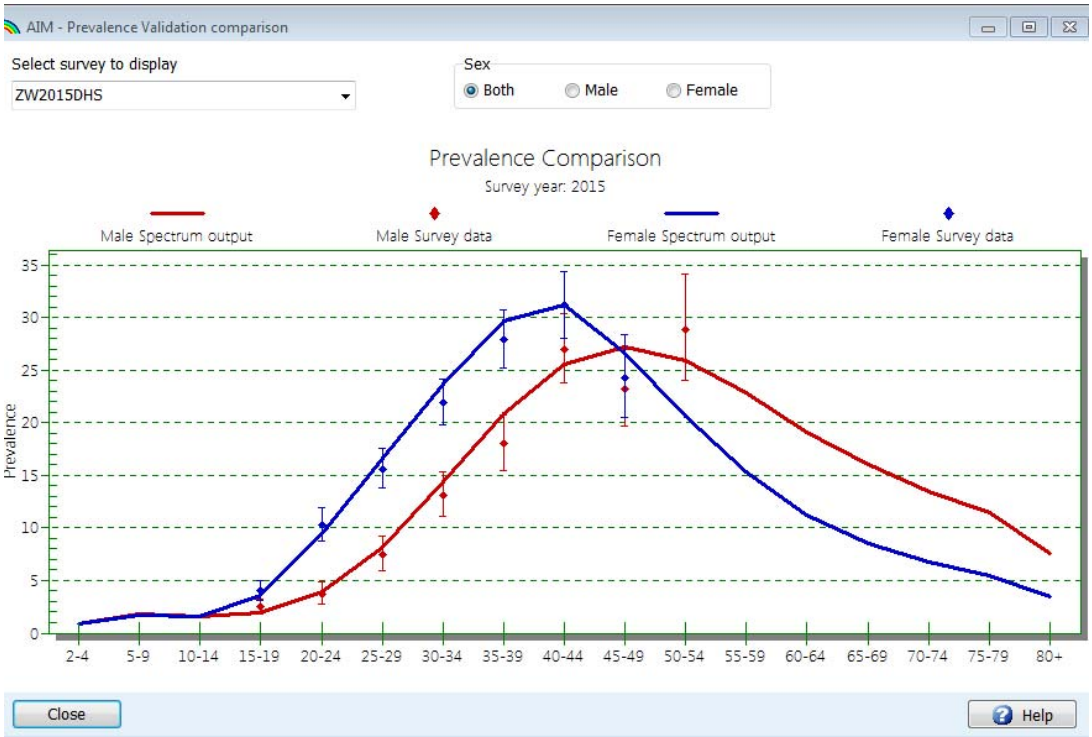
If the results do not fit well to the case diagnoses and death data, you may want to **Adjust IRRs** during the fit**.**

Step 12. Set the pattern of incidence by sex and age

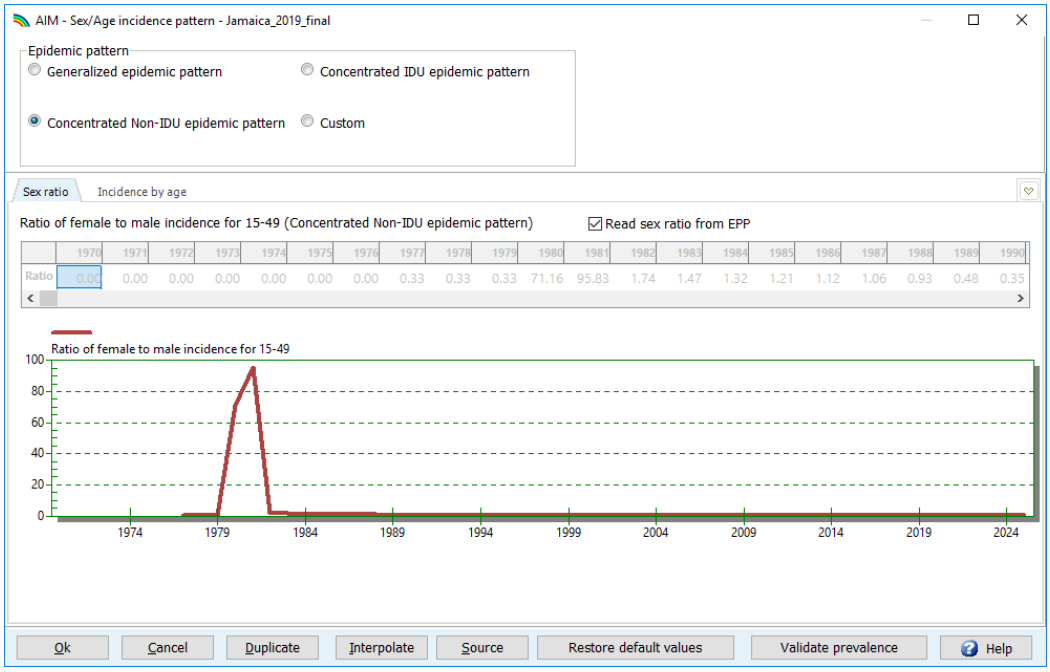
The sex/age pattern tab provides information on the assumed sex and age distribution of incidence. For generalized epidemics a default pattern will be automatically used that describes the general pattern of an increasing proportion of female infections reaching a ratio of **1.38** ten years after the start of the epidemic. If a country has a national household survey the user can improve the age and sex distribution based on available household survey results. To apply this option, the user needs to first reset to default values. Then select 'Fixed incidence ratios over time' and then select **Fit Incidence Ratios**. The model requires a few minutes to run and will produce a set of incidence rate ratios based on the prevalence in household surveys. The user can also choose Time dependent incidence ratios and determine which option has the better fit depending on which has the lower Akaike information criteria score.



The user should then select "validate prevalence" button at the bottom of the screen to ensure the resulting prevalence is reasonably close to the survey results.



You can review the sex ratio trend by select the **Sex/age pattern** menu item. It will show a screen like this:



You should examine the chart and determine if this trend is appropriate for your country. If it is not, you can enter a new pattern.

Note: For countries with concentrated epidemics the curve fitting process will produce an estimate of the sex ratio (the ratio of female prevalence to male prevalence), which is selected if the "Read sex ratio from EPP" box is ticked. If you invalidate the sex ratio from EPP by unchecking the box and selecting a different pattern, estimates of incidence and prevalence by sub-population in the Results menu should not be used.

The second tab in this editor (HIV age distribution) allows you to examine and change the ratios of incidence by age to the reference age group (25-29). In most cases you should accept the default pattern.

Step 13. Validation

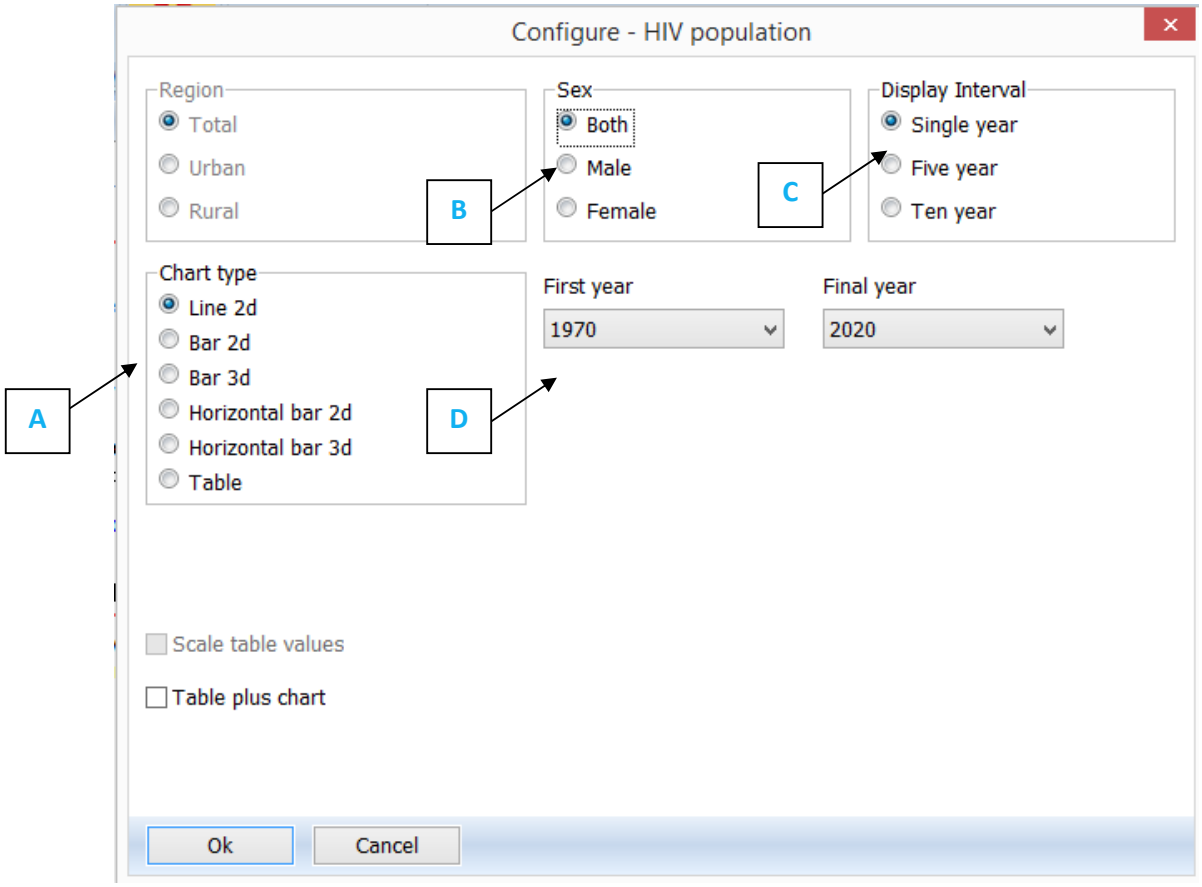
This tab allows you to compare the results to other information as a validation step. For example you can compare HIV prevalence against survey results by age group, or the number of people receiving ART as estimated by Spectrum by age group. In addition the overall mortality (under five, 15+ or other standard mortality indicators) and AIDS-related mortality can be compared to what Spectrum estimates. This review of the data against alternative sources should be done before finalizing the file.

Step 14. Results

Select the **Results** menu item to see a drop-down menu with the categories of HIV/AIDS indicators. They are:

- Dashboard
- Total population
- Adults (15-49)
- Adult 15+
- Adults 50+
- Young adults (15-24)
- Adolescents (10-19)
- Children (0-14)
- Children under 1
- Children 1-4
- Children under 2
- PMTCT
- ART – Dec 31
- Sub-populations
- AIDS impacts
- Orphans

Each category contains indicators that Spectrum can display. Choose one of these indicators, for example, **HIV population.** The following screen will appear:



On this screen you can set the options for displaying the results.

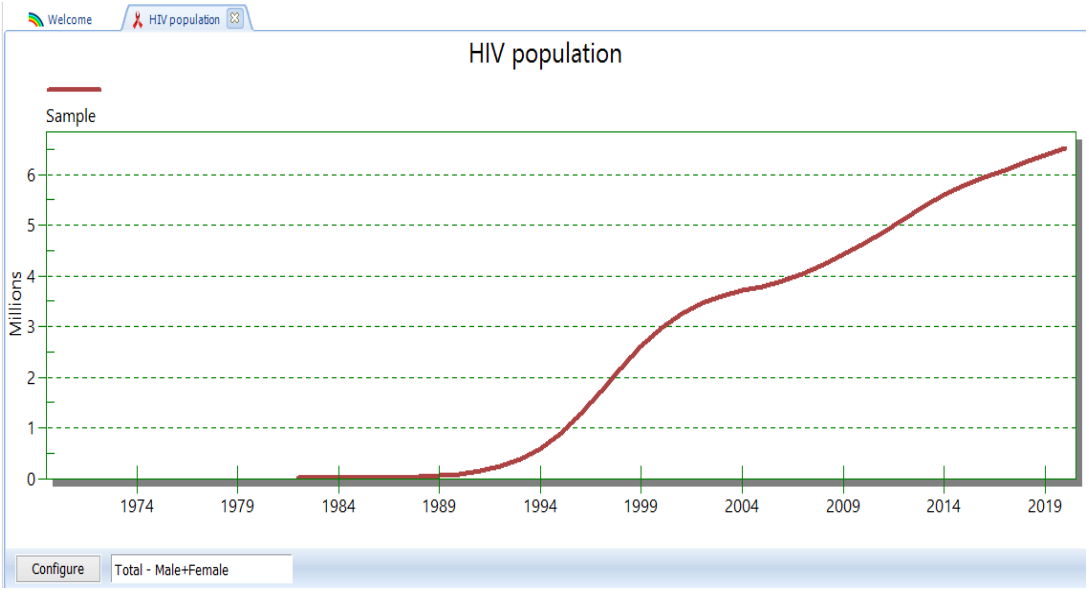
A. **Chart type.** Select the type of chart you wish to display.

B. **Sex.** By default this is set to display both sexes, but you can change it to male or female only.

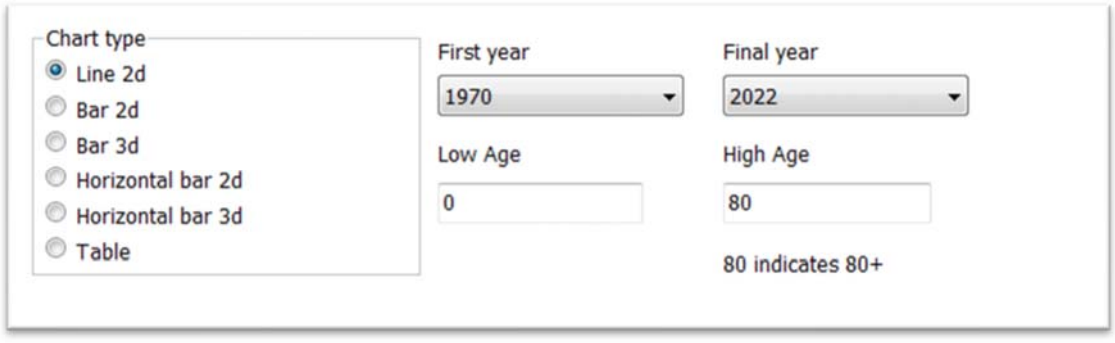
C. **Display interval.** By default this is set to display every year.

D. **First year** and **Final year.** By default this is set to the first and final year of your projection.

Once you have set the options, click **Ok** at the bottom of the screen. This will display a chart showing the indicator you have chosen, according to the variables you have selected on the previous screen. The following is an example of a line graph:



The user can also display results for specific age groups from the Total Population page. Options to display results for HIV age distribution 0-80 years allow the user to define which age group should be included in the presented results.

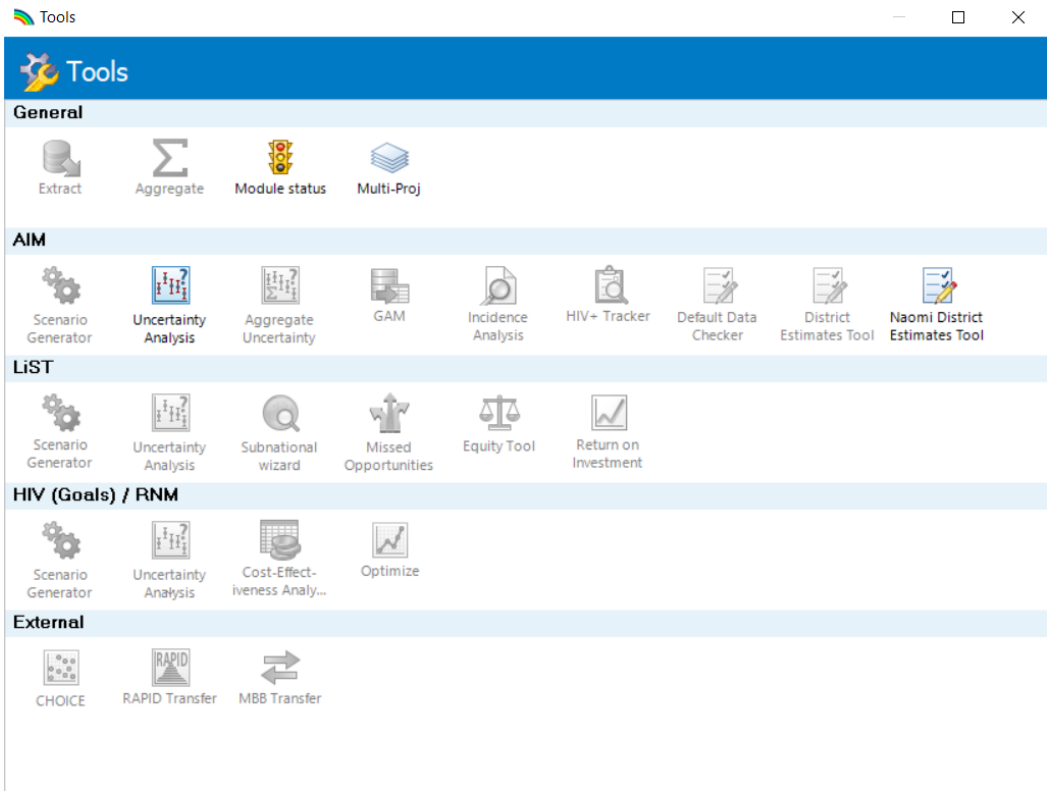


You can open up to 10 projections at one time and display the results in the same chart. The name of each projection that you open will appear at the bottom of the screen.

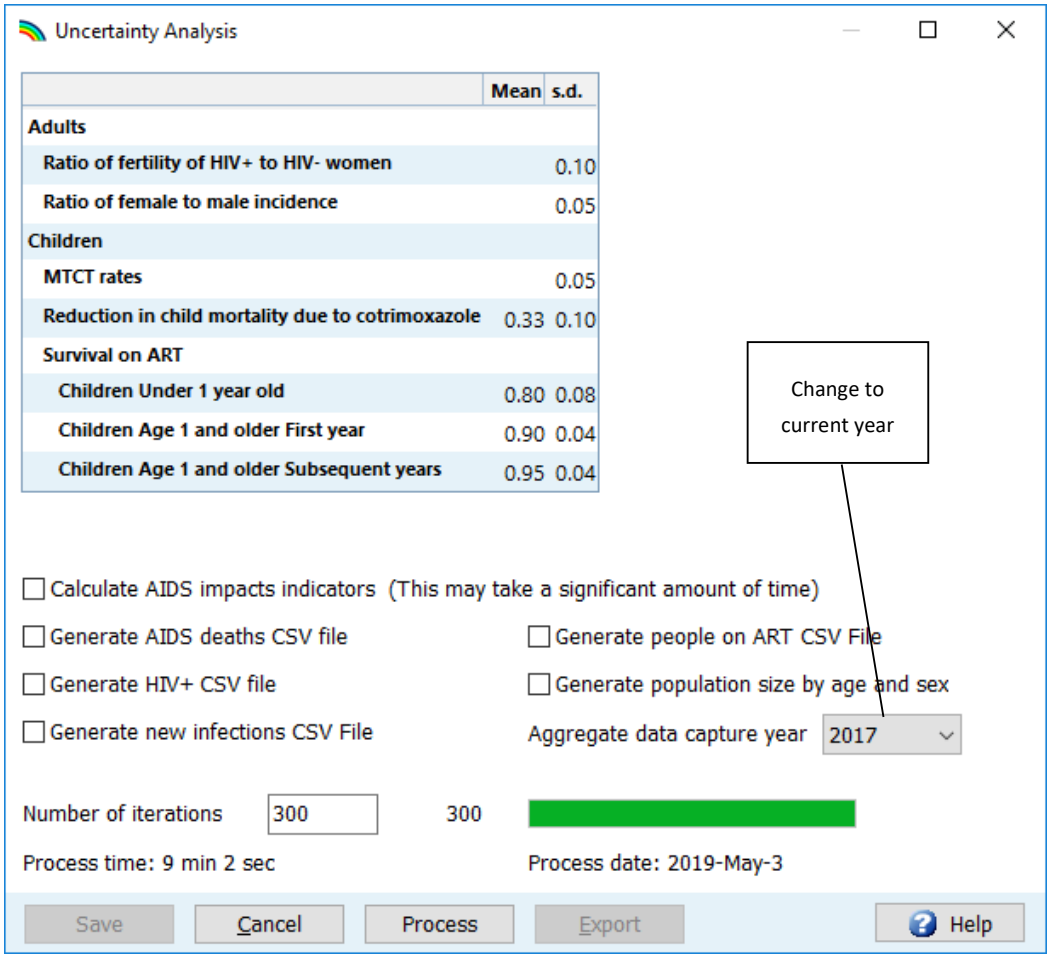
Step 15. Uncertainty analysis

Spectrum can calculate the range of plausible values for each of the output indicators. To use this feature you should open one, and only one, projection. If you have more than one projection open the uncertainty menu option will not appear.

To start an uncertainty analysis, select **Tools** from the main menu and then click on **more tools** then on **Uncertainty Analysis** icon as shown in the visual below.



You will see a display like the one below.



The column labeled '**s.d.**' shows the standard deviation (as a proportion of the mean value) used in the uncertainty analysis. You can change any of these standard values if you wish to try a larger or smaller range. The uncertainty analysis will randomly select parameter values for each of these indicators for each iteration.

By default, the number of iterations is set to 300. It will take 10-15 minutes to generate 300 runs. You can test the procedure by changing this to a smaller number but should generate 300 curves for your final analysis.

When you are ready to go, click the 'Process' button to start the analysis. When it is finished click the Save button to save the results. Once you have run the uncertainty analysis, most of the displays will show the 95% plausibility bounds. Note that bounds will only be shown when a single projection is open. If you open multiple projections, then the bounds will not be shown.

Other tools are available on the Tools menu. The most commonly used tools include:

Extract: to extract indicators from multiple Spectrum files. The results are written to a CSV file.

Aggregate: to aggregate multiple Spectrum files. This is useful for aggregating sub-national files to get national totals.

Default data checker: to compare the advanced parameters in the current Spectrum file with the default values.

Step 16. Save the projection

Save the projection by click the Spectrum menu button and selecting **Save** or **Save As** or by selecting **Home** and clicking the **Save** icon. Please be sure the file name includes the country name.

Step 17. Comparing projections

If you want to compare your new projection with a previous one you can open a 'Read Only' projection. Click on the Spectrum menu icon in the upper left corner of the Spectrum window and select 'Read Only' then select the previous projection. You will now have two projections open in Spectrum. Any charts you display will show both the current and the comparison projection so that you can see what has changed. You can use the editors to see the inputs to the comparison projection but you will not be able to change anything. When Spectrum re-projects the current projection it will not re-project the comparison projection. This maintains the integrity of the previous projection and uses it only for comparison purposes.

Step 18. Creating alternate projections

You can compare alternate projections by opening two or more files that have the same inputs except for one indicator that you wish to examine. For example, you might want to see the effect on AIDS deaths of increasing ART coverage. The easiest way to do this is to start by opening the base file. Then open the same file again. When you try to do this Spectrum will recognize that you are trying to open the same file twice. It will ask you if you want to go ahead and do this or if you want to rename the projection as you load it. If you choose to rename it, you can provide a new name, such as 'Expanded ART'. Then you will have two projections opens that are the same. You can then edit the 'Expanded ART' projection and change the projected ART coverage. Then you can display the number of AIDS deaths to see the effect of expanded coverage.

When multiple projections are open Spectrum will display the names of the projections at the bottom of the screen and show an asterisk next to the active projection. This is the projection that will appear when you edit the data. To edit a different projection, click the **Set Active** button (when the **Modules** menu item is selected) and select the projection to edit.

ANNEX 1. Managing Templates

What is a template and how do I use it?

Templates are predefined national epidemic structures for use in EPP. The various templates provided each consist of a number of special sub-populations (i.e., specific groups of people affected by HIV epidemics) that tend to occur frequently in national epidemics globally.

The three *default* templates provided automatically in EPP and the associated sub-populations are:

- *Urban Rural (G)* – a template for use in generalized epidemics
  - Urban – the national population living in urban areas
  - Rural – the national population living in rural areas
- *Concentrated (C)* – a template for use in concentrated epidemics
  - IDU – the national population of injecting drug users
  - MSM – the national population of men who have sex with men
  - Sex work clients – the national population of men who visit female sex workers regularly
  - Sex workers – the national population of female sex workers
  - Male remaining pop – all males in the country not in one of the other groups
  - Female remaining pop – all females in the country not in one of the other groups
- *From UNAIDS Workbook* – a template for fitting trends from the UNAIDS Workbook
  - Workbook trend – the entire national population

Any template can be applied to a national epidemic (or to a sub-epidemic) by right-clicking on that epidemic in the "National Epidemic Structure" tree on the Define Epi Page (see figure below)

You then just select a template in the list and click on it and the sub-populations defined it in will be added to the national epidemic structure for your country.

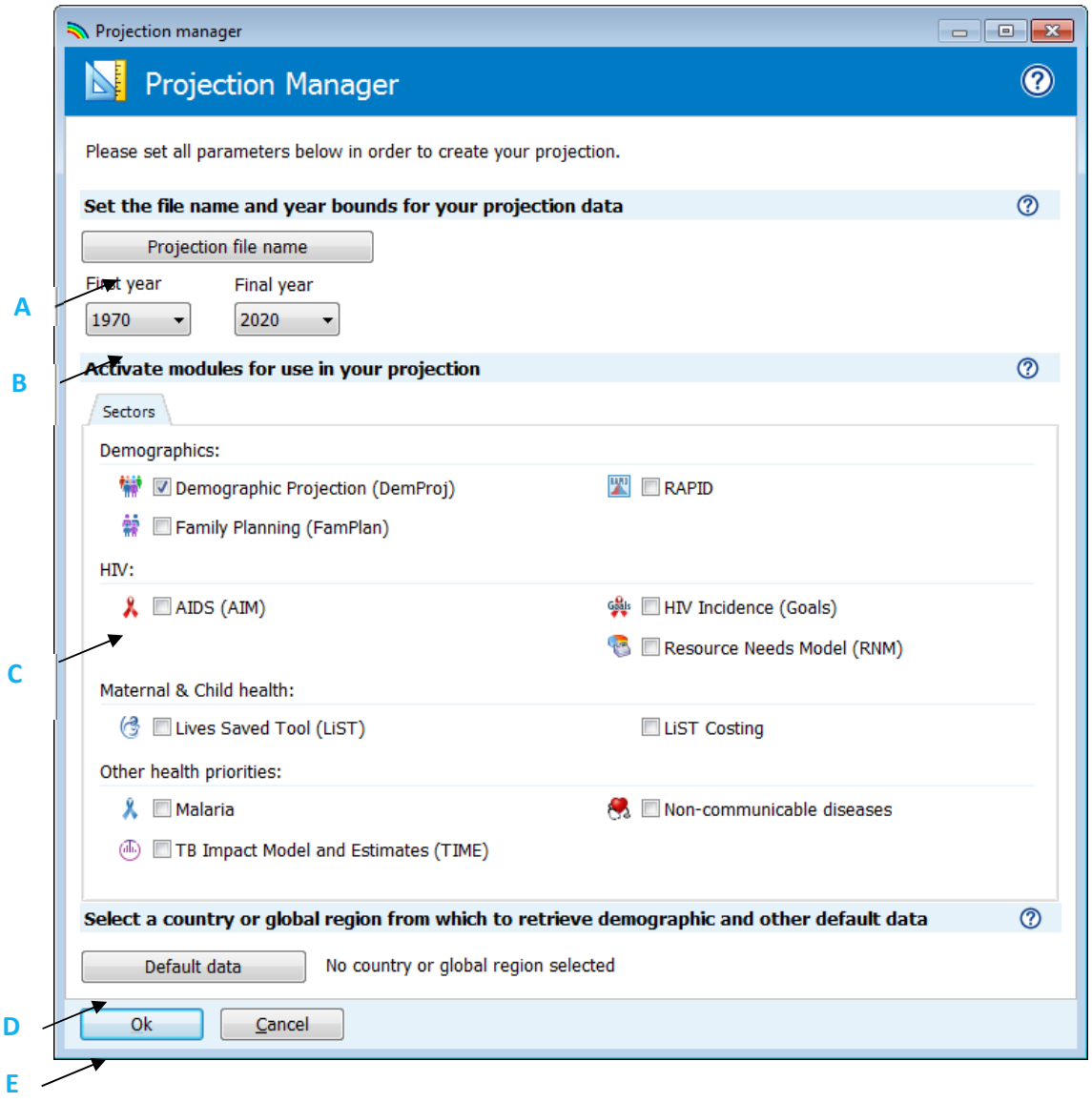
Creating your own templates describing your local epidemic situation

Suppose you have your own special set of epidemic structures. Consider, for example Vietnam, where there are often two distinct epidemics among people who inject drugs, one among older PWIDs and one among younger PWIDs. Since this occurs in many provinces, they may want to define this particular structure one time and then apply it repeatedly in a number of provinces.

For assistance with creating unique or advanced epidemic structures please request assistance from your UNAIDS strategic information adviser or write to estimates@unaids.org.

ANNEX 2. Creating a new population projection

When you create a new projection you will see the "Projection manager" dialogue box.



Follow these easy steps to complete the "Projection manager" screen:

A. Click the **Projection file name** button and enter a file name for the projection.

B. The **First year** and **Final year** should be set to 1970 and 2021. You can change them if you wish, but projections submitted to UNAIDS should use these settings.

For projections using AEM (AIDS Epidemic Model), the first and final year should be respectively 1975 and 2050.

C. Click the check box next to **AIDS (AIM)** to add the AIM module to the projection.

D. Then click the **Default Data** button. A list of countries will appear. Once you select your country from the list Spectrum will automatically load all the demographic data you need for your projection.

   Spectrum will load data on HIV incidence, and number of people receiving ART, cotrimoxazole and PMTCT services from data published by UNAIDS and WHO. It is important that users compare these inputs with their program data and make any revisions that might be necessary. In particular, the data provided on PMTCT and ART services should be reviewed.

E. When you are done click the **OK** button.

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