QUICK START GUIDE FOR SPECTRUM
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Part I. Overview of estimates and projections tools

Introduction

A. Purpose of estimation and projection tools

A well planned response to the HIV epidemic requires specific information on the projection of the disease over time. This projection needs to be based on measures of HIV prevalence in the population as well as programme data on coverage and effectiveness.

UNAIDS and partners have developed software to assist countries to map their HIV epidemic and determine the consequences of the HIV epidemic. Consequences such as number of people living with HIV, number of new infections, number of pregnant women infected with HIV, mortality due to AIDS and treatment needs are all provided from these programs. From these results countries can estimate their potential service and pharmaceutical needs, can plan for health care service requirements, and can get a general understanding of the overall impact of their response.

In addition, the HIV estimates produced through this process are currently used by development partners, such as the Global Fund for AIDS, Tuberculosis and Malaria and the US Government, to monitor the impact of their support.

B. Reference Group on Estimates, Modeling and Projections

The computer programs used to create the HIV estimates are informed by a Reference Group of experts from multiple disciplines and institutions. These experts include epidemiologists, demographers, clinicians, modelers, as well as implementers from countries with different types of epidemics. The functions and assumptions used in the models are based on the recommendations of this Reference Group. The Reference Group meets at least annually and updates the software every year. For more information on the Reference Group go to: www.epidem.org.

C. Processes to create estimates and projections

As of 2013 UNAIDS and partners request that countries update their Spectrum file annually. The update should be done by a national HIV estimates team that is made up of appropriate stakeholders in the country. Ideally this will include epidemiologists from
the national HIV coordinating body conducting HIV surveillance, statisticians from the government statistical agency, and development partners who are working on the HIV response as needed.

To support this work, UNAIDS and partners hold regional trainings every other year to explain new features and review the files with the HIV estimates teams. These teams work in groups at the trainings to update the estimates with the country’s most recent surveillance and programme data. As a result, the country is able to use the software to estimate and project the future consequences of the epidemic for the country.

National HIV estimates teams are encouraged to validate the input and refine and share the outcomes with other interested parties in the country. Once the models are completed the country provides the final file to UNAIDS headquarters to inform the regional and global estimates of HIV. Countries are also encouraged to create estimates and projections reports for their individual countries and to communicate the results to a broad range of potential users of the data.

**D. Data Required for Estimation and Projection**

The quality and accuracy of the estimates depend on the quality and accuracy of the data used for the models. If very little information is available on HIV prevalence in the country the model will rely heavily on assumptions used in the model. On the other hand, countries which have conducted routine surveillance and covered groups which are most important to the epidemic will be able to inform the models with substantial data resulting in high quality estimates and projections.

In generalised epidemics (see box 1 for epidemic classifications), data from sentinel surveillance sites at antenatal clinics (ANC) are required. Data from population based surveys are also very useful for informing the models. The models are able to utilize data to create urban and rural epidemics or prepare different regional epidemics.

In concentrated epidemics more specific information is required about the populations that are at increased risk to HIV. The software separates the epidemic into sub-populations. However the user must have information on each of the sub-populations that are used in the epidemic structure. For example if a country specifies female sex workers and injecting drug users as important risk categories they will be required to enter data for those two sub-populations and the remaining general population. Data required for each sub-population include estimates of the population size, HIV surveillance data from the group over time, and estimates of how long people remain in that sub-population.
Box 1: Epidemic classifications
Different epidemics require different types of surveillance and modeling techniques. The data required for Spectrum depend on what type of epidemic prevails in a country. The following classification can be used to differentiate the type of data required for the epidemics:

Generalised Epidemic
- HIV is firmly established in the general population.
- Although sub-populations with higher risk may continue to contribute disproportionately to the spread of HIV, sexual networking in the general population is sufficient to sustain an epidemic independent of subpopulations at higher risk for infection.
- Numerical proxy: HIV prevalence is consistently over 1% in pregnant women. In generalised epidemics, the prevalence among pregnant women is usually a fairly good indicator of prevalence in the total adult population. Prevalence is usually higher in urban areas than in rural areas. Therefore, most countries with generalised epidemics can be modeled using two distinct sub-populations (an urban population and a rural population). Increasingly countries with generalized epidemics are shifting to regional or provincial/state models to better inform decision making at both national and local levels.

Concentrated Epidemic
- HIV has spread rapidly in at least one defined sub-population, but is not well-established in the general population. Most often more than one subpopulation with higher risk is affected.
- This epidemic state usually suggests active networks of risk exist within and between the sub-populations.
- Numerical proxy: HIV prevalence is consistently over 5% in at least one defined subpopulation. HIV prevalence is below 1% in pregnant women in urban areas.

In concentrated and low-level (low prevalence) epidemics HIV infection is primarily concentrated in certain sub-populations. Therefore, countries with concentrated epidemics are usually modeled by combining epidemic curves for several subpopulations.

The type of epidemic also determines which computer programmes are necessary for modeling the epidemic and how to use those programmes.

For all epidemic types, the software requires additional programme data on the number of men, women and children on ART, the number of women receiving ARVs for prophylaxis (PMTCT) and other demographic and epidemiological information to determine the impact of HIV.

Many countries require sub-national estimates allowing programme managers to develop provincial level estimates. Spectrum does allow for such estimates. Sub-national estimates require HIV prevalence data, programme data and demographic data from each of the sub-national entities. See Box 2 for more information on this option.
If there are no recent data, for example no data in the past four years, on HIV prevalence available in the country then alternative forms of non-surveillance data sources should be identified to help inform the estimates process for recent years and the results of the estimates should be used cautiously.

**E. Computer Programmes for Fitting an HIV Epidemic Curve**

This guide describes the Spectrum program that has been developed to support national estimates and projections. The 2014 version of Spectrum includes the Estimation and Projection Package (EPP) used to generate an epidemic curve. EPP was previously a standalone program, but in now tightly integrated into Spectrum. A number of countries have also chosen to use the Asian Epidemic Model (AEM) to determine the trajectory of their HIV epidemic. Spectrum will soon be able work with the output of AEM to provide the same indicators that are available to a country that uses the EPP programme. Please consult with the East-West Center if your country would like to use the AEM model. Some countries with very little surveillance data may also use an Excel-based program called Workbook. The Workbook programme will generate an HIV point prevalence estimate for a given year. This should be repeated for several years; these prevalence estimates are then used in EPP to generate an epidemic curve. Consult with UNAIDS if your country needs to use Workbook. EPP now contains multiple models that can be chosen based on the amount of data available (the models are described in Step 9).
Part II. Using the Spectrum Software

Introduction
This Quick Start Manual describes how to:

- Create a demographic projection using data from the United Nations Population Division.
- Create an HIV/AIDS projection using surveillance data.
- Display various HIV/AIDS indicators such as the number of people infected, the number of new infections, AIDS cases, AIDS deaths, the number of people needing ART and the number of orphans.

The Manual also explains how to update a file that has already been created. To avoid re-entering data it is advised to update existing Spectrum files.

Step 1. Installing Spectrum
The latest Spectrum program can be downloaded from www.futuresinstitute.org. Spectrum will run on any computer running Windows Vista or later Windows versions. It requires about 170MB of hard disk space.

Once you have downloaded the software from the internet you can install Spectrum by double clicking on the file named “SpecInstall.exe”. This will start the installation program. Just follow the instructions on the screen to complete the installation.

If you have trouble installing Spectrum it may be that you do not have the appropriate permission to install programs on your computer. In that case you should contact your IT support office to do the installation for you.

Step 2. Changing the language in Spectrum
The first time you run Spectrum after installing it, all the displays will be in English. You can change to another language by selecting the Spectrum Menu Button (the rainbow icon at the top left of the screen), then “Options” and from the Spectrum menu. Then select the language you want to use and click on the “Ok” button. If you select a language other than French, Spanish or Portuguese, you must have the proper fonts or version of Windows to display the language correctly. The EPP component of Spectrum supports English, French, Russian and Spanish and will automatically change languages based on the language chosen in Spectrum.
**Step 3. Start Spectrum**

Start the Spectrum program by selecting it from the “Start” menu on your computer (Windows 7 or earlier) or your Start Screen (Windows 8). When the program starts you will see an opening screen giving you the option to select ‘New Projection’, ‘Open existing projection’, select a ‘Recently opened projection’ or use ‘Spectrum online support’.

If you have a projection file from previous rounds of estimates you can start with that file by opening an existing projection, or you can start over by creating a new projection. We recommend you use an existing projection for national HIV projections.

If you saved your previous Spectrum file with Export Projection to create a single compressed file with a .zip extension you would normally have opened it using Import Projection. In the latest version of Spectrum that command is no longer available. Instead when you see the File Open dialogue box asking you to select the file, you can click on the All projection files button in the lower right hand corner and select Zip files (*.ZIP). Then you will be able to open your file.

**Step 4. Create or update the population projection**

When you create a new projection you will see the “Manager” dialogue box, shown below. If you are updating a projection you will need to click on Manager to open this box.
Follow these easy steps to complete the “Projection manager” screen:

4.1 If you are creating a new file you should click on the Projection file name button and enter a file name for the projection. We recommend that this be the country name followed by the year of the projection, i.e. “Argentina 2014”. If you are using an existing projection you will change the file name using the Save As function from the Spectrum menu under the rainbow icon.

Tip: Keep file names short. Longer file names can cause the software to hang. Use a date at the end of the file name for version control. For files that will be sent to Geneva please avoid using Cyrillic or Arabic characters in the file name.

4.2 The First year and Final year will be set to 1970 and 2021 by default. In most cases you should accept these values. You can change them if you wish, but projections submitted to UNAIDS should use the default settings. Projections more than five years from the latest surveillance will not be reliable.
4.3 Click the check box next to AIDS (AIM). The box next to Demographic Projection (DemProj) should already be checked.

4.4 Then click the Default Data button. If you are updating a file you may receive a message alerting you that the data are missing and you will need to download the data from the internet. Click on yes and let the data be downloaded. Once it is complete you will need to identify that you would like to load the DemProj data. This will update the demographic data in the file. If you are creating a new file a list of countries will appear after selecting Default Data. Once you select your country from the list Spectrum will download the demographic data you need for your projection from the internet. Your computer needs to be connected to the internet for this to work.

Once the data are downloaded Spectrum will ask whether you want to install the default data. You should select DemProj to load the demographic data. If you also selected the AIM button Spectrum will also load data on HIV incidence, and number of people receiving ART, cotrimoxazole and PMTCT services based on the previous round of estimates. It is important that you review your program data and make any revisions that might be necessary.

When you are done click the OK button to exit the Manager

**Step 5. Display the AIM menus**

Select Modules from the Spectrum menu and click the AIM icon to display the AIM menu as shown below.

![AIM menu](image)

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

**Step 6. Enter program data**

Click on the Program statistics menu item to see the program data editor. It will look like this:
Enter your program data using the three tabs at the top for: PMTCT (prevention of mother-to-child transmission of HIV), men and women receiving ART, and Child treatment (including ART and cotrimoxazole).

In each of these editors you may enter data as the number of people receiving the service. If you enter a percent coverage, Spectrum will calculate the number receiving the service when it makes the projection of the people in need of the service. Usually you will enter numbers from program statistics for all historical years. For future years you may enter either numbers or percent coverage. You can enter numbers for some years and coverage for other years but you cannot mix numbers and percent coverage in the same year. The PMTCT editor has a number of rows. You can use the drop-down menu in the upper right of the screen to select to show (1) just the rows for numbers, (2) just the rows for coverage or (3) both.
The grey numbers displaying the estimated number in need are based on the last time the projection was run. These grey numbers cannot be modified by the user. They are calculated by the software. Substantial changes to the inputs (surveillance data or programme data) will result in a change in the calculation of the need. Consider the needs in grey as indicative values.

All Spectrum editors have duplicate and interpolate functions to make it easier to enter all the data required. To use these features just select a range of data with your mouse and either click the Duplicate or Interpolate buttons or right click with the mouse and select Duplicate or Interpolate from the menu.

- **Duplicate** copies the data from the first cell of the range to all the other cells in the range. It is useful when you want values to remain constant over time.
- **Interpolate** calculates values for the cells between the first and last cell in the range by interpolation. Spectrum will perform a linear interpolation if you click the Interpolate button. It you right click you will see a menu allowing you to choose the interpolation method: linear, S-shaped, exponential, and front loaded.

The PMTCT ARV input page has two sections: the top half describes what medications were taken pre-natally (during pregnancy and delivery) and another section on what medication was taken post-natally during breastfeeding. The post-natal data should only include women and their infants who are taking the medication as a prophylaxis. It does not include women who are receiving lifelong ART. The numbers of women in the post-natal prophylaxis are generally a sub-set of the women who were receiving Option A or Option B in the pre-natal data.

After entering the PMTCT data, users should review the data in the Breastfeeding tab. These data describe the percentage of children born to HIV+ women who are not breastfeeding by the age of the child. Separate data are required for women in the PMTCT programme, women outside of the PMTCT programme and for different years. This allows the model to reflect changes in breastfeeding policy over time.

After entering data for PMTCT, users should enter the Adult treatment data (separately for men and women) and for children.

Data for years beyond the current year can reflect any national targets that have been set.

When you are finished entering data, click the Ok button to save the changes.
Step 7. Specify eligibility for treatment

Select the **Eligibility for treatment** menu item to see the editor shown below.

In the top part of the screen you can specify the eligibility for ART in terms of CD4 count. By default, eligibility is set to 200 cells/µl until 2010 and to 350 cells/µl for 2011 and later. You should modify these inputs to match your country’s actual guidelines.

The second part of the editor allows you to specify that people living with HIV in certain population groups may be eligible for treatment regardless of CD4 count. Specify eligible populations by clicking the check box next to the name and set the year in which the guidelines were changed to include that population group. Spectrum will calculate the number of HIV+ pregnant women but for all other groups you need to specify the percentage of HIV+ adults that are in that population group. Spectrum contains default estimates for most countries. The percentage of HIV+ adults that are co-infected with TB has been estimated by WHO based on HIV surveillance studies among HIV+ adults. The percentage that are in sero-discordant partnerships is based on the most recent national HIV survey if one exists, otherwise it is estimated as using a regression equation derived from fitting to Demographic and Health Survey data (percent serodiscordant = 44.332 x e^{-0.047 x prevalence}). The percentages that are sex workers, MSM or injecting drug users are taken from national estimates of the sizes of these populations from EPP estimates or Modes of Transmission studies. Regional averages are used when country-specific estimates are not available.
For children, ART eligibility has three components:

- **Age.** Enter the age below which all HIV+ children should be on treatment. By default this is set to 12 months from 2007 to 2009 and to 24 month thereafter.
- **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 of the three criteria.

**Step 8. Advanced options**

The **Advanced options** menu item gives you access to the default parameter values used in the projection. These parameter values are based on special studies and surveys from a number of sites around the world. In most cases the default values should be used. This section allows you to see these default patterns, and change them if you have the information to do so. The patterns are grouped into four categories:

- **Transition parameters.** These include the amount of time a typical HIV+ adult spends in each CD4 category, the distribution of new infections by CD4 count, HIV-related mortality by CD4 category without ART, HIV-related mortality on ART by CD4 count at the initiation of treatment, survival on ART for children, the patterns of progression from new infection to death for children, 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.
- **Orphans.** This section is used to indicate the relative fertility of the HIV+ population in concentrated epidemics in order to provide a better estimate of the number of orphans caused by AIDS.
Calculating Incidence

When you select Incidence from the menu you will see a drop down menu with six choices: Configuration, Surveillance, Curve fitting, Restore values, Direct incidence input, Review. If you are creating a new projection only Configuration and Direct incidence input will be active. Once you choose Configuration and enter the necessary details then the Surveillance item will become active and once you enter surveillance data, the Curve fitting item will become active. Each of these options in described in detail in Steps 9-11.

Direct input of incidence is used only when you already have an incidence projection that you want to use. In most cases you should go through the Configuration, Surveillance, and Curve fitting steps to create an incidence projection.

NOTE: If you do not have the Java Runtime version 7 or later 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 on the internet, 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. If you currently have Java 6 or earlier installed, you will need to update to Java 7 before you will be able to run EPP.
Step 9. Incidence: Configuration

The first step under incidence is to define the epidemic structure of the country by selecting an appropriate template.

Define the epidemic structure.

9.1 Right click on the top entry under National epidemic structure. Select the appropriate template. There are three template options: Concentrated (C), From UNAIDS Workbook, and Urban/rural (G). For most countries with generalized epidemics use the Urban/Rural template. For most other countries, use the Concentrated template.

Alternatively, create a custom national epidemic structure 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 on the right and choose "Rename".

Define the sub-population characteristics

9.2 Highlight the sub-population in the epidemic structure.
9.3 Click on the characteristic of that sub-population (for examples sex workers should be “FSW” and the “General pop women” should be “low risk”).
9.4 Repeat this for each sub-population
9.5 Click on “Save and continue”
Generalised epidemics:
For many countries with generalised 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.

Box 2: Producing estimates for sub-national regions
In some settings it might be necessary to create estimates based on sub-national regions to provide locally relevant estimates. Three options are available to help countries create sub-national estimates.
Option 1. Create a national Spectrum file using the urban/rural configuration and apply the HIV prevalence by region through an excel sheet
Option 2. Create a national Spectrum file using sub-regions (instead of urban/rural) to fit curves and display a regional summary table within Spectrum
Option 3. Create separate regional Spectrum files

Option 1
Fit two epidemic curves for urban and rural areas for generalized epidemics or fit curves to develop a single Spectrum file for the national projection. Use a spreadsheet to allocate key results by sub-national region based on regional prevalence from a national HIV prevalence survey or surveillance.
Use this option when at least one national survey exists. The disadvantage is that estimates are only for regions with HIV prevalence in the national survey and it assumes epidemic dynamics are the same in each region of the country.
Option 2
Create an epidemic structure in the configuration page using sub-national regions. Assign the surveillance 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 a number of surveillance sites are available in each region. This option captures the different epidemic dynamics for each region. However the results are only allocated on the basis of prevalence or incidence and miss any differences in fertility or mortality between the sub-national regions.

Option 3
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 (programme data, size estimates, non-AIDS population data). This option produces full epidemic information (all variables) for each region. However it requires that all of the demographic projection information is available by region.

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 population, and average time spent with the risk behaviour for those sub-populations of persons with high risk behaviour. Do not create sub-populations for which no data are available.

In concentrated and low level epidemics, if there are less than 3 data points from consistent surveillance sites for sub-populations at increased risk to HIV, then use the Workbook template. (As described earlier, you will need to derive point prevalence estimates for several years using Workbook and then will enter those into the incidence page to generate a curve.)

Tip: In countries with well documented concentrated epidemics in which HIV in the general population has increased beyond 1% (such as, Russia, Ukraine, Myanmar, Thailand), the concentrated epidemic template should continue to be used.

Tip: The full population needs to be represented in the sub-populations. Thus it is important to include a population that includes the remaining population. This should be done separately for men and women. For example there should be a remaining female population that includes the low-risk female population and a remaining male population that includes the low-risk male population.

Define the populations
The Define Pops page allows you to define the size of each sub-population.
Generalised epidemic (urban/rural template):
In a generalised 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. 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.

Generalised 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 a non-AIDS population projected by Spectrum). You must assign all of this population to different groups within the epidemic structure.
9.6 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 as shown in the first column above.

**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.

9.7 When done entering all population, 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:

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

9.9 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.

9.10 Fill in the percentages for the final year, 2020, 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.
9.11 Click on the button “Calculate Proportional Values” and the software will fill in the additional entries for the entire table.
9.12 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 is more challenging. There are two sub-pages. On the first page (“1. Population”), the user should provide 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.

9.6 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). See Box 3 for regional estimates of population sizes.
Box 3. Estimates of the size of key populations at increased risk to HIV (For low and 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 on the basis of 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 IDU) 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
(MSM and clients as % of male pop ages 15-49; FSW as % of female pop ages 15-49)

<table>
<thead>
<tr>
<th>Men having sex with men</th>
<th>Injecting drug users</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>General</td>
</tr>
<tr>
<td>E. Asia</td>
<td>3 – 5%</td>
</tr>
<tr>
<td>S &amp; SE Asia</td>
<td>6 – 12%</td>
</tr>
<tr>
<td>E. Europe</td>
<td>6 – 15%</td>
</tr>
<tr>
<td>Latin America</td>
<td>6 – 20%</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Female sex workers</th>
<th>Clients of sex workers</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sub-Saharan Africa</td>
<td>All</td>
</tr>
<tr>
<td>Asia</td>
<td>Central Africa</td>
</tr>
<tr>
<td>Russian Federation</td>
<td>Eastern and southern Africa</td>
</tr>
<tr>
<td>E. Europe</td>
<td>Asia</td>
</tr>
<tr>
<td>W. Europe</td>
<td>Latin America</td>
</tr>
<tr>
<td>Latin America</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>0.4 – 4.3%</th>
<th>0.2 – 2.6%</th>
<th>0.1 – 1.5%</th>
<th>0.4 – 1.4%</th>
<th>0.1 – 1.4%</th>
<th>0.2 – 7.4%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sub-Saharan Africa</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asia</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Russian Federation</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>E. Europe</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>W. Europe</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Latin America</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>


For concentrated epidemics, additional information is required on the proportion of each 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 page 2 of the define populations page titled “% Male and Turnover” if you are using a concentrated epidemic template.

9.7 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 check the box under
“Turnover”. Populations that are static such as the remaining populations will have no turnover.

9.8 For each sub-population with turnover, 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 particular are known in most countries to have a short average duration (few years). See box 4

9.9 If turnover has been selected you will need to specify the sub-population where members of the group will return after “turnover”, i.e., after they have left the most at risk population.

9.10 You also need to determine whether to add the prevalence of each sub-population turning over to the overall prevalence in the receiving sub-population or to replace it. You should choose “add prevalence” if those who are HIV positive from the former at-risk group members are to be added to the HIV positive members of the receiving sub-population. This means they have NOT been captured in surveillance for the receiving sub-population. You will need to “replace prevalence” if some of the people who are found HIV positive in surveillance in the receiving population come from the former at-risk populations. That is, if the surveillance data for the receiving population detects them, then choose “Replace prevalence”. EPP then calculates the remaining infections that occurred “within group” and this information will be available on the Fitting Results page. Under “assign prevalence to” identify the sub-population to which the group members go after leaving the behaviourally at-risk sub-population.

9.11 If your epidemic includes populations of people who inject drugs (PWID), then it is important that you review the entry at the bottom of the page labeled “IDU mortality”. This specifies the non-AIDS crude mortality rate for HIV positive and HIV-negative people who inject drugs. The values currently set are based upon a Reference Group review of existing studies, but if there are local studies of this mortality, they should be entered here. These numbers determine the number of non-AIDS deaths occurring among people who inject drugs.
**Box 4. 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 injecting drug users then, we would want to add these additional infections into the overall prevalence in the male population. In long running concentrated epidemics, this turnover can make a substantial contribution to overall prevalence.

**Estimates of time in most at risk populations by region**

*Average duration of female sex work, by region*

<table>
<thead>
<tr>
<th>Region</th>
<th>Duration of behaviour in years</th>
</tr>
</thead>
<tbody>
<tr>
<td>Africa</td>
<td>5.5 (4 studies)</td>
</tr>
<tr>
<td>Asia/Oceania</td>
<td>2.9 (12 studies)</td>
</tr>
<tr>
<td>North America</td>
<td>10.2 to 11.0 (3 studies)</td>
</tr>
<tr>
<td>Europe</td>
<td>8.4 to 10.0 (10 studies)</td>
</tr>
<tr>
<td>Latin America</td>
<td>11.2 to 12.0 (6 studies)</td>
</tr>
</tbody>
</table>

*Average duration of injecting drug use, by region*

<table>
<thead>
<tr>
<th>Region</th>
<th>Duration of behaviour in years</th>
</tr>
</thead>
<tbody>
<tr>
<td>Africa</td>
<td>5.6 (1 study)</td>
</tr>
<tr>
<td>Asia</td>
<td>8.7 (6 studies)</td>
</tr>
<tr>
<td>Oceania</td>
<td>17 (1 study)</td>
</tr>
<tr>
<td>Europe</td>
<td>13.9 (1 study)</td>
</tr>
<tr>
<td>North America</td>
<td>9.5 (1 study)</td>
</tr>
<tr>
<td>South America</td>
<td>21 or 19.6 (9 studies)</td>
</tr>
</tbody>
</table>

Step 10. Incidence: Entering surveillance data

Once the epidemic structure and populations have been defined it is time to enter the available HIV prevalence data. From the AIM menu choose: Incidence and then select Surveillance Data (EPP). This will take you to the Surveillance Data page. There is a separate data entry spreadsheet for each sub-population. When the page is initially open it only has one row (each row represents the data from one site).

10.1 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 a number of sites at a time using “Add Multiple” and entering the number of sites to be added.

10.2 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 workset. 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.

10.3 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 workset.

**Tip:** Prevalence estimates should be entered as whole numbers not as percentages. So 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 a site has 0% prevalence in multiple years it will be virtually impossible for the software to develop a curve for this site. It will be even more difficult if there are numerous sites for one population and the values are all 0. For such situations it is best to take the following steps.
1. Turn off all but one site in the sub-population. This will reduce you to a single site and will allow the software to calculate a likelihood based on different equations that work as long as there are no zero prevalence values before the epidemic start year.

2. Under Model Parameters, pick a range of start years before the first data point, e.g., choose 1990 to 1995 for a first data point of 0.00% in 1997.

3. Set the f values low to drive up the samples of low curves (0 to 0.01).

4. Fit – this will produce a very low epidemic (effectively zero). It won’t be precisely zero because the software will introduce some HIV in the start year, but it will be low enough that it will not increase. This will effectively give you a zero prevalence curve through the whole projection period.

This will be quite useful if you have a low prevalence population, e.g., remaining males, where most of the HIV prevalence comes from turnover. It will allow EPP to then send turnover to this population using “add prevalence” and this prevalence from former members of behaviourally at-risk populations will then be displayed on the graphs and in the Reassignment table available on the Fitting Results page.

**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.

10.4 Enter survey data. If your country has collected HIV prevalence in a national population based survey you can add those data here to inform your curve. Data can be entered for up to 5 surveys. Be sure to include the prevalence, survey year,
standard error, and sample size for the survey. HIV prevalence values which have been adjusted for non-response should be used in the model.

If your country does not have HIV prevalence data from a national population survey, click on the button labeled “Do not include any surveys in the fitting process”.

Step 11. 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 three models that can be used for the curve fitting:

- R-Spline: This will be the best model for most applications.
- R-Trend: This will be the best model for countries with many years (8+) of surveillance data and many (7+) surveillance sites.
- EPP Classic. This will be the best model for countries with few data points.

*Figure 1: Decision tree on use of estimates tools*
11.1 Select the model you wish to use in the upper left portion of the screen.

11.2 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. This number of curves will take much longer to run. However the National run will give a more precise fit. The national run should be made before finalizing the estimates. Note that the curve might change when the National run is completed.

11.3 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.

11.4 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.
11.5 If you are satisfied with the fit choose “Save and continue” and move on to fitting a curve for the next sub-population.

11.6 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 Box 5). For example if there is little data for early on 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).

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**Box 5. 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. **Constraints on start years and prevalence should be used sparingly and with careful consideration of the following guidance:**

1. **Before applying prevalence conditions make sure the start year covers the full range of possible start years (a range of about 15-20 years) if using the R-Trend or EPP Classic models.** 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...
possible. NOTE: this does not apply to R-Spline where the start year is already set in a country-specific way. In general, users of R-Spline should not change this start year without checking with UNAIDS support staff.

2. **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. In some cases, it may also prevent the models from obtaining good fits to the 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, shown by the dashed blue lines, may reflect the true uncertainty in your epidemic’s future when data is sparse.

It is important to know that some calibration may be done during the fitting procedure. If you have entered surveys in either a generalized or concentrated epidemic, they are used during the fitting to set the appropriate level for the curves being explored as possible fits. Once the fit is complete, an adjustment will be made to the display of the ANC data in the graph to calibrate it to the level of the epidemic trend determined by the combination of the ANC data and the surveys. It should be noted that the final curve will not always pass exactly through the survey point itself – this is normal, do not be concerned by it. You can change it on the next page, the Calibration Page.

If you do not have surveys, but are in a generalized epidemic, then regionally specific adjustments of the final fitted curve will be made. These adjustments are based on averaging the observed urban and rural differences between national surveys and surveillance data in a number of other countries in the same region. Again, these adjustments are done automatically during the fitting procedure for generalized epidemics. For concentrated epidemics, no such global adjustments are made at present, although again normally some downward adjustment will need to be made for surveillance data done with women attending antenatal clinics. This adjustment can be made on the Calibration Page that follows the Project Page.

On the Calibration tab you can calibrate the curve based on additional data sources.
Generalised epidemics:
On this page you are able to adjust the curves based on any national population based survey data that you have entered. If you have had one or more national surveys then you can use all of the data from those surveys. Alternatively you could use the most recent survey if it better represents HIV prevalence than the earlier survey.

If you have not had a national population based survey then leave the default setting on “Use the modeling results as they are”. As described earlier, this has already shifted urban and rural prevalence down to in accordance with regional evidence from surveys in nearby countries that ANC surveillance most often overestimates adult HIV prevalence.

There are additional options available for adjusting the curves, which are described in the next section, but these are not normally used in generalised epidemics.

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

To use the calibration section:
11.7 Select the sub-population you wish to scale in the list of sub-populations shown
11.8 Select one of the options
i. *Use the modeling results are they are.* This option keeps the calibration that was established during the fitting.

ii. *Adjust the results taking into account all surveys.* This calculates an average offset between the EPP fitted curve and the survey values in the years where surveys are done. This is then applied to modeled prevalence curve.

iii. *Adjust the result for this projection to agree with most recent survey.* This calculates an offset that assures the adjusted EPP curve goes directly through the survey most recently completed and applies it to the modeled curve.

iv. *Adjust the results to global defaults for urban/rural bias in surveillance data.* In the case of generalized epidemics, this adjusts all urban and rural sub-population projections downward by UNAIDS-specified urban and rural amounts developed by comparing national surveys with ANC data in a number of countries. This approach has been replaced in the current version of EPP by the country-specific adjustments described above for countries without surveys in generalized epidemics, but is kept for comparison purposes with earlier projections.

v. *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.

vi. *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.

vii. Remove all calibrations. This removes all calibrations done during the curve fitting and uses the EPP curve without any upward or downward adjustments.
Box 6. Adjusting prevalence for the “remaining population” (low risk populations)

HIV Prevalence from antenatal clinics (ANC) can be used to 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 to avoid biases from the selection of pregnant women who are not using condoms and often younger than the general population and who are attending facilities that are included in the sentinel surveillance. These biases often lead to higher estimates of HIV prevalence. Comparing data available from ANC against HIV prevalence coming from population based surveys in 20 low and concentrated epidemic countries (or states), show that on average, HIV prevalence among all women was 0.47 percent of that measured in ANC prevalence. Thus a proposed adjustment value for women in the remaining population of 0.47 is recommended when assigning the ANC data to the remaining female population. The option “Scale HIV by factor of” should be chosen and 0.47 should be entered into the cell.

For men a similar analysis showed that the scale of HIV prevalence in the remaining male population is approximately 0.56 of ANC prevalence. Thus the adjustment from ANC data to men in the general population should be 0.56.

Note that the lower calibration values will result in lower overall HIV prevalence than the calibration values recommended in 2012.

Limitations: Every epidemic has a different history and thus the relationship between data from the ANC and the male remaining population will vary between countries as well as over time. While the above suggested calibration values can be used when there is a lack of other data, it is important to pursue data that might give a better estimate for your country. One example is to identify data which can provide a sex ratio of HIV+ males to HIV+ females. This ratio can be used to determine the calibration between ANC and the male remaining population.

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 does not increase their risk to HIV) these data can also be used to inform prevalence among the male remaining population. In using such data, however, it is also important to consider adjusting for the age and geographic origin of those in service.

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 also see the national trend that is produced by combining the trends for all the sub-populations.
11.9 Select the population you want to examine from the list at the top right of the page.

11.10 You may also compare your new results with the prevalence trends from a previous projection by clicking the ‘Compare’ button. That will display a screen like the one shown below.

11.11 Click the ‘Load’ button and select the comparison projection’s Spectrum (*.SPT) file which contains the necessary information from 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 (prevalence 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.

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

For concentrated epidemics the curve fitting process will produce an estimate of the sex ratio (the ratio of female prevalence to male prevalence). 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.
You can review the sex ratio trend by select the Sex/age pattern menu item. It will show a screen like this:

![Sex/age pattern menu item}

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. It is particularly important to review this chart in concentrated epidemics where the relative timing of the start of the epidemic in male and female sub-populations and poor estimates of their population sizes can sometimes produce unrealistic female-male ratios. This may require you to go back and carefully review and adjust the start times of each sub-population’s epidemic or the sizes of your male and female sub-populations.

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. Results

Select the Results menu item to see a drop down menu with the categories of HIV/AIDS indicators. 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.

13.1 Chart type. Select the type of chart you wish to display.
13.2 Sex. By default this is set to display both sexes, but you can change it to male or female only.
13.3 Display interval. By default this is set to display every year.
13.4 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:

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 14. Save the projection**

Save the projection by clicking the Spectrum menu button and selecting Save or Save As or by selecting Home and clicking the Save icon. If you created a new projection the file will be saved in PJNZ format. This format combines all the individual Spectrum files
associated with a single projection into one file. It can be easily transferred to another person by e-mail or flash disk. If you started by opening a file created in an earlier version of Spectrum then, by default, your file will be saved in PJN format which includes 10-20 individual files. In that case you should change the default file type to PJNZ by clicking the Save as file type button and selecting PJNZ.

Step 15. Comparing projections
If you want to compare your new projection with a previous one you can open a ‘Comparison Projection’. Click on the Spectrum menu icon in the upper left corner of the Spectrum window and select ‘Open Comparison’ 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 16. Creating alternate projections
You can compare alternate projections by opening two or more files that have exactly 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 exactly 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.
Step 17. 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 the Uncertainty Analysis icon. You will see a display like the one below.

![Uncertainty Analysis](image)

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 1000. It will take 20-40 minutes to generate 1000 runs. You can test the procedure by changing this to a smaller number but should generate 1000 curves for your final analysis.
When you are ready to go, click the ‘Process’ button to start the analysis. When it is finished you can select any of the indicators to display the average curve and the 95% plausibility bounds. A summary table, shown below, is available to display the ranges for all indicators for a selected year.

![Summary Table]

<table>
<thead>
<tr>
<th>2012</th>
<th>Lower 2.50%</th>
<th>Median 50%</th>
<th>Upper 97.50%</th>
</tr>
</thead>
<tbody>
<tr>
<td>HIV Adults + Children</td>
<td>1,573,034</td>
<td>1,644,635</td>
<td>1,723,666</td>
</tr>
<tr>
<td>HIV Adults 15+</td>
<td>1,388,762</td>
<td>1,442,161</td>
<td>1,518,505</td>
</tr>
<tr>
<td>HIV 15+ female</td>
<td>786,737</td>
<td>821,162</td>
<td>864,361</td>
</tr>
<tr>
<td>HIV population - Children</td>
<td>176,267</td>
<td>202,474</td>
<td>233,846</td>
</tr>
<tr>
<td>Prevalence Adult</td>
<td>5.90</td>
<td>6.12</td>
<td>6.28</td>
</tr>
<tr>
<td>Prevalence - Males aged 15 to 24</td>
<td>1.28</td>
<td>1.59</td>
<td>2.11</td>
</tr>
<tr>
<td>Prevalence - Females aged 15 to 24</td>
<td>2.88</td>
<td>3.49</td>
<td>4.46</td>
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<tr>
<td>HIV Prevalence - Children</td>
<td>0.94</td>
<td>1.09</td>
<td>1.26</td>
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<tr>
<td>New HIV infections - Adult</td>
<td>82,475</td>
<td>87,360</td>
<td>98,187</td>
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<tr>
<td>New HIV infections - Children</td>
<td>7,195</td>
<td>10,126</td>
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</tr>
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<td>Annual AIDS deaths</td>
<td>46,417</td>
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<tr>
<td>Annual AIDS deaths - Adult</td>
<td>36,977</td>
<td>41,625</td>
<td>48,833</td>
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<td>Annual AIDS deaths - Children</td>
<td>8,712</td>
<td>10,861</td>
<td>13,570</td>
</tr>
<tr>
<td>Need for ART - Adult (15+)</td>
<td>622,589</td>
<td>643,536</td>
<td>669,368</td>
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<tr>
<td>Need for ART - Children</td>
<td>128,402</td>
<td>148,027</td>
<td>171,590</td>
</tr>
<tr>
<td>Mothers needing PMTCT</td>
<td>76,079</td>
<td>85,710</td>
<td>96,937</td>
</tr>
<tr>
<td>AIDS orphans</td>
<td>965,374</td>
<td>1,032,799</td>
<td>1,102,472</td>
</tr>
<tr>
<td>HIV population (15-49)</td>
<td>1,254,941</td>
<td>1,299,251</td>
<td>1,330,835</td>
</tr>
<tr>
<td>Number of new HIV infections</td>
<td>90,456</td>
<td>97,486</td>
<td>107,517</td>
</tr>
<tr>
<td>Incidence Adults 15-49</td>
<td>0.38</td>
<td>0.40</td>
<td>0.44</td>
</tr>
<tr>
<td>Annual AIDS deaths - Children (1-4)</td>
<td>1,897</td>
<td>2,538</td>
<td>3,350</td>
</tr>
<tr>
<td>HIV+ pregnant women with CD4 counts &lt; 350</td>
<td>37,955</td>
<td>40,383</td>
<td>42,775</td>
</tr>
<tr>
<td>New HIV infections - Males aged 15 to 24</td>
<td>9,354</td>
<td>12,520</td>
<td>14,412</td>
</tr>
<tr>
<td>New HIV infections - Females aged 15 to 24</td>
<td>21,353</td>
<td>24,935</td>
<td>31,860</td>
</tr>
</tbody>
</table>
ANNEX 1: Steps to update your Spectrum file in 2014

1. Download the updated software from www.futuresinstitute.org and load the software on your computer. Ensure you have the latest version of Java (Java 7) installed on your computer.

2. Open your most recent Spectrum file. Save a new file of the projection with a new name. Please keep the name short. Such as “CountryName XXJan2014”.

3. Spectrum has a new feature whereby all of the files related to the projection are included in one file which has the extension “.pjnz”. This function removes the need to export or import the files. You should change the default file type to PJNZ by clicking the Save As file type button and selecting PJNZ.

4. Update the population data by clicking on Manager then Default data. Be sure to click on DemProj to update the demographic data. To include the new demographic data you will need to be able to connect to the internet.

5. Open the programme statistics and enter the data on PMTCT and ART for 2013. Be sure to review the data from previous years to ensure it is accurate. Also remember that you must include either all percent values or all numbers for any single year. So for 2013 you cannot include 400 women on Option A and 13% receiving ART before the pregnancy. Check that the number of women on post-natal prophylaxis includes only those women who are receiving either option A or Option B (not Option B+) and that the post-natal numbers reflect the per-natal numbers.

6. Update any changes to the eligibility criteria for ART.

7. Select Advanced Options / Transition Parameters and choose “Use default values”.

8. Select Incidence / Configure. The following warning will appear:

   ![Warning](image)

   Click on ‘Invalidate’ this will reset your EPP curves. Click ok to move through each of the sub-populations and move on to the Define Populations page. NOTE: this will appear even if you have not changed your ART numbers because EPP now only uses ART in those aged 15-49, removing the ART for those over 50.

9. If you are a concentrated epidemic or a sub-national epidemic you will need to click on “Adjust to changed pop” on the define pops page.

10. Select Incidence / Surveillance. Add any additional surveillance or survey data.

11. Select Incidence / Curve fitting. Again the above invalidate pop-up window will appear. Click on ‘Invalidate’. Review the “Model parameters” for each sub-

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population and if there are large numbers of prevalence conditions or changes to EPP defaults, consider removing them or restoring the defaults before fitting. Make sure you have chosen the National run and Select “Fit All”

12. On the calibration page choose the appropriate calibration. The software will reset the calibration to the first calibration. If you have forgotten what option was used previously you can click on “Show startup calibrations” to see what the setting was in the previous file.

13. Review the prevalence and incidence curve under Fitting results. It might be useful to compare the epidemic curve results to your previous estimate. That can be done using the Compare button at the bottom left of the screen.

14. Click on Save Results

15. View the results from Results menu. Note the new estimated ART coverage available which can present coverage according to the National ART criteria or the percent of all people living with HIV who are receiving ART. The latter will be reported in future global reports.

16. Also look at the Results / AIDS Impact. Spectrum can estimate the number of deaths averted due to ART in your country or the number of child infections averted due to PMTCT.

17. Run the uncertainty analysis by selecting Tools (from the options at the top of the page), then Uncertainty Analysis. You should run the uncertainty using 1000 curves.

18. Finally, save the file. You should save the file as a PJNZ file. Do this by clicking on the button for “Save as Type” at the bottom of the save window and selecting PJNZ. Be sure to use the naming convention described in step 2 above.

19. Upload one file with the extension PJNZ to your designated Dropbox folder. Please write to Estimates@unaids.org if you need the link to the folder. Please alert Estimates@unaids.org when it is uploaded.
ANNEX 2: Checklist before submitting file

- Have PMTCT data been updated? Do they match GARPR?
- Have ART data been updated? Do they match GARPR?
- Are breastfeeding data correct?
- Have you updated population sizes (primarily for concentrated epidemics)?
- Have you reviewed the results, such as HIV prevalence, other key variables, AIDS impact variables
- Have you examined the graph of female-male ratio being used in Spectrum? This is especially important in concentrated epidemics where EPP sets this trend.
- Do the results seem comparable to alternative data sources?
- Have you added any notes to the source information?
- Have you run uncertainty?
- Have you included the resample results file in the export? The file size should be more than 5 MB.
- If yes to all of the above, please upload the file with extension PJNZ to Dropbox.