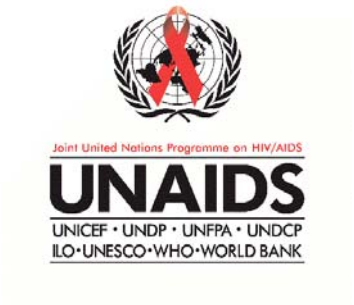

Estimating and Projecting National HIV/AIDS Epidemics

The models and methodology of the UNAIDS/WHO approach to estimating and projecting national HIV/AIDS epidemics

The UNAIDS Reference Group on Estimates, Models and Projections

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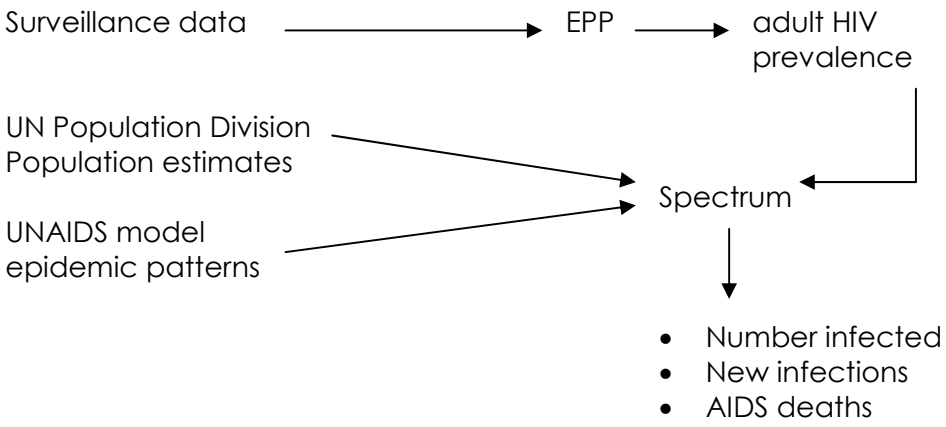
I. Quick Start Tutorial

This manual explains the methodology and computer programs used by UNAIDS/WHO to prepare national HIV/AIDS estimates. It is intended for use by national AIDS programs that wish to review and revise the estimates prepared for their country by UNAIDS/WHO. This chapter provides an overview of the procedures required to use the models to make a national estimate and projection. It describes the most basic application. Additional details on the methodology and assumptions and the procedures for customizing estimates are provided in the following chapters.

The UNAIDS/WHO approach to national HIV estimates requires the use of two special computer models: EPP (Estimation and Projection Package) and Spectrum. EPP and Spectrum are provided on CD-ROM and are available for download from the websites at UNAIDS (www.unaids.org) and the Futures Group (www.FuturesGroup.com). You may run the programs from the CD-ROM or install them on your computer.

The estimate is based on surveillance data. For generalized epidemics surveillance data from antenatal clinics are used. For concentrated and low-level epidemics the estimate is based on surveillance data from special populations, such as sex workers, men who have sex with men and injecting drug users. Data files for many countries are provided with EPP or data can be entered directly using the EPP data editor. The EPP program fits a simple epidemiological model to find the best fitting curve that describes the evolution of adult HIV prevalence over time. The Spectrum program reads the prevalence projection produced by EPP and calculates the number of people infected, new infections, AIDS cases and AIDS deaths. These calculations are based on population estimates provided by the United Nations Population Division and model patterns prepared by the UNAIDS Reference Group that describe the progression from infection to death, the distribution of infection by age and sex, transmission from mother-to-child and the effect of HIV infection on fertility.

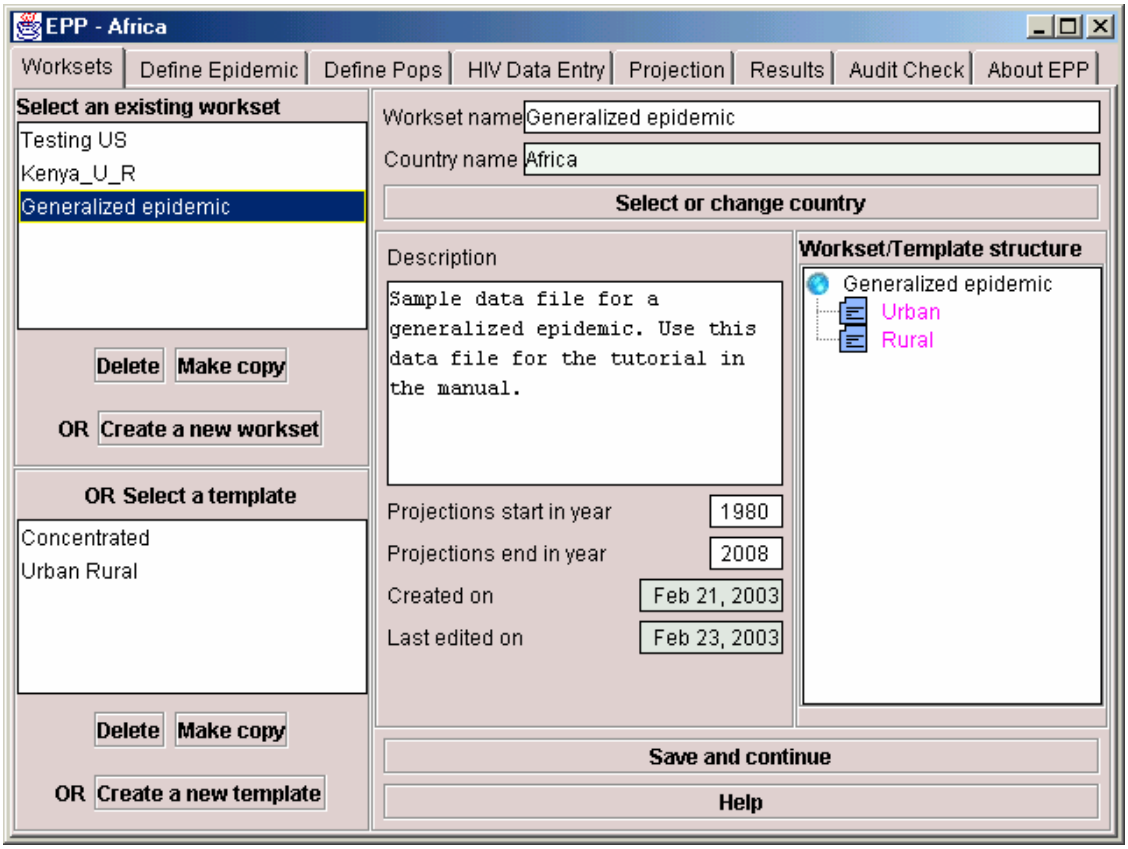


Step 1. Install EPP. You can install the EPP program from the CD-ROM. Put the CD-ROM in your drive. It should start automatically and display a menu. (If it does not start automatically, you can do this manually by starting Internet Explorer from the Windows "Start" menu, selecting "File", "Open", "Browse", clicking on the CD-ROM drive and double clicking on the file named "index.htm"). Select the first option from the CD-ROM menu. This will install the Java Runtime Environment (JRE) required by EPP and the EPP program itself. See Chapter III for more details.

Step 2. Start EPP. Start EPP by clicking the Windows "Start Menu" icon on the bottom left of your screen, choosing "Programs" and selecting "EPP". (Alternatively you can start Windows Explorer to find and double-click on the file named "EPP_multi.jar". If you accepted the standard installation it will be in the directory "C:\Program files\EPP" directory.) Be patient, it may take a moment for EPP to load.

Step 3. Selecting the country file. The EPP screen will look like the one below. Select the country you want to use by selecting the country from the list under the label "Select an existing workset". For this tutorial select the file named "Generalized epidemic."

Once you select a data file, the details of the file will be displayed. These include the country name, a description and the workset structure. The structure describes the different epidemics that will be modeled. For generalized epidemics the structure usually contains urban and rural epidemics while for concentrated epidemics the structure usually includes special sub-populations, such as sex workers and men who have sex with men. The screen will also display the first and last year of the projection. To use this file click on the button "Save and continue."



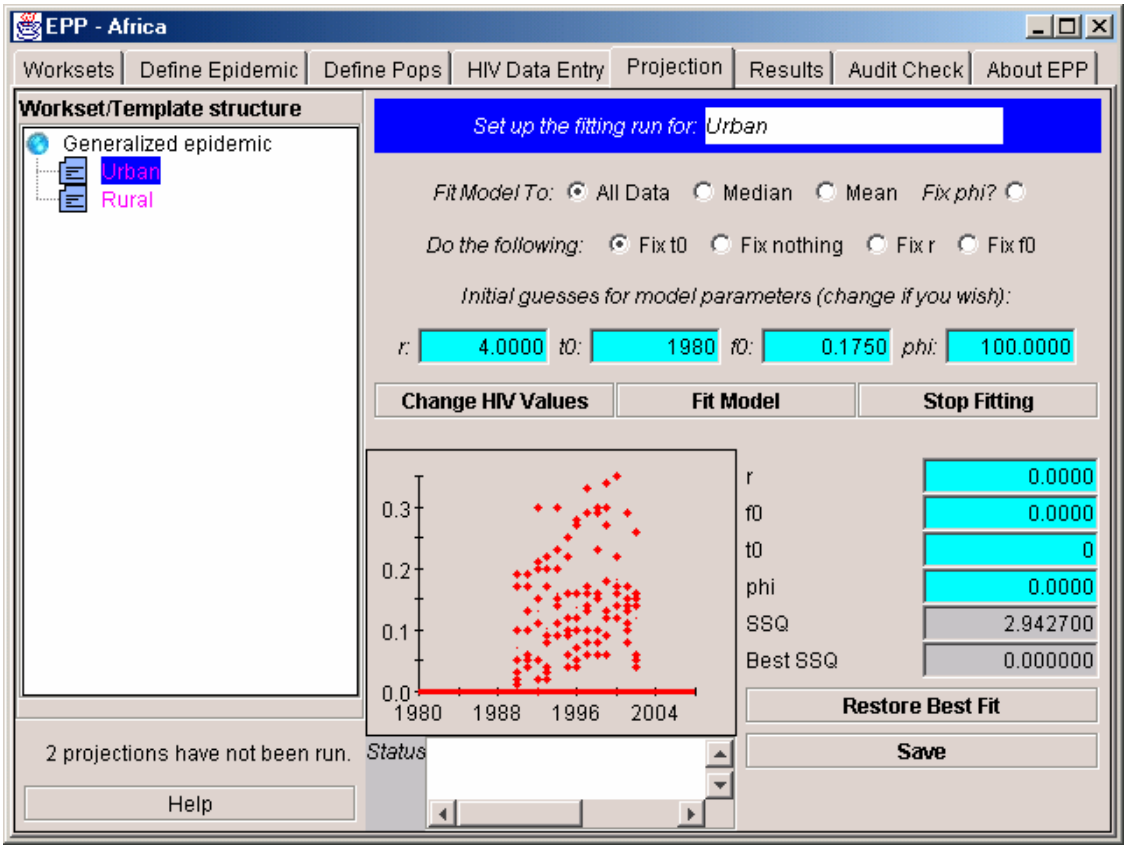
Step 4. Define epidemics. The program will now display the "Define epidemics" tab. This sheet is used to define or modify the types of sub-epidemics that will be modeled. For this tutorial we will not change the epidemic structure. To accept the current structure and continue, click "Save and continue."

Step 5. Define populations. This screen allows you to enter or modify information about the characteristics of the population associated with each sub-epidemic. For this tutorial, we will accept the default values provided. To accept these values and continue, click "Save and continue" for each sub-epidemic until the program advances to the "HIV data entry" tab.

Step 6. HIV data entry. This screen allows you to enter surveillance data for each sub-epidemic. For this tutorial we will accept the data provided. Click the "Save data" button for each sub-epidemic until the program advances to the "Projection" tab.

Step 7. Projection.

This screen allows you to fit an epidemic curve to the surveillance data for each sub-epidemic. The screen will look like the picture below.



You should see the surveillance data points for the urban epidemic appear in the graph at the bottom of the screen.

The radio buttons on the top right of the screen set several options. The buttons following "Fit Model To:" allow you to select all the surveillance data or just the median or mean values for each year. Make sure the button for "All data" is selected.

The button for "*Fix phi?*" should also be selected.

The buttons next to "Do the following:" allow you to tell the program how to fit the data. Make sure that the button for "Fix t0" is selected. This will fix the start year of the epidemic and let the model find the remaining parameters that give the best fit to the surveillance data. The value for "t0" should set to the first year of the epidemic, generally one or two years before the year of the first reported AIDS case. The value for "phi" should initially be set to 100. Later you can test the effects of a lower value of "phi" which is used when prevalence is declining.

Now click the button labeled "Fit model" to start the fit. The program will search for the parameter values that provide the best fit to the surveillance data. When the program finishes, it will display the best fitting curve on the graph.

If you do not like the curve produced by the program, you can modify it by changing the values of some of the model parameters. You do this by changing "r", "f0", "t0", or "phi" in blue cells to the right of the graph. To change any of these values, type in a new value and press the Enter key. This changes the curve directly and allows you to modify the curve to fit the data better. The "best" fit will be one that reduces the sum of squared errors ("SSQ") to a minimum. If you change any values be sure to press the "Enter" key after typing the value.

The four parameters that you can change and their effects on the prevalence curve are as follows:

- **t_0** – The start year of the HIV/AIDS epidemic. An earlier start year will cause the curve to rise earlier and a later start year will produce a curve that starts later.
- **r** – The force of infection. A large value of r will cause prevalence to increase rapidly while a small value will cause it to increase slowly.
- **f_0** – The initial fraction of the adult population that is exposed to the risk of infection. The parameter determines the peak of the epidemic curve.
- **phi** – The high-risk adjustment parameter. The value of phi determines the amount of decline in prevalence after it reaches a peak. A large value of phi will produce a small prevalence decline, while a small value of phi will produce a large prevalence decline.

Additional details on how to modify the model fit are provided in Chapter IV.

Once you are satisfied with the curve for the rural epidemic click "Save" to save the results and move to the rural epidemic. Repeat the process for the rural epidemic: click "Fit model" to find the best fit and then modify the parameters if necessary.

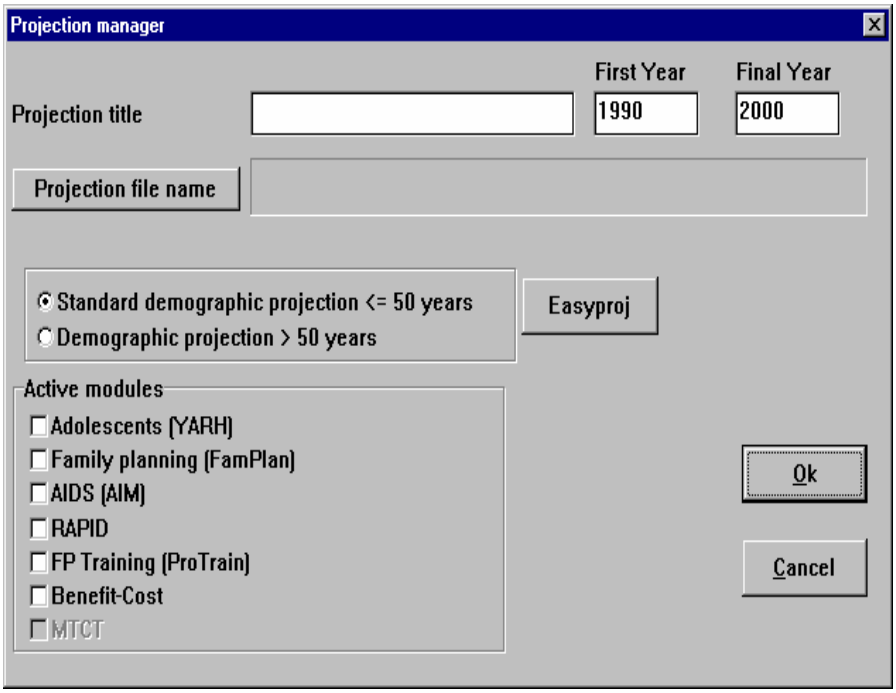
Once you have fit the urban epidemic click "Save" to save the results and move to the "Results" tab.

Step 8. Results. In the "Results" display you can see the curves for the rural and urban epidemics and the combined curve for the entire country. Select the curves you want to see by checking the boxes next to the epidemics in the box in the upper right of the display. You can see the results in table form by clicking the button "Numerical results".

Step 9. Save the results. Once you are satisfied with the curve fits, save the results in a Spectrum file by clicking the button "Write Spectrum file." This button is only shown when you have selected "Numerical results."

Step 10. Start Spectrum. Start the Spectrum program by selecting it from the menu on the CD-ROM or by selecting it from the "Start" menu on your computer.

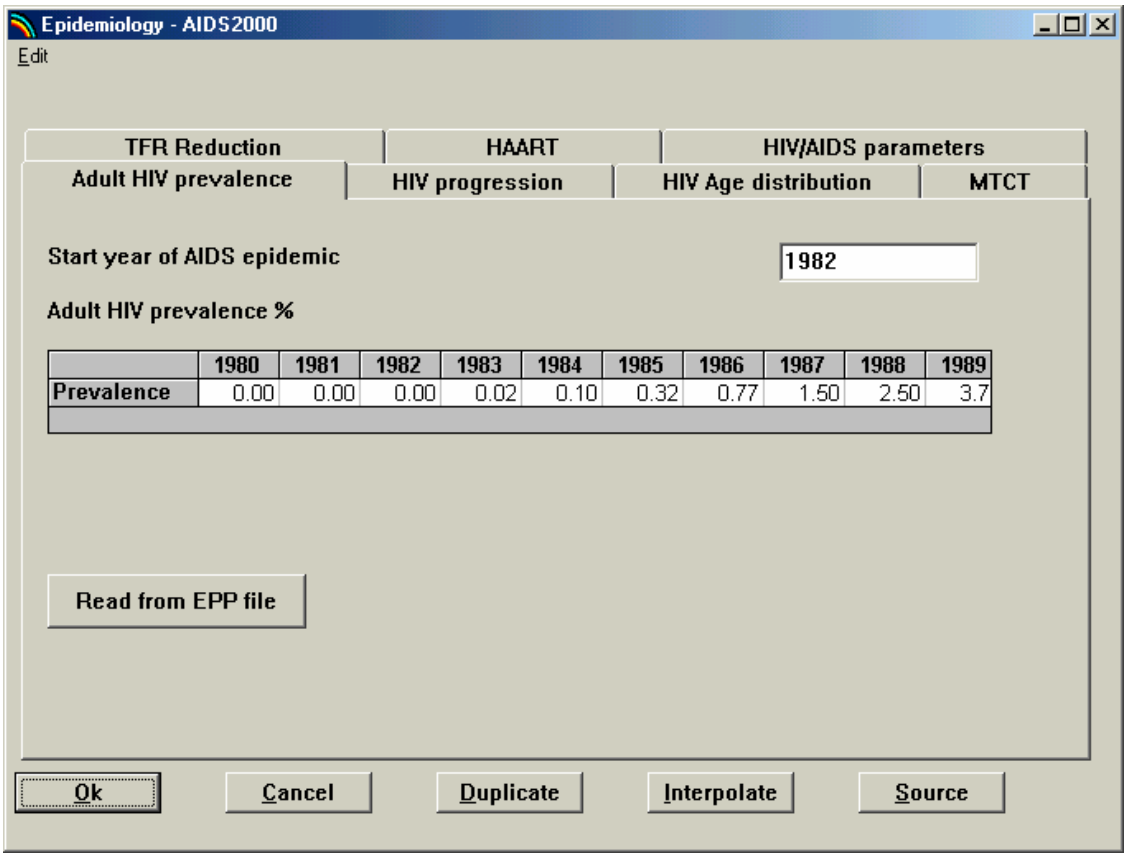
Step 11. Create a population projection. Create a new population projection by selecting "File" and "New" from the Spectrum menu. The "Projection manager" dialogue box will appear and will look like the following screen:



Click in the box next to "Projection title" and type a title for the projection. Set the "First year" to 1980 and the "Final year" to 2005. Click on the "Projection file name" button and enter a file name for this projection. (Be sure to select a location on the hard disk, C:, drive for the file and not on the CD-ROM since the program cannot write a file to the CD-ROM.) Click the check box next to "AIDS (AIM)" to add the AIM module to the program. Then click the "EasyProj" button. From the EasyProj screen choose your country from the list. Once you click "OK", the program will load all the necessary demographic data.

Step 12. Read the prevalence estimate. Select "Edit" and "AIDS (AIM)" from the Spectrum menu and "Epidemiology" from the dialog box. Then you will see the editor for the prevalence projection. It will look like the screen shown below. Click the button "Read from EPP file". This will display a "file open" dialog box. Navigate to the directory where your EPP output file is stored (for example C:\Program files\EPP\eppout) and select the appropriate file. The prevalence projection from EPP will be read into

Spectrum and displayed in the editor. Click the "Ok" button to complete this step.



Step 13. Display the output. From the main Spectrum menu, select "Display", "AIDS (AIM)" and "Epidemiology". You will then see a drop down menu with a list of HIV/AIDS indicators. The key indicators are summarized in the last two choices in the list "Adults 15-49 summary" and "Child AIDS summary". Select one of these choices. The first time you select a display after you have changed input values, you will see the message "Inputs have been changed. Re-project population now?" Click on the "Yes" button to tell Spectrum to re-calculate the projection. Next you will see the display configuration dialog box. Click OK and you will see a table displaying the results of the projection.

Step 14. Save the projection. Save the projection by selecting "File" and "Save" or "Save As" from the Spectrum menu.

II. Introduction

UNAIDS and WHO prepare estimates of the magnitude of the HIV/AIDS epidemic every two years. Global and regional estimates include the number of adults and children living with HIV, the annual number of new infections and the current and cumulative number of AIDS deaths. These estimates are disseminated widely and used by many international and national organizations for advocacy and planning.

UNAIDS/WHO prepare estimates for each country in the world. These country estimates are aggregated to produce the regional and global figures that are released on World AIDS Day. The first draft of the country estimates is produced at UNAIDS headquarters in Geneva. These estimates are then sent to the AIDS control programs in each country for comments and revisions. The country comments are then incorporated into revised country estimates that become the basis for the official figures released at the World AIDS Conferences.

The purpose of this manual is to explain the methodology and computer programs used by UNAIDS to prepare the country estimates. This manual is intended for use by national experts who will be asked to review the initial UNAIDS estimates. It is designed to help them understand how the UNAIDS estimates are prepared and to use the same computer models to review and revise these initial estimates. Additional detail on these methods and assumptions is available in Walker, *et al*. "Improved methods and assumptions for estimation of the HIV/AIDS epidemic and its impact: Recommendations of the UNAIDS Reference Group on Estimates, Modelling and Projections" *AIDS* 2002;16:W1-W14.

The national estimates are based primarily on HIV surveillance data from each country. The methodology for producing national HIV prevalence estimates from surveillance data has been developed by the UNAIDS Reference Group on Estimates, Models and Projections. This methodology is implemented through two computer programs: the Estimates and Projection Package (EPP) and Spectrum. The 2001 round of estimates was prepared using this methodology and these computer programs and the 2003 round will be prepared using the latest version of these programs.

The following chapters provide information on the methodology, data needs, assumptions, outputs and computer programs used to produce these estimates. The program can be downloaded from web sites at UNAIDS (www.unaids.org) and the Futures Group (www.FuturesGroup.com). Chapter III describes how to install the computer models. Chapter IV Describes the process for estimating the time trend of adult HIV prevalence based on surveillance data using the EPP model. Chapter V describes how to use the prevalence projection in Spectrum to estimate the numbers of people infected, new infections and AIDS deaths.

Chapter VI provides the details on the methodologies employed. Chapter VIII provides additional information on resources available to provide assistance and training in the use of these tools.

The members of the UNAIDS Reference Group on Estimates, Models and Projections who participated in the work described here are Marc Artzrouni, Tim Brown, Griff Feeney, Geoffrey Garnett, Peter Ghys, Nicholas Grassly, Stefano Lazzari, David Schneider, Karen Stanecki, John Stover, Bernhard Schwartländer, Neff Walker, Peter Way, Ping Yan, Basia Zaba, and Hania Zlotnik. Many others provided data and participated in discussions about generalizing the available data to apply to the global estimates. The EPP model has been programmed by Panuchart Bunyakiati, Tim Brown and Wiwat Peerapatanapokin at the East West Center. Spectrum is a product of the USAID-financed POLICY Project implemented by the Futures Group.

III. Installing the computer models

The UNAIDS/WHO approach to preparing national HIV estimates involves the use of two computer models: the Estimates and Projections Package (EPP) and Spectrum. These models are available on CD-ROM from UNAIDS and other sources. Both models can also be downloaded from web sites at UNAIDS (www.unaids.org) and the Futures Group (www.FuturesGroup.com).

A. Requirements

To use EPP and Spectrum you will need a computer system with the following characteristics:

- 32MB or more of RAM
- 40 MB of free space on your hard disk
- Windows 95, Windows 98, Windows Me, Windows 2000 or Windows XP

B. Installing EPP

Follow these steps to install the EPP model.

1. If you have the CD-ROM version of EPP, install the EPP model on your hard disk by selecting "Install EPP" from the menu of the CD-ROM.

2. If you do not have the CD-ROM, you can download the EPP program from the Internet (at www.FuturesGroup.com) and follow the instructions provided. (Note that EPP requires the Java Runtime Environment (JRE) version 1.3.1. You can download the installation program for the JRE from the following web site: http://java.sun.com/j2se/1.3/jre/download-windows.htm. This will put a file on your computer called: j2e-1_3_1_01-win.exe. Double click on this file to install the Java Runtime Environment on your computer.

   The EPP installation program will create several subdirectories. The most important are:

   epproj – stores input files. Any EPP input files should be saved in the *epproj* directory. If they are stored in this directory they will then appear in window of the EPP model and can be easily selected. Each projection is stored as a separate file named *.epr for *EPP projection*. The file consists of the country name, the complete set of urban and rural input data, the

model fits which have been made to this data, any adjustments made to make to those fits, and a comment field to document the projection.

eppout – stores output files. Output from EPP will be written to this directory by default. Output is stored in a file with the extension "*.spt". Files in this format can be read by Spectrum.

epppop – holds the UN pop database. It holds the database (*UNPop2000.csv*) of demographic variables required by EPP.

3. To run the EPP model:
    a. Click on the Windows "Start" menu button, select "Programs" and then select "EPP"; or
    b. Use Windows Explorer to go to the EPP directory and double click the file names EPP_multi.jar; or
    c. Click on the "Start" button, select "Run", browse to the EPP directory, select the EPP_multi.jar file, click "Open" and click "Ok".

C. Installing Spectrum

The Spectrum program is distributed on CD-ROM and through the Internet at http://www.FuturesGroup.com. It can be run from a CD-ROM or installed on a hard disk. Spectrum will run on any computer running Windows 95 or later Windows versions. It requires about 9MB of hard disk space.

To install Spectrum from a CD-ROM or from a file downloaded from the internet, just double click on the file named "spectrum.exe". This will start the installation program. Just follow the instructions on the screen to complete the installation.

D. 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 "Options" and "Environment" 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.

IV. Estimating adult prevalence of HIV-1

A. Introduction

The EPP model is used with the available surveillance data to estimate the time trend of adult prevalence of HIV-1 at the national level. The methodology behind this approach is described in detail in Chapter VI.

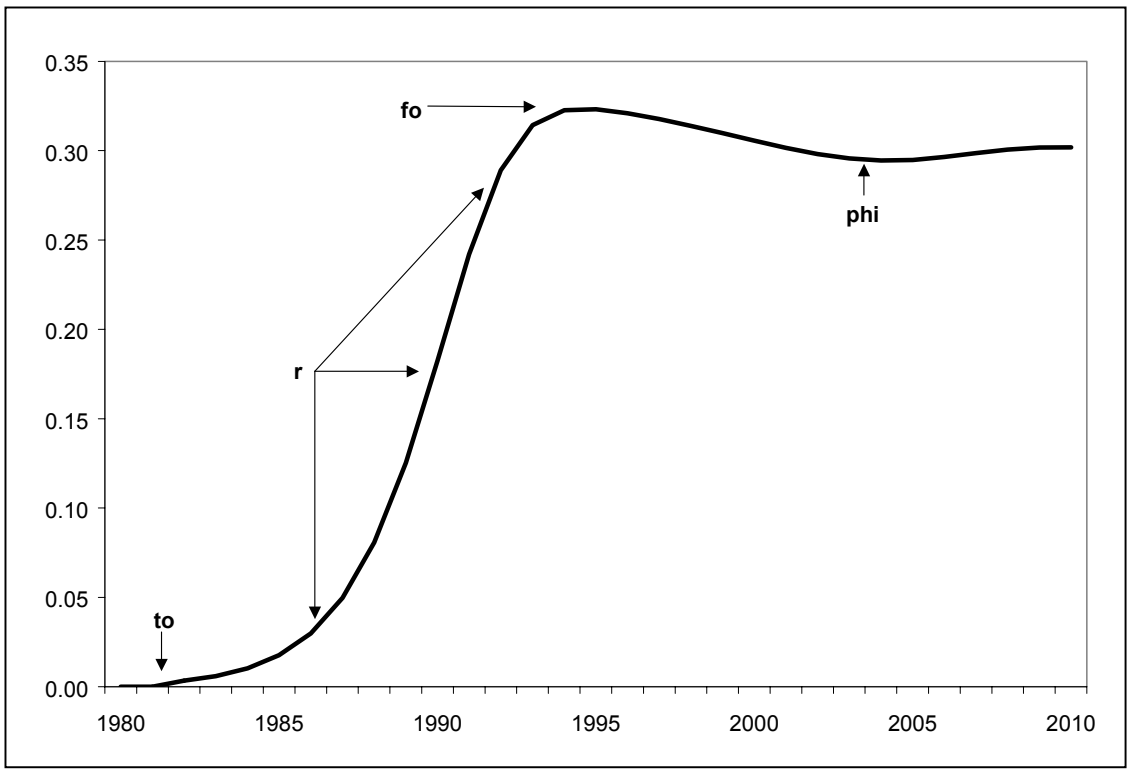
The time trend of HIV prevalence is estimated by fitting a simple epidemiological model to surveillance data. In generalized heterosexual epidemics the model is fit to urban and rural data separately. These estimates are then combined to produce a national estimate. For concentrated and low-level epidemics the epidemic curves are fit to special population groups (such as sex workers, men who have sex with men, and injecting drug users). The separate epidemic curves are aggregated to produce the estimate and projection for the entire country.

The model uses four parameters to fit the surveillance data. The shape of the epidemic curve and the influences of these four parameters are shown in Figure 1.

These parameters are:

- **t_0** – The start year of the HIV/AIDS epidemic.
- **r** – The force of infection. A large value of r will cause prevalence to increase rapidly while a small value will cause it to increase slowly.
- **f_0** – The initial fraction of the adult population that is exposed to the risk of infection. The parameter determines the peak of the epidemic curve.
- **phi** – The high-risk adjustment parameter. This parameter determines the degree to which susceptible people who die from AIDS are replaced by people who previously were not at –risk. The value of phi determines the amount of decline in prevalence after it reaches a peak. A large value of phi will produce a small prevalence decline, while a small value of phi will produce a large prevalence decline.

Figure 1. The parameters determining the shape of the epidemic curve



The next sections explain how to prepare the input data, run the model, find an appropriate fit to your data, and save your results.

B. Preparing the input data

The distribution copy of EPP has country data files for most countries in the world. You can examine the data file for your country and modify it as necessary. If there is no data file for your country, you can create one by entering the data directly into EPP.

For generalized heterosexual epidemics surveillance data from antenatal clinics are most appropriate. For concentrated and low-level epidemics surveillance data from special population groups, such as sex workers, men who have sex with men, injecting drug users, STI patients, etc. can be used to estimate separate epidemics that can be aggregated to a national estimate.

For generalized epidemics, sites may be classified as urban or rural or each site can be examined separately. The UNAIDS estimates usually classify the sites as

belonging to "major urban areas" or "outside urban areas". You may want to review the sites and classifications to make sure they are appropriate for your country. Since good information is often lacking regarding the characteristics of surveillance sites you may find that some data needs to be re-classified. Where possible, the classification of surveillance sites should match the census classifications. That is, sites in towns that are classified as urban by the census should be classified as urban in the EPP data file. This will ensure that the urban and rural prevalence estimates are appropriate for the population figures used to combine the urban and rural estimates into a national estimate.

The EPP model contains epidemiological parameters that describe the dynamics of HIV-1 infection. It is not appropriate for projecting HIV-2 prevalence. Only surveillance data relating to HIV-1 should be used.

C. Creating an epidemic structure

EPP is generally used to estimate and project the HIV/AIDS epidemic in a particular country. A national epidemic is made up of many smaller epidemics among special populations. HIV will start spreading earlier in some groups than others. The pace and ultimate magnitude of the epidemic will differ by population sub-group. Surveillance data are usually collected to monitor the status of the epidemic in different sub-populations. These might include pregnant women in urban or rural areas, sex workers, men who have sex with men (MSM), injecting drug users (IDU), STI patients, TB patients, blood donors, migrants, military personnel, truck drivers and others. EPP allows you to estimate different epidemic curves for each important sub-population and then combine them into a national estimate.

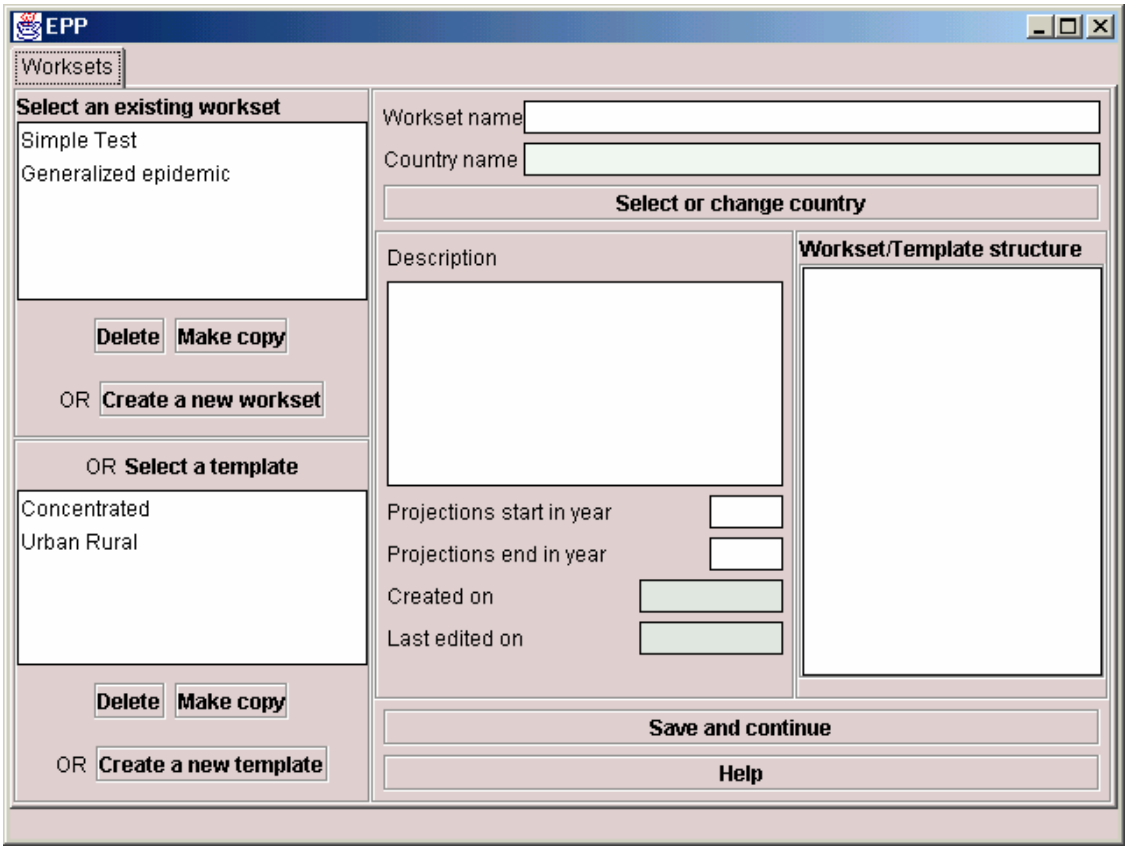
In ***generalized epidemics***, the prevalence among pregnant women is usually a good indicator of prevalence in the total adult population. Prevalence is usually higher in urban areas than in rural areas. Therefore, most countries with generalized epidemics can be modeled as consisting of two sub-epidemics: urban and rural epidemics among adults.

In ***concentrated and low-level (low prevalence) epidemics*** HIV infection is primarily found in certain sub-populations. In these countries prevalence among pregnant women is not a good indicator of total adult prevalence. Therefore, countries with concentrated epidemics are usually modeled with several sub-epidemics. The particular sub-epidemics selected for each country will depend on the surveillance data available. Typical sub-epidemics include sex workers, clients of sex workers, MSM, IDU patients with sexually transmitted infections (STI).

More complicated epidemic structures can be defined, but one of these two general types will be appropriate for most countries.

D. Understanding the EPP screens

When you start EPP you should see a screen that looks like the one shown below.



Basic interface

The interface for this version of the EPP uses a "tabbed" model. Each of the key functions of the model is kept on a separate "tab" to keep the interface clean and uncluttered. The tabs are: 1) Worksets; 2) Define epidemics; 3) Define pops; 4) HIV data entry; 5) Projection; 6) Results; 7) Audit check and 8) About EPP. These are described in more detail below. You create a projection by stepping through these tabs in order.

The Worksets Tab

This is the opening panel and the starting point for all projections. Here you select an existing projection or start a new one.

Select an existing projection by clicking on the projection name in the list of existing projections. This list is found in the box on the upper left corner of the screen under the label "Select an existing workset". Click on the projection you want to use. When you select a projection from the list, the relevant information for that projection will appear in the right hand part of the window. This information includes:

1. *Workset name* – which can be any legitimate Windows filename. The files themselves are stored as *<Workset name>.epr* in the *eppproj* directory.
2. *Country Name* – which is chosen from the United Nations list of existing countries when the projection is first created.
3. *Description* – a text description of this projection. This is created when you create or edit the projection. This description can be of arbitrary length and if it is too large to fit in the space provided, scrollbars will appear.
4. *Projections start year and Projections end year* – these are the years in which the projection begins and ends. Note that this is not the same as the start date of the epidemic. You may decide to start your projection in 1980, because it is a census year, but the HIV epidemic may not have started until 1985.
5. *Created on* – date on which the projection was first created
6. *Last edited on* – date on which the projection file was last changed in any way (this can include editing projection information, adding or changing data, running a new fit, or changing any of the model results.)

Create a new workset by selecting one of the three option buttons:

- *Create a new workset*. This option creates a new workset only. You will have to specify the types of sub-epidemics for this workset.
- *Select a template*. This option creates a new workset using one of the available templates. This is the easiest option and should be used when ever one of the standard templates is appropriate for the country you are using.
- *Create a new template*. This option lets you define an epidemic structure that can be applied to a number of different epidemics.

1. ***Create a new workset***. Click on the button "Create a new workset". You should then fill in each of the items described above: workset name, country name, description, projections start year and projections end year. Select the country name by clicking on the button "Select or change country." The

program will read the appropriate demographic data for that country from a database of information prepared by the United Nations Population Division.

2. ***Select a template***. The templates have sub-epidemic structures already defined. There are two general templates: "Concentrated" and "Urban rural." The concentrated epidemic has sub-epidemics for sex workers, sex worker clients and injecting drug users (IDU). The "Urban rural" template has sub-epidemics for urban and rural populations. It is most appropriate for generalized epidemics, where prevalence in antenatal clinics is above one percent.

3. ***Create a new template***. You can also create a new template. This option is similar to "Create a new workset" except that it allows you to save the epidemic structure to use with other data sets.

Once you have entered all the data required on the "Worksets" display, click the "Save and continue" button. The display will move to the "Define epidemics" tab.

The Define Epidemics Tab

In this display, the program will show the structure of the epidemic. If you have selected a country that has a generalized epidemic, then the epidemic structure will look like this:

- Generalized epidemic
    - Rural
    - Urban

If you have selected a concentrated epidemic the epidemic structure will look something like this:

- Concentrated epidemic
    - Sex workers
    - IDU
    - MSM
    - Clients
    - Remaining population

In both cases the national epidemic is composed of sub-epidemics. The sub-epidemics must add up to the national total. For this reason, the category "Remaining population" may appear. In the concentrated epidemic not all infections will occur in the sub-populations specified. In this case, "Remaining population" refers to the rest of the adult population not included in any of the specified sub-populations.

If you have selected prepared country file or decided to create a new file from a template, then the epidemic structure should already be correct. In this case, you can click the "Save and continue" button to go to the next tab.

If you want to modify the epidemic structure, you can add an epidemic or a projection. A ***projection*** is a component of an ***epidemic***. The generalized and concentrated epidemic templates have a single national "epidemic" composed of a number of "projections" (urban and rural or sex worker, IDU, clients, etc.). If you wanted to make separate estimates for different regions of the country, each with data on sub-populations, you might create a structure like this:

- Concentrated epidemic
  - East
    - IDU
    - MSM
    - Sex workers
    - Remaining population
  - West
    - IDU
    - MSM
    - Sex workers
    - Remaining population
  - North
    - IDU
    - MSM
    - Sex workers
    - Remaining population
  - South
    - IDU
    - MSM
    - Sex workers
    - Remaining population

You can create this example by clicking the "Add epidemic" button to add the epidemics "East", "West", "North" and "South." Then select each epidemic in turn and click the "Add projection" button to add "IDU", "MSM" and "Sex workers."

Once you are satisfied with the epidemic structure, click the "Save and continue" button to advance to the next tab.

The Define Populations Tab

In this screen you provide demographic information about each sub-population. The program will start with the first sub-population in the epidemic structure.

Once you enter the information for this sub-population click the "Save and continue" button and the program will advance to the next sub-population. An indicator at the bottom left of the screen will show "Populations not defined:" This is the number of populations for which you have not yet entered the demographic information.

If you are working with a country data set that came with EPP then you should not have to do anything on this page. You can simply advance to the next tab by clicking on the "HIV Data Entry" tab. If you need to modify the population data or you are creating a new projection then you will need to follow the instructions below.

When entering information be sure to press "Enter" after typing each number. This will make the program accept the entry. If you do not press "Enter" the number will not be accepted.

For each sub-population you need to enter the following information:

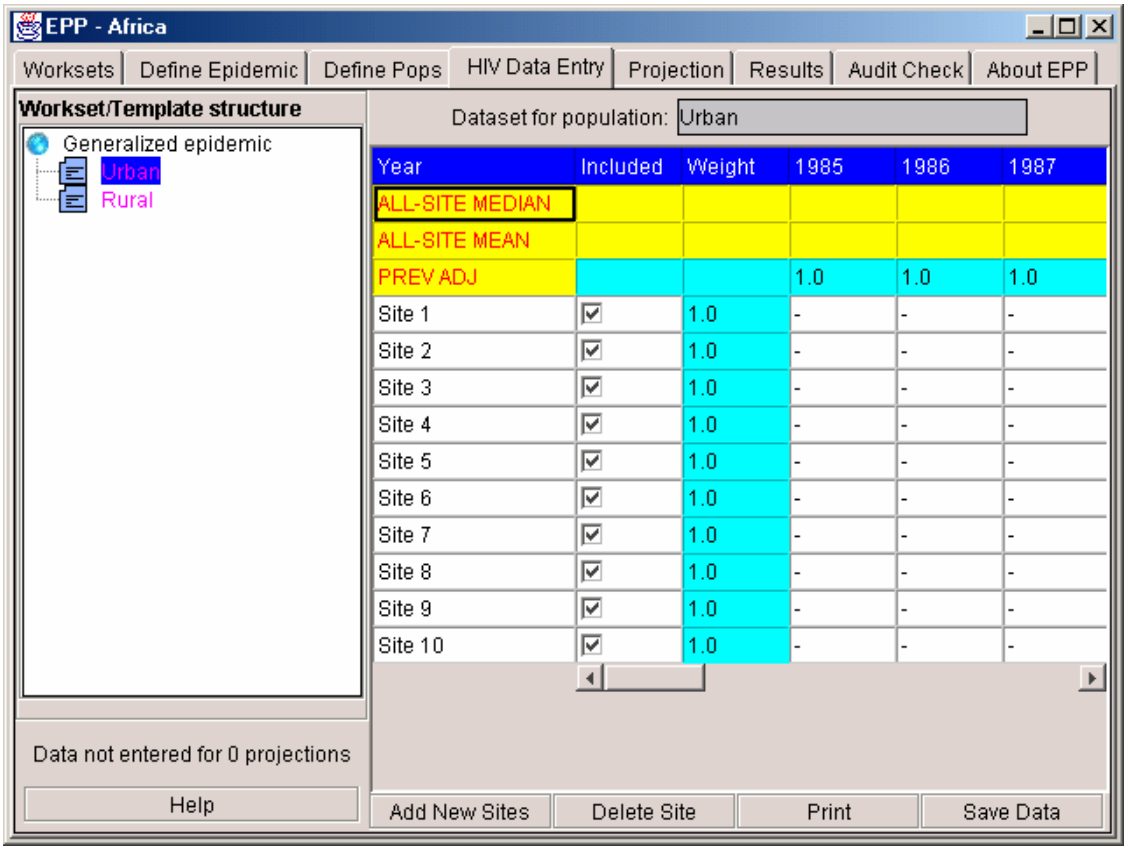
- *Total population in the workset*: This is the number of adults 15 and older in the national population in the year specified in the next box.
- *Year*: The year for which the population size is provided. Generally this should be the first year of the projection.
- *Remaining population to be assigned*: You do not enter this number. It is calculated to show you how much of the population still needs to be assigned to a sub-population.
- *Urban, rural or both*: Select the appropriate button to specify the type of population.
- *Special pop?:* If the population you are defining is FSW (female sex workers), IDU (injecting drug users) or MSM (men who have sex with men) then select that button. Otherwise select to "No" button.
- *Population 15 and over*: The number of adults 15 years and older in the sub-population.
- *Percentage male*: The percent of the population that is male.
- *Birth rate in 15+(b)*: The annual number of births divided by the population 15 and older. For special populations, such as FSW, IDU or MSM, this rate should reflect the number of new members entering the group each year divided by the size of the group.
- *Survival to age 15 (l15):* The proportion of births that survive to age 15.
- *Mortalty in 15+ (mu)*: The proportion of the population that dies each year from causes other than AIDS.
- *15+ growth rate (gr):* The annual growth rate of the population.

When you finish entering the data for a population click the "Save and continue" button to advance to the next population. Once you have defined all the populations, the "Save and continue" button will take you to the next tab.

The HIV Data Entry Tab

The HIV Data Entry Tab is the place to enter your surveillance data. If you are using one of the pre-defined data sets the surveillance data may already be entered. In that case you can review the data for completeness. If it is complete you can advance to the "Projection" tab.

The screen will look something like this:

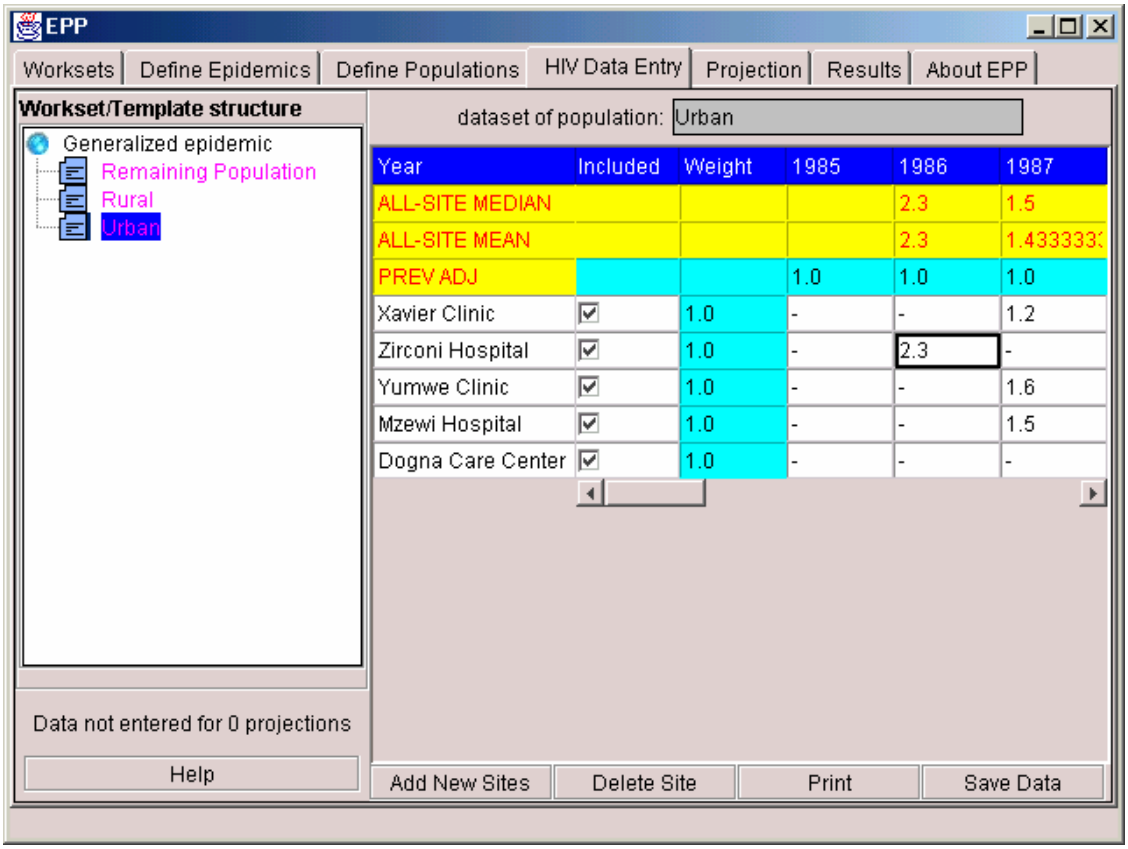


There is a separate data entry spreadsheet for each population. In the example shown above, there is a separate sheet for "Urban" and "Rural". Surveillance data are entered in the white cells of the spreadsheet. Use a separate row for each surveillance site. You can add new rows by clicking the "Add new sites" button. Enter the name of the site in the first column. The second column should be checked if that site is to be included in the projection. You can remove the check if you want to omit that site from the projection. The "weight" column allows you to assign a weight to each site. You might want to assign weights less than one if the site represents a small population or if the quality of the data from the site is suspect. Assigning a weight of zero is the same as omitting the site from the projection.

For each site enter the surveillance data that are available in the corresponding years. You may leave years blank if there are no data for those years.

In the row labeled "Prev adj" you can enter an adjustment factor for all the prevalence data in that year. This feature is often used with data from rural sites. In many cases rural sites are located in the largest rural settlements and may over-estimate prevalence in the most remote areas. To make the rural surveillance data more representative of the total rural population, you might set the prevalence adjustment to 0.8 for all years.

After entering data for a number of sites the screen might look something like this:



Note that a prevalence estimate of 12% should be entered as 12, not as 0.12.

The second and third rows contain the *annual medians* and *means* for all sites entered for that year. These values are automatically updated by the spreadsheet each time a value is entered into a cells.

The color-coding is as follows:

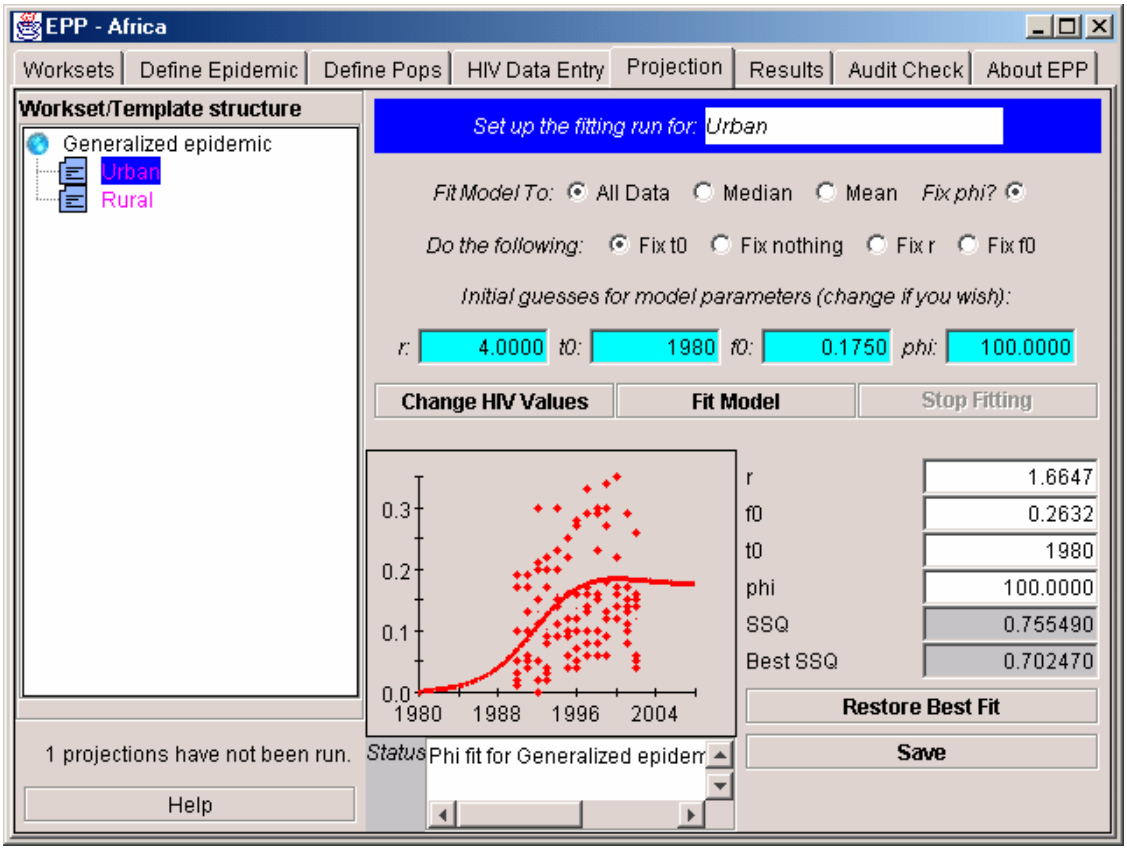
- Yellow cells – are calculated by the program from the data you enter.

- Light blue cells – defaults are provided by the program (1.0 in the case of prevalence adjustment), but you can change these if so desired.
- White cells – are user-entered data. In this case this includes both site names and actual prevalence data values.

Once you have entered all the surveillance data for each population, click the "Save data" button to save the data and advance to the Projection tab.

The Projection Tab

This screen is used to fit epidemic curves to the surveillance data. It will look something like this:



You need to fit an epidemic curve for each of the populations shown in the workset structure. To fit the curve, follow these steps:

1. Select an option next to "Fit Model To:" You can fit the curve to all the surveillance data or to the median or mean for each year. Usually you will use all the data. You might want to use the median if you have some data points that appear to be extraneous outliers. You might want to try

the mean or median if you have so many points that it is hard to see the trend in the data. **You should generally select the option "*Fix phi?*" This will allow you to fit the model first with the default assumption that prevalence is not declining. Later you can see whether a curve with declining prevalence provides a better description.**

2. Select an option next to "Do the following:" In the most general use of the model, it will search for the best values for all four parameters: t_o, r, f_o and phi. However, generally you will know the start year of the epidemic. This is often estimated as two years before the first AIDS case report. If you do know the start year of the epidemic then it is best to select the option to "Fix t_o." This will allow you to find the best fitting curve more quickly. You can also fix r or f_o and have the model fit the other parameters. You might do this if you were fitting several similar epidemics and wanted them to all use the same value of r or f_o. You can also choose to "Fix nothing" but the model may take a long time to find the best fit.
3. The next row shows the initial guesses for each of the model parameters. In general these values will not have much influence on the final fit. However, if you choose to fix t_o, r or f_o then you should make sure that the initial guess for that parameter is set correctly, since the model will not change it. Typically you would fix t_o and then enter the start year of the epidemic next to t_o in this row. If you have selected the option "*Fix phi?*" then you should make sure that phi is set to a large value, such as 100.
4. Once you have completed the first three steps you can click the "Fit model" button. The program will search for the best fitting curve for the surveillance data. The result will be displayed as a red line in the graph and the parameter values will be shown in the boxes to the right of the graph.
5. There are four HIV related parameters in the model, which are set to default values. These values have been determined by the Reference Group based on a review of available evidence. You should not normally have to change them. To view or change values, click the "Change HIV Values" button. A window will pop up showing the values for thefour parameters:
   - *Alpha and beta*. The parameters defining the survival curve.
   - *Vertical transmission*. The rate at which HIV infected women transmit HIV to their newborns.
   - *Fertility reduction*. The reduction in fertility of women living with HIV. This should be a value from 0 (no fertility) to 1 (full fertility).
6. If you are satisfied with the fit you can select the next population from the workset structure and repeat the fitting process.

Exploring the effects of changing the parameters

Having done a fit, it is sometimes useful to be able to see the effect of changing the model parameters. This can be done by entering a new value for any of the parameters to the right of the graph and pressing ENTER. The model will then be recalculated using that new value and the result displayed in the graph.

If at any point you wish to return to the program's estimate of the best-fit model, just click the "Restore Best Fit" button and these values will be returned. This will discard the current values.

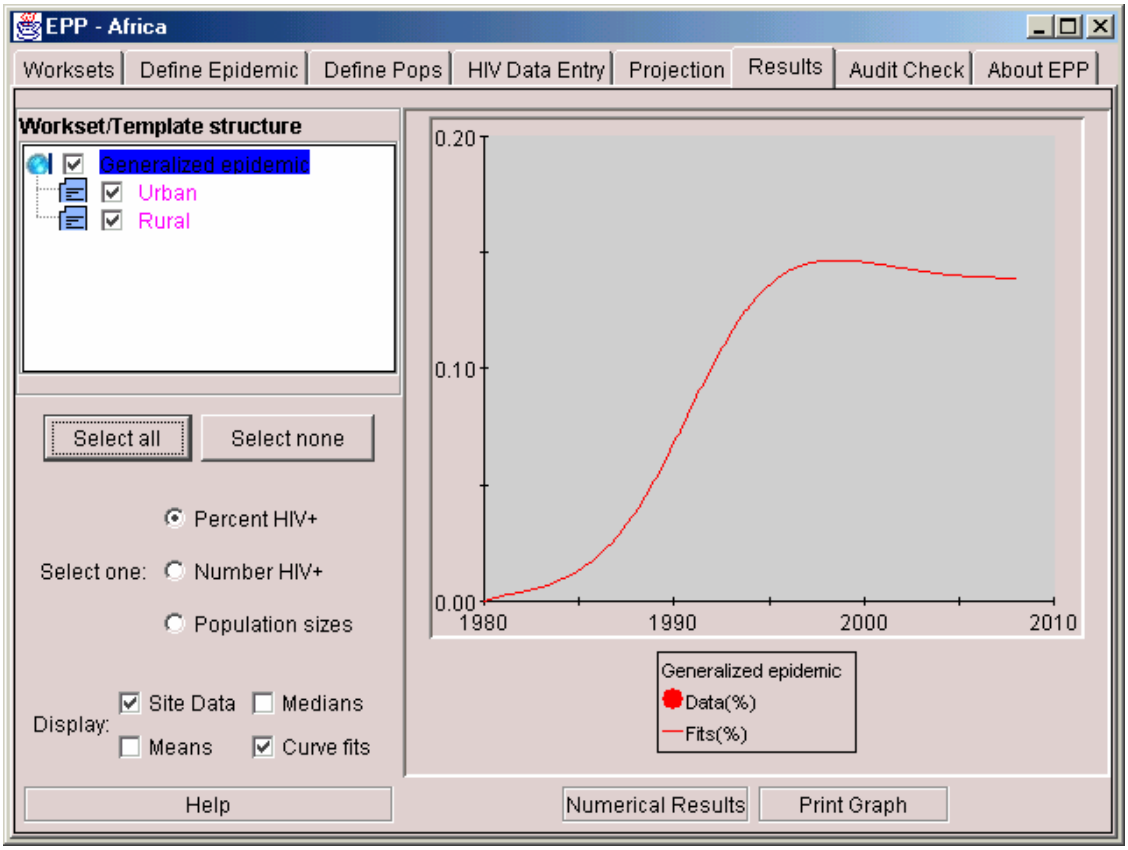
See section E. Fitting the Model below for more details on how to modify the fit to produce the most reasonable result.

Once you have an acceptable fit, click the "Save" button and these values will be stored in the projection file along with the best-fit values.

You should then repeat this procedure for each population in your workset. Once you have completed all the populations you can advance to the Results tab.

The Results Tab

The Outputs Tab is illustrated below.



This screen displays the results of all the projections you have made. If you click the "Select all" button the data and projections for all populations will be shown in the graph. You can add or delete check marks next to the population names in the box in the upper left corner to change which populations are shown in the graph.

Using the radio buttons next to "Select one:" you can set the graph to show the "Percent HIV+", the "Number HIV+" or the "Population Sizes".

Using the radio check boxes next to "Display:" you can display or hide the "Site data", "Medians", "Means" and "Curve fits" (the epidemic curves).

To examine the results as a table, click the "Numerical results" button bellow the graph.

To write the results to a file that can be read by Spectrum, click the "Write Spectrum File" button that is visible when you are examining the "Numerical results". You will be requested to provide the name of the file.

To print the graph, click the "Print" button.

You can move to any of the other tabs to review or revise previous steps by clicking on the tab at the top of the screen.

The Audit Check Tab

This tab is primarily used with concentrated epidemics. It will check the projected sizes of the special populations to see if they are unusually large. If you specified that the population of injecting drug users is growing at 10 percent per year. It is possible that after a few years the number of IDUs could be an unreasonably large percentage of the total population. This audit check will examine the population sizes and display an alert if there are any potential problems. You should examine the messages and consider returning to the "Define pops" tab and revising some of the estimated growth rates.

The About EPP Tab

This tab contains information about the model, where to report problems or errors, and acknowledges the agencies that funded this work.

E. Fitting the model

When you fit a model in the "Projections Tab" you need to examine the results to see if they are reasonable. In some cases the program may show a curve that does not fit the data well at all. This is most likely to happen when there are few

data points. In this case, you will need to customize the fit. You can do this by specifying different initial values or by fixing certain parameter values. The most appropriate action to take will depend on the problem encountered. Table 1 shows common problems and the most likely solutions.

Table 1. Common problems and likely solutions

Problem	Possible solutions
Prevalence curve is too high early in the epidemic (it passes well above the surveillance data points)	• Use a later start year, **t_o** • Use a lower value of **r**
Prevalence curve is too low early in the epidemic	• Use an earlier start year, **t_o** • Use a higher value of **r**
Peak prevalence is too low	• Use a higher value of **r** • Use a higher value of **f_o**
Peak prevalence is too high	• Use a lower value of **r** • Use a lower value of **f_o**
Prevalence declines too rapidly after the peak	• Use a higher value of **phi**
Prevalence does not decline enough after the peak	• Use a lower value of **phi**

The program can be used to customize the curve to provide a better fit to the surveillance data. Two different approaches can be used.

- **Change the initial values.** You change the initial values of any of the parameters (in the boxes under "Initial guesses for model parameters") and then re-fit the curve. This causes the model to start from a different point that may allow it to find a better fit. This is not always the case, however. Many times the model will find the same fit no matter what the starting conditions are.
- **Fix the values of model parameters.** Instead of allowing the model to vary all the parameters you can specify values for some of them. There are two ways to do this.
    - **Refit.** You can specify that either **t_o**, **f_o**, or **r** should remain fixed at the initial value by using the "*Fix r, Fix t_0* or *Fix f_0*" radio buttons. Select the parameter you want to remain fixed. Be sure that the initial value for that parameter is set as you want it. Then click the "Fit Model" button. The model will try to find the best fit by varying the other parameters.

- **Recalculate.** Alternatively, you can change the value of any or all of the parameters and re-calculate the curve. To do this, change any of the parameter values in the blue boxes to the right of the graph. Remember to hit "Enter" after changing a value. As soon as you hit Enter, the curve will change to reflect your new value.

Examining multiple start years. The default setting of EPP is to have the start year fixed. If you are not sure about the start year of the epidemic, you can let EPP search for the best start year. To do this, change the selection of the radio button from "Fix t_o" to "Fix nothing". This allows all four parameters to vary. The values tried for start year of the epidemic will vary from the start year of the projection to the first year before there is non-zero prevalence in the data file.

Refitting with a different start year. If the epidemic curve seems to start too early or too late, you may want to change the start year of the epidemic. To change the start year type a new value in the box for t_o and hit Enter. Click the "*Fix t_o*" box and click the "Fit Model" button. This will use your new set of initial guesses and rerun the fitting algorithm.

Improving the fit by modifying r, f_o or phi. Depending on the problem you are facing you may want to try difference values of **r**, **f_o**, or **phi**.

- A lower value of **r** will produce a slower epidemic while a higher value will produce a faster one. Typical values range between 0 and 10 with most around 0.5 to 2.5.
- A lower value of **f_o** will reduce the peak of the curve and a higher value will raise it. Typical values are between 0 and 0.40.
- A lower value of **phi** will cause the curve to decline more rapidly from its peak while a higher value will cause it to decline less. Typical values are between –2 and 100.

To make any of these changes you can try changing the initial values and then refitting the curve to see if that makes any difference. If that does not work, you can change any of these values directly in the boxes to the right of the graph. Remember to press "Enter" after making a change. The model will recalculate the curves with these new parameter values. In many cases you will be able to tell if the new curves is better or worse just by looking at it. A more precise measure is to look at the figures displayed next to the "SSQ" label. This value is the sum of the squared errors. (The errors are the distance between the surveillance data points and the epidemic curve.) The best fitting curve is the one with the lowest sum of squared errors. You can compare two different values for a parameter by seeing which one produces a lower sum of squared errors.

Working with limited data. The EPP model will generally do a very good job of finding an epidemic curve to fit your surveillance data if lots of data are available for all parts of the epidemic. However, the model cannot determine the shape of the curve when no data are available. For example, if the surveillance data do not show any downward trend after the peak, then the model will have no way to determine the value of **phi**, the parameter that

governs the shape of the curve after the epidemic. Similarly, if the surveillance data indicate that prevalence has not yet peaked, it will be difficult for the model to determine the best value of $\mathbf{f_o}$, the parameter that determines the peak of the curve. In these cases, almost any value of **phi** or $\mathbf{f_o}$ will produce an equally good fit (e.g., a similar value for the sum of squared errors).

In these cases human judgment must be used. You will have to try different values of the parameters, look at the shape of the epidemic curve and select the one that seems best to you.

In most surveillance sites in mature epidemics prevalence rises to some peak value and then either stabilizes at that value or declines slightly. As a result, if you have no surveillance data past the time of peak prevalence, it is generally best to use a high value of **phi** (50 or more) so that prevalence will remain relatively stable after the peak.

If prevalence has not yet peaked, it will be difficult to determine the best value for $\mathbf{f_o}$. Today, national prevalence ranges from 0 to around 35 percent. Values of $\mathbf{f_o}$ above 0.35 would be very extreme.

Determining whether prevalence is declining. The epidemic model underlying EPP uses four parameters to fit an epidemic curve to the surveillance data. The phi parameter determines how rapidly prevalence declines from its peak. In most cases, the best fitting curve will be one in which prevalence declines significantly. This is because the extra degree of freedom will allow EPP to find a better mathematical fit when the epidemic curve changes direction than when it stays constant at peak prevalence. This does not necessarily mean that prevalence is, in fact, declining. You need to use your own judgment and consider additional factors before deciding whether prevalence is actually declining or not.

It is recommended that you first fit a curve with *phi* fixed at a value of 100. After examining this fit, you may want to remove the button from "*Fixed phi?*" and fit the curve again. The sum of squares (SSQ) will indicate how much better the fit is with the optimum value of *phi*. Generally if the SSQ for the optimum *phi* is within 10 percent of the SSQ with *phi* fixed at 100 you should reject the hypothesis that prevalence is declining. You should also consider other information in making this decision. Has prevalence declined for at least three years in a row? Is prevalence declining at more than one site? Are the declines at different sites occurring at about the same time? If none of these is true, then it will generally be best to be conservative and assume that prevalence is not declining.

F. Saving the results

When you are satisfied with the model curves, save the results by clicking the "Results" tab and clicking "Write Spectrum file" button. Type a name for the file

and click on the “Save” button. By default, the program will store your output files in the “eppout” directory under the EPP directory.

V. Estimating numbers infected and AIDS deaths

The prevalence projection created with EPP can be used to estimate the numbers of people infected, new infections and AIDS deaths. These estimates are made using the Spectrum program. Spectrum is a policy modeling system. It contains modules for a number of reproductive health areas. For the purposes of making a national HIV estimate two Spectrum modules are used: DemProj (for the demographic projection) and AIM for the epidemiological projection. This manual describes the basics of using these modules to make a national HIV projection. Additional details are available in the manuals for these modules:

- Stover, John and Sharon Kirmeyer. ***DemProj Version 4. A computer program for making population projections***. Washington, DC: The POLICY Project/Futures Group, November 1999.
- Stover, John. ***AIM Version 4. A computer program for making HIV/AIDS projections and examining the social and economic impacts of AIDS***. Washington, DC: The POLICY Project/Futures Group.

These manuals are available from the POLICY Project 1050 17th Street, Washington, DC 20036 or from the Futures Group web site at www.FuturesGroup.com.

You can start Spectrum by clicking on the "Start" button and selecting "Spectrum" from the programs list.

The following steps are required to use Spectrum:

1. Create a population projection
2. Read the EPP prevalence projection into Spectrum
3. Review the assumptions regarding age distribution of HIV, the sex ratio, the pattern of progression from infection to death and revise them if necessary.
4. View the results.

Each of these steps is described below.

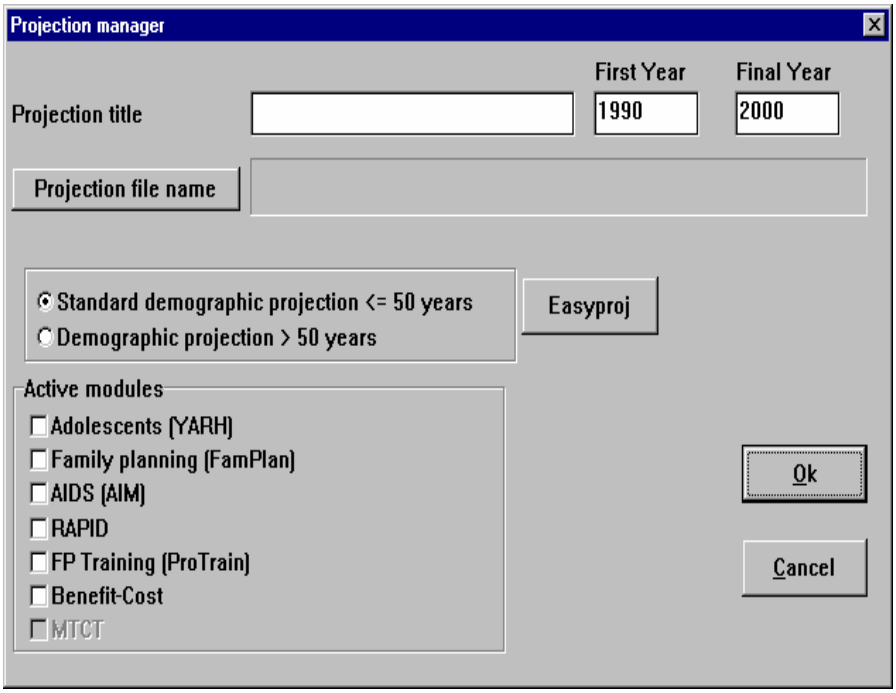
A. Creating a population projection

Spectrum contains a feature called EasyProj that will create a population projection automatically for any country in the world using the estimates and projections from the United Nations Population Division.

To create a new projection:

1. Select "File" from the menu bar.
2. From the pull-down menu that appears, choose "New projection."

The "Projection manager" dialogue box will appear and will look like the following screen:



The following information is required to create a new projection:

Projection title: Enter the title you wish to assign to this projection. This title will be printed at the top of all printed output.

Projection file name: You must also assign a file name to the projection. This is the name that will be used to store all data files associated with this projection. This name must obey the usual DOS-based rules for file names, i.e., it should not be more than eight characters in length and should not contain any illegal characters (you may use letters, numbers, and certain symbols such as a hyphen). Do not enter an extension with the file name; the program will automatically assign the extension ".pjn" to the projection file.

1. Click on the "Projection file name" button to open an edit box and type the file name.
2. Click on "Ok" to accept or "Cancel" to reject.

First year: Click in the "First year" box to enter the first year of the projection. In most cases this should be 1980 – the same as the first year of the projection in EPP. (Note this is not the same as the first year of the epidemic in EPP. The first year of the epidemic may be much later than 1980, but the population projection starts in 1980.)

Final year: Click in the "Final year" box to enter the final year of the projection. In most cases this should be 2005, the same final year used in EPP.

Active modules. These check boxes let you select other Spectrum modules that will be used with the population projection. You should select the "AIDS (AIM)" module.

EasyProj. EasyProj is a special feature that allows you to use data prepared by the United Nations Population Division and published in *World Population Prospects*. Click on the EasyProj button. From the EasyProj screen choose your country from the list. In most cases you should select the "medium" projection. Once you click "OK", the program will load all the necessary demographic data.

This is all you need to do to create the population projection. If you want to customize the projection you can select "Edit" and "Demography" from the Spectrum menu and change any of the demographic assumptions. See the DemProj manual for additional information.

B. Making the HIV/AIDS projections

Importing HIV prevalence from EPP

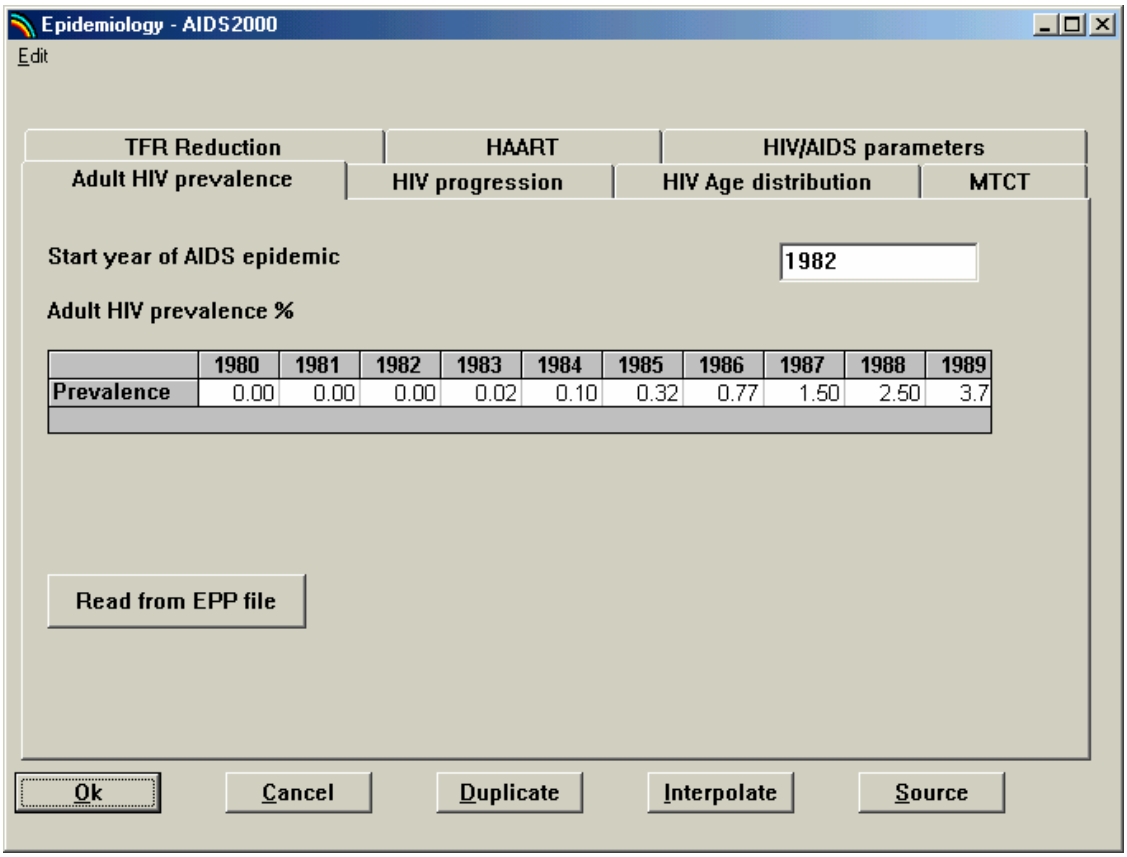
The next step is to read the HIV prevalence projection from the file created by EPP. To do this, select "Edit" and "AIDS (AIM)" from the Spectrum menu and "Epidemiology" from the dialog box. Then you will see the editor for the prevalence projection. It will look like the screen shown below.

Click the button "Read from EPP file". This will display a "file open" dialog box. Navigate to the directory where your EPP output file is stored (for example C:\Program Files\EPP\eppout) and select the appropriate file. The prevalence projection from EPP will be read into Spectrum and displayed in the editor.

If the first and last years of the projection are the same in EPP and Spectrum then the prevalence projection will match perfectly. If they are different Spectrum will do the following:

- If the prevalence projection from EPP starts earlier or extends later than the Spectrum projection, the extra values will be discarded.
- If the Spectrum projection extends beyond the last year of the EPP projection then the last value from the EPP projection will be duplicated for all remaining years.

- If the Spectrum projection starts before the beginning of the EPP projection, prevalence in these early years will be set to zero.



Accepting the default values for other epidemiological factors

The rest of the inputs required by Spectrum will be set to default values that are appropriate for most of sub-Saharan Africa. These factors include the pattern of progression from HIV infection to death, the distribution of HIV infection by age and sex, the reduction in fertility due to HIV infection, the mother-to-child transmission rate, and HAART treatment. You do not need to change any of these. To accept the default values, simply click the "Ok" button on the editor, click "Close" on the next dialog box and you will be ready to examine the projection.

Reviewing and changing other epidemiological factors

You can review or change any of the other epidemiological factors by selecting the appropriate tab at the top of the editor. For the progression pattern from infection to death and the age and sex distribution of HIV infection, buttons are

provided to select patterns for different types of epidemics. All of these other factors will initially be set to default values that are appropriate for sub-Saharan Africa. Details on these factors and the default values are provided in Chapter VI, "Understanding the methodology", section 2 "Spectrum". After reviewing or changing the other factors, click the "Ok" button on the editor to end the editing session. Then click "Close" on the next dialog box and you will be ready to examine the projection.

Parameters for calculating AIDS orphans

Spectrum can calculate the number of AIDS and non-AIDS orphans. It displays the number of maternal, paternal and dual orphans due to AIDS and other causes. In order to calculate dual AIDS orphans, two addition inputs are required: the percent of women aged 15-19 who have never been married and the percentage of married women 15-49 who are in monogamous unions. Both of these values are available from DHS reports. Values for selected countries are shown in table 2.

Table 2. Percent of women 15-19 never married and percent of married women in monogamous unions from various DHS reports

	Percent 15-19 never married	Percent of married women in monogamous unions
Benin 2001	76.1	54.2
Botswana 1988	93.9	
Burkina Faso 1998/99	65.2	45.3
Burundi 1987	93.2	88.3
Cameroon 1998	64.2	66.9
CAR 1994/95	57.7	71.5
Chad 1996/97	51.4	60.8
Comoros 1996	88.5	74.7
Cote d'Ivoire 1998/99	74.6	65
Eritrea 1995	62.4	92.9
Ethiopia 2000	70	86.4
Gabon 2000	77.6	78
Ghana 1998	83.6	77.3
Guinea 1999	53.9	46.3
Kenya 1998	83.3	83.7
Liberia 1986	64	61.9
Madagascar 1997	66.3	96
Malawi 2000	63.2	
Mali 1995/1996	50.3	55.7
Mauritania 2000/01	72.3	88.4
Mozambique 1997	52.9	71.5
Namibia 1992	92.3	74.6
Niger 1998	38.1	62.2
Nigeria 1999	72.5	64.3
Rwanda 1992	90.2	85.6
Senegal 1997	71	51.4
Sudan 1990	84.1	79.6
Tanzania 1999	72.8	
Togo 1998	80.1	57.2
Uganda 2000/01	67.7	67.3
Zambia 1996	72.7	82.9
Zimbabwe 1999	77.3	

C. Examining the output

From the main Spectrum menu, select "Display", "AIDS (AIM)" and "Epidemiology". You will then see a drop down menu with a list of HIV/AIDS indicators. The key indicators are summarized in the last two choices in the list "Adults 15-49 summary" and "Child AIDS summary".

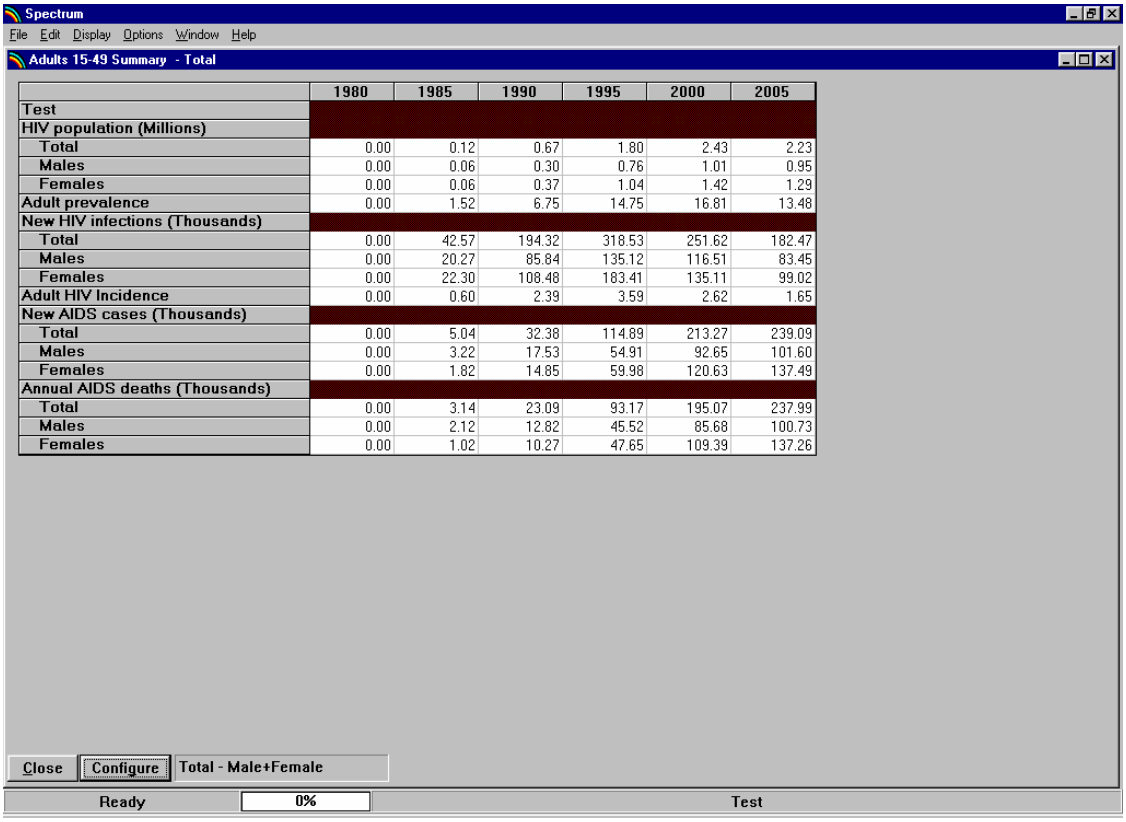
The first time you select a display after you have changed input values, you will see the message "Inputs have been changed. Re-project population now?" Click on the "Yes" button to tell Spectrum to re-calculate the projection.

Next you will see the "Configure" dialog box. This allows you to customize the display. The choices available vary depending on the indicator. For the summary tables there are three choices:

- **Display interval.** You can display values for every year or just for every five or ten years. You may want to select five or ten year intervals if you want to print the projection on a single page.
- **Final year.** You can set the final year of the display to something other than the last year of the projection, although usually you will want the display to show all years.
- **Scale table values.** Normally Spectrum will scale large numbers by displaying them as "thousands" or "millions" in order to make the display easier to read. If you do not want values to be scaled, remove the check mark from the "Scale table values" check box.

Once you have made any required changes to these options, click the "Ok" button to see the display.

A sample display is shown below.



	1980	1985	1990	1995	2000	2005
Test						
HIV population (Millions)						
Total	0.00	0.12	0.67	1.80	2.43	2.23
Males	0.00	0.06	0.30	0.76	1.01	0.95
Females	0.00	0.06	0.37	1.04	1.42	1.29
Adult prevalence	0.00	1.52	6.75	14.75	16.81	13.48
New HIV infections (Thousands)						
Total	0.00	42.57	194.32	318.53	251.62	182.47
Males	0.00	20.27	85.84	135.12	116.51	83.45
Females	0.00	22.30	108.48	183.41	135.11	99.02
Adult HIV Incidence	0.00	0.60	2.39	3.59	2.62	1.65
New AIDS cases (Thousands)						
Total	0.00	5.04	32.38	114.89	213.27	239.09
Males	0.00	3.22	17.53	54.91	92.65	101.60
Females	0.00	1.82	14.85	59.98	120.63	137.49
Annual AIDS deaths (Thousands)						
Total	0.00	3.14	23.09	93.17	195.07	237.99
Males	0.00	2.12	12.82	45.52	85.68	100.73
Females	0.00	1.02	10.27	47.65	109.39	137.26

Six types of indicators are displayed:

- **HIV population.** The number of people between the ages of 15-49 living with HIV. This includes those with AIDS.
- **Adult prevalence.** The percent of the population 15-49 living with HIV/AIDS.
- **New infections.** The number of adults between the ages of 15-49 newly infected with HIV in that year.
- **Adult HIV incidence.** The percentage of adults 15-49 who are not infected with HIV that becomes newly infected in that year.
- **New AIDS cases.** The number of adults 15-49 who progress to AIDS in that year.
- **Annual AIDS deaths.** The number of adults 15-49 who die from AIDS in that year.

You can change the configuration of the display (interval, last year of display, scaling) by clicking the "Configure" button. You can print the display by

selecting "File" and "Print" from the Spectrum menu. To close the display, click on the "Close" button. Note that it is not necessary to close the display before displaying another table. It will remain open in a window that can be accessed from the "Window" selection in the horizontal Spectrum menu.

The "Child AIDS Summary" can be displayed in the same way as the adult summary. The indicators in this display are:

- **HIV population.** The number of children 0-14 living with HIV infection.
- **New HIV infections.** The number of HIV-positive births each year.
- **New AIDS cases.** The number of new AIDS cases among children 0-14.
- **Annual AIDS deaths.** The number of AIDS deaths among children 0-14 in each year.

There is also an "HIV/AIDS Summary" display that shows indicators for the entire population.

Individual indicators can be displayed by choosing them from the display menu. Individual indicators can be shown as line graphs or bar charts as well as tables. If more than one projection is loaded, all projections will be shown in the graphs and tables.

Special pyramid and table displays show the distribution of HIV infection, new infections and AIDS cases by age and sex.

The indicators available in Spectrum are:

- **Number infected with HIV:** The total number of people who are alive and infected with HIV. This includes those with AIDS.
- **Adult HIV prevalence:** The percentage of adults aged 15 to 49 who are infected with HIV.
- **Adult HIV incidence:** The percentage of uninfected adults 15-149 who become infected in each year.
- **HIV age distribution:** The number of infected people, by age and sex. This information can be displayed as a table or a pyramid chart.
- **HIV incidence by age:** The number of new infections per year by age and sex. This information can be displayed as a table or a pyramid chart.
- **New AIDS cases:** The annual number of new AIDS cases.
- **AIDS deaths:** The annual number of deaths due to AIDS.
- **Cumulative AIDS deaths:** The cumulative number of AIDS deaths since the beginning of the projection.

- **AIDS age distribution:** The number of people alive with AIDS, by age and sex. This information can be displayed as a table or a pyramid chart.
- **HIV/AIDS summary:** A table with all the above indicators shown for a selection of years. All input assumptions are also shown on this table.
- **Adults 15-49 summary.** A table of HIV/AIDS indicators for adults 15-49. It includes number infected, prevalence, number of new infections, incidence, AIDS cases and AIDS deaths.
- **Child AIDS summary.** A table of HIV/AIDS indicators for children 0-14. It includes number infected, new infections, AIDS cases and AIDS deaths.

There is also an orphans summary table that is displayed by choosing "Display", "AIDS", "Orphans" and "Summary table." It will display the following indicators:

- **Maternal AIDS orphans**
- **Paternal AIDS orphans**
- **Dual AIDS orphans**
- **All AIDS orphans**
- **Maternal non-AIDS orphans**
- **Paternal non-AIDS orphans**
- **Dual non-AIDS orphans**
- **All non-AIDS orphans**
- **All orphans**

An orphan is defined as a child under the age of 15 who has lost a parent. Maternal orphans are children whose mother has died. Paternal orphans are children whose father has died. Dual orphans are children who have lost both parents. "All orphans" refers to children who have lost one or both parents. AIDS orphans are children who have lost a parent to AIDS, while non-AIDS orphans are children who have lost a parent to a cause other than AIDS.

D. Saving the results

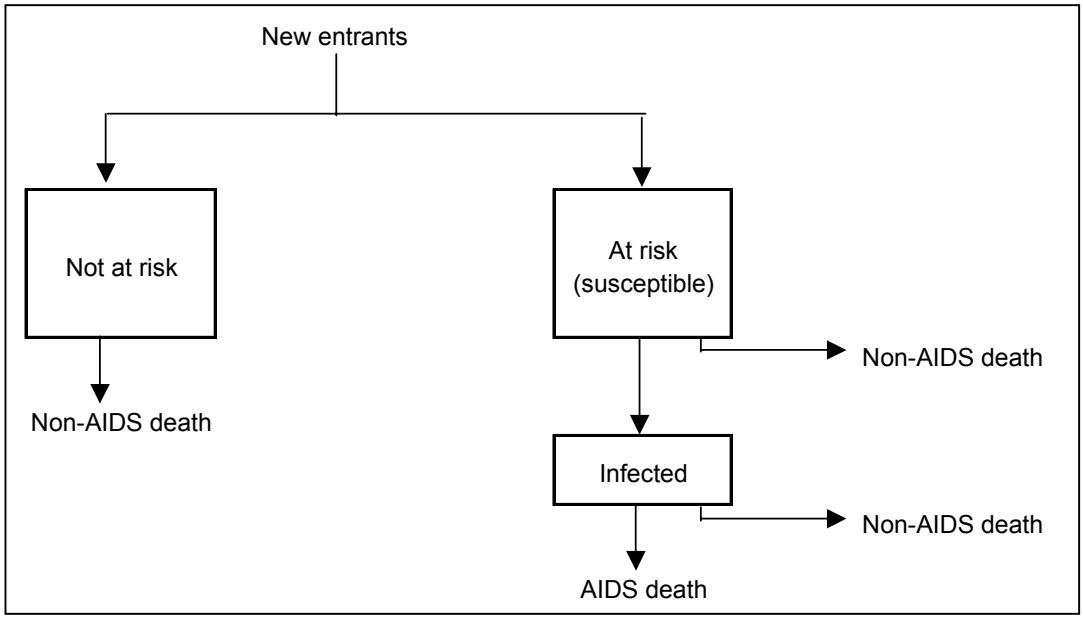
You can save your projection by selecting "File" and "Save" or "Save As" from the Spectrum menu.

VI. Methodology and Assumptions

A. Estimating HIV prevalence - EPP

The methodology for estimating prevalence from surveillance data was developed by the UNAIDS Reference Group on Estimates, Models and Projections. This new model, called the Estimation and Projection Package (EPP) replaces EpiModel, which was used by WHO's Global Programme on AIDS and UNAIDS to make previous estimates (Chin, 1996; Chin and Lwanga, 1989). EpiModel was developed by the Global Programme on AIDS at a time when very little surveillance data was available. The new EPP model is designed to take advantage of the much larger number of sites and years for which surveillance data is not available in many countries.

EPP is a simple epidemiological model that produces the basic epidemic curve shapes found in most HIV epidemics. The model structure is shown below.



The population is initially divided into two parts, those who are not at risk of HIV infection and those who are at risk. People would not be at risk if they are not sexually active, if they have only one partner who has no outside partners, or if they successfully use condoms all the time. New entrants are children reaching the age of 15. They can enter either population group. Some of those who are at risk will become infected and progress to AIDS death. All population groups are subject to this risk of dying from causes other than AIDS.

The dynamics of this model are described by four parameters:

- **t_0** – The initial year of the epidemic.
- **f_0** – The initial proportion of the population that is in the at-risk category.
- **r** – The force of infection. This governs the rate at which people in the susceptible population become infected.
- **ϕ –** A parameter that affects the distribution of new entrants to the not at-risk and at-risk categories.

The model is defined as follows:

Z = at-risk population
X = not at-risk population
Y = infected
N = *X* + *Y* + *Z*

$$\frac{dX}{dt} = (1 - f(X/N)).E_t - \mu X$$

$$\frac{dZ}{dt} = f(X/N).E_t - (\mu + rY/N + \iota)Z$$

$$\frac{dY}{dt} = (rY/N + \iota)Z - \int_0^t (rY_x/N_x + \iota_x).Z_x.g(t-x)\mathrm{dx}$$

where $f(X/N)$ is the fraction of those individuals entering the adult population (E_t) who enter the at-risk group *Z*, and is given by

$$f(X/N) = \frac{\exp\left[\phi(\frac{X}{N} - (1 - f_0))\right]}{\exp\left[\phi(\frac{X}{N} - (1 - f_0))\right] + \frac{1}{f_0} - 1}$$

μ = the non-AIDS death rate
ι = 1 for the first year of the epidemic and 0 for all other years
g = function describing the proportion progressing to AIDS death by the number of years since HIV infection

The population not at risk (X) is increased by new entrants and reduced by non-AIDS deaths (μX). The population at risk (Z) is increased by new entrants and reduced by non-AIDS deaths and new HIV infections (rY/N). The infected population (Y) is increased by new infections (rY/N and ι) and decreased by progression to AIDS death.

The function *f*(X/N) determines the proportion of new entrants to the adult population that enter the at-risk population. Initially this proportion is set by *f*o. As

the epidemic progresses those in the at-risk category become infected with HIV and die. Since the death rate will be higher in the at-risk category than among those not at risk, the proportion of the population at risk will gradually decline. This will produce a prevalence curve that rises to a peak value and then declines rapidly to low levels. In many epidemics, however, prevalence stabilizes at or near its peak value. This can be simulated by directing more entrants to the at-risk category as the proportion of the population in the at-risk category declines. The parameter ϕ determines the size of this effect. At high values of ϕ new entrants will join the at-risk category in large enough numbers so that the proportion of the total population in the at-risk category remains nearly constant. When ϕ is zero the proportion of entrants going to the at-risk category does not change from its initial value. Negative values of ϕ cause the proportion of entrants to the at-risk category to drop as AIDS deaths increase.

These equations can produce a prevalence curve that can fit a wide variety of epidemic shapes by adjusting the four parameters: **t_0**, **f_0**, **r**, and **phi**.

EPP uses this model to find prevalence curves that fit available surveillance data. The parameter μ (the non-AIDS death rate) is estimated for each country from the population estimates and projections of the United Nations Population Division. The progression to AIDS death (g) is assumed to be constant throughout the projection. It is a weibull function that has been fitted to available information on survival times. The progression pattern used in EPP is discussed below.

New entrants to the adult population at time *t*, E_t are calculated from the births of HIV negative children B^-_{t-15} occurring 15 years previously and the probability of surviving to age 15, *l*. The number of births is simply the birth rate multiplied by the size of the adult population. However, some children will be born infected. We assume that they do not survive to age 15. Thus the number of children born without HIV infection is determined by calculating births to HIV-negative adults (b(X+Z)) and HIV-negative births to HIV-positive adults (b'Y(1-v) where v is the perinatal transmission rate and b' is the birth rate adjusted for the reduction in fertility caused by HIV infection, ε.

$$E_t = B^-_{t-15} \cdot l$$

$$B^-_{t-15} = b \cdot \left[X_{t-15} + Z_{t-15} + (1-\nu) \cdot \varepsilon \cdot Y_{t-15} \right]$$

This approach is implemented in the EPP model by assuming that the parameters l (survival to age 15), b (birth rate), ε (fertility reduction caused by HIV), v (perinatal transmission rate) and the distribution g (progression from infection to AIDS death) are fixed. The initial values of the population size, survival to age 15 and the birth rate are derived from the population estimates of the United Nations Population Division.

EPP searches for the best values of the four remaining parameters $\mathbf{t_0}$ (start year), $\mathbf{f_0}$ (fraction at-risk), **r** (force of infection and **phi** (adjustment for AIDS deaths). The best values are defined as those that produce the prevalence curve that best fits the surveillance data. The best fit is determined by minimizing the sum of the squared errors (the differences between the model curve and the surveillance estimates in each year).

B. Estimating numbers infected, new infections and AIDS deaths – Spectrum

Equations

The Spectrum model combines the epidemiological calculations of HIV/AIDS with demographic calculations to translate the prevalence estimate from EPP into estimates of numbers of people infected. Spectrum contains a demographic projection model that projects the population by age and sex on the basis of fertility, mortality and migration. The full details of this methodology are provided in the DemProj manual (Stover and Kirmeyer, 1999).

The HIVAIDS calculations are implemented by age and sex and are described fully in the AIM manual (Stover, 1999). A simplified version of the equations is shown here.

The number of adults 15-49 infected with HIV in any year is simply the number of adults multiplied by the HIV prevalence provided by EPP.

HIV_t = adult population$_t$ x prevalence$_t$

This calculation is made for each age group and for both males and females. The distribution of prevalence by age and sex is described in the next section.

The number of new infections each year is calculated as the number required to achieve the specified prevalence. Thus, new infections are calculated as the number of infections expected in year t minus the number of infections surviving from the previous year. Surviving infections are the number of infections in the previous year minus deaths occurring during the previous year. (In the full age-specific set of equations the number of infected people aging out of the 15-49 age group and the number aging into this age group are also considered.)

New HIV infections$_t$ = HIV_t – (HIV_{t-1} – AIDS deaths$_{t-1,t}$ – non-AIDS deaths to HIV+$_{t-1,t}$)

AIDS deaths are a function of the number of new infections in previous years and the rate of progression from AIDS to death.

$\text{AIDS deaths}_{t-1,t} = \Sigma_{i=0,20}\ \text{New HIV infections}_{t-i} \times \text{Proportion progressing to death}_i$

Child infections occur when an HIV positive mother passes the infection to her child during gestation or birth or after birth through breastfeeding.

$\text{New child infections}_t = \text{HIV+WRA}_t \times \text{TFR}_t \times (1\text{-TFRreduction}) \times \text{PTR}_t$

Where:

HIV+WRA = the number of HIV positive women of reproductive age
TFR = total fertility rate
TFR reduction = the reduction in fertility caused by HIV infection
PTR = the perinatal transmission rate

Children progress from infection to AIDS and death in the same manner as described above for adults, although the progression rates are different.

The next sections describe the assumptions and patterns used to determine the progression from infection to death, the distribution of prevalence by age and sex, the perinatal transmission rate and the reduction in fertility caused by HIV infection.

Progression from HIV infection to AIDS death

The progression period describes the amount of time that elapses from the time a person becomes infected with HIV until he or she dies from AIDS. AIM uses the cumulative distribution of the progression period. This distribution is defined as the cumulative proportion of people infected with HIV who will die from AIDS, by the number of years since infection. For example, it might be that for all people infected in a certain year, 1 percent will die ; 3 percent will die within two years; 7 percent within three years; etc. The progression period can be specified for up to 20 years. The cumulative percentage dying from AIDS by year 20 will be the percentage that ever dies from AIDS. Thus, if this value is equal to 95 percent, it implies that 5 percent of people infected with HIV will never die from AIDS. AIM uses separate incubation distributions for adults and children.

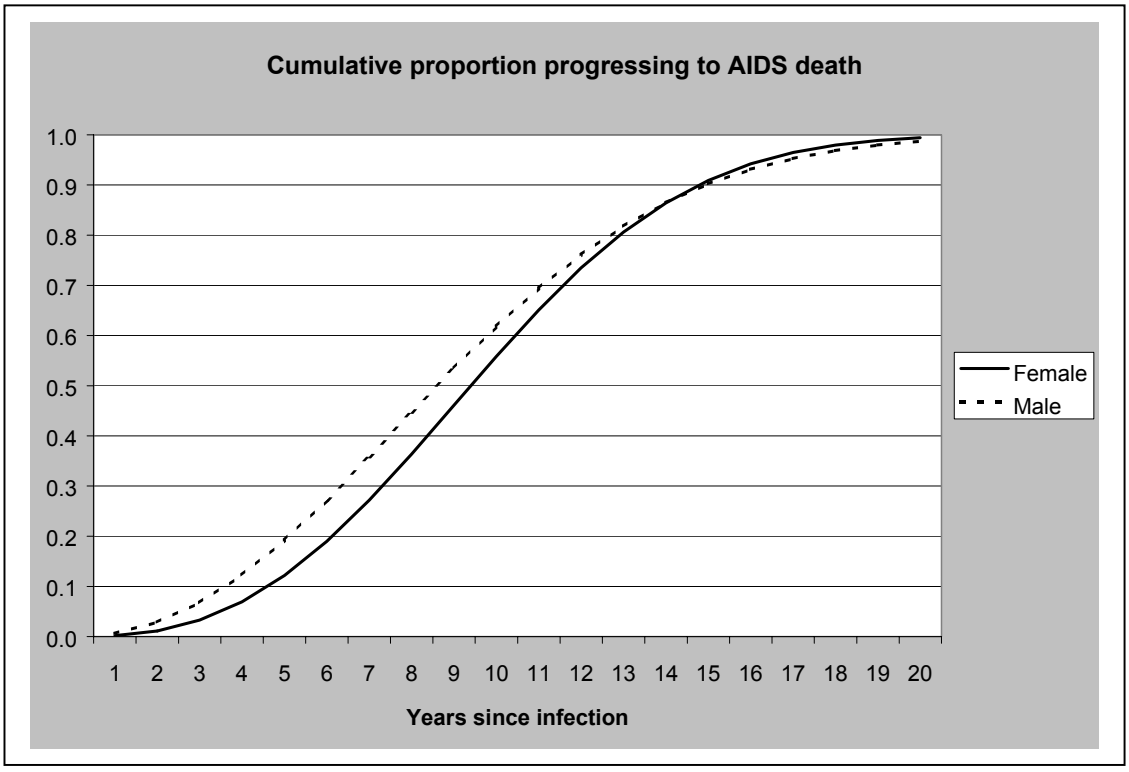
Adult Progression Period

A number of studies have calculated the distribution of the progression period (time from infection to death) for different groups of adults (Alcabes et al., 1994; Buchbinder et al., 1994; 1996; Chevret et al, 1992; Chiarotti et al., 1994; Downs et al., 1991; Hendriks et al., 1992, 1993; Hendriks, Satten et al., 1996; Law, 1994; Operskalski et al., 1995; Veuglers, 1994). Estimates of the median time from infection to AIDS range from 6.5 to 16.1 years, with most of the estimates at 9-10 years. Estimates of the mean time to AIDS generally are slightly longer. Differences are due to a variety of factors. Progression to AIDS occurs faster in

older people and in those infected through male homosexual contact. Aside from these factors, the mode of infection does not seem to affect the progression to AIDS.

Most of the studies of progression to AIDS have been done in industrialized countries. Very little information is available from developing countries. A study in Masaka, Uganda began following a cohort of infected people in the early 1990s. That study indicates that the rate of progression to death in Uganda is similar to industrialized countries. There is evidence that older people progress to AIDS and death faster than younger people. As a result, women generally progress slower than men since they tend to be infected at a younger age. (UNAIDS, 2001A)AIM has two default progression patterns available: fast (for developing countries) and slow (for industrialized countries). These patterns are based on the assumption that better health care leads to a somewhat longer survival period in industrialized countries. Thus, the median time from infection to death is assumed to be 9 years in developing countries (8.6 years for males and 9.4 years for females) and 10 years in industrialized countries. These survival periods refer to people who are not receiving treatment with anti-retroviral drugs. The effects of anti-retroviral drugs are considered in a separate section. The default patterns are shown in Figure 2. A pattern can be selected in Spectrum by clicking the appropriate button ("Fast pattern" for developing countries, "Slow pattern" for industrialized countries) or a custom pattern can be entered directly.

Figure 2. Progression from infection to death for adults

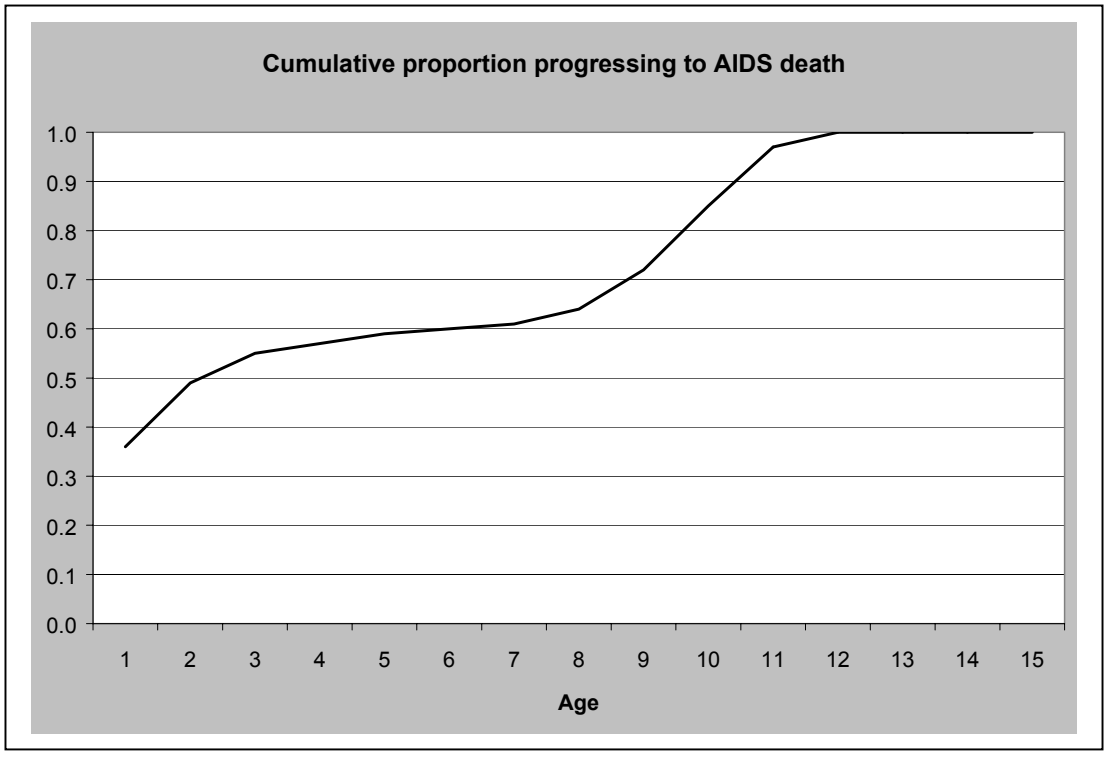


Child Progression Period

Children who are infected perinatally generally progress to AIDS faster than adults. Studies have reported median time from birth to AIDS to range from one year to 6.3 years (Auger et al., 1988; Commenges et al., 1992; Downs, Salamini, and Ancella Park, 1995; Jones et al., 1989; Lui et al., 1988; Oxtaby et al., 1992; Pliner, Weedon, and Thomas, 1996; Salamini et al., 1992;). Several of these studies have found that some children (perhaps 40%) progress to AIDS within a few months while the rest take considerably longer.

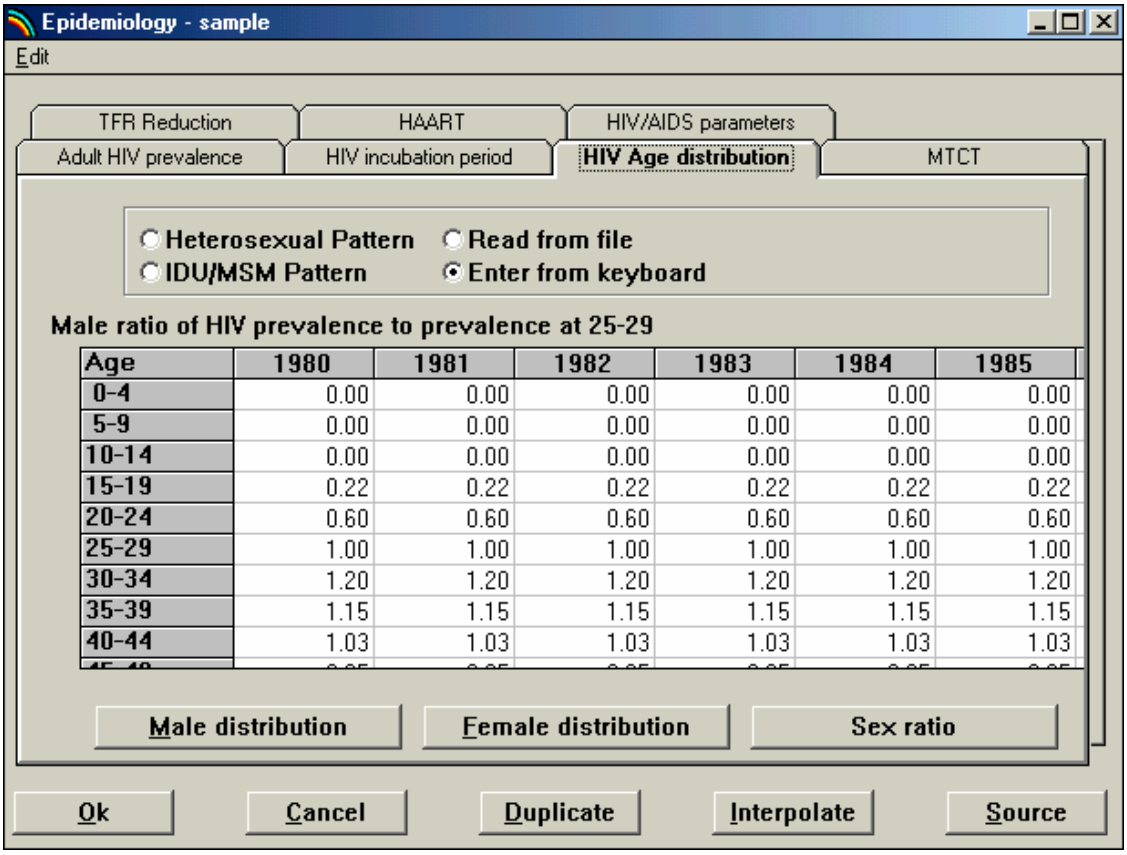
A UNAIDS review of available evidence (UNAIDS 2001B) suggests that the survival is best described by a rapid progression from infection to death for some children and much slower progression for others. The default pattern used in AIM is shown in Figure 3.

Figure 3. Progression from infection to death for children



Age distribution of HIV infection

Once the progression patterns are specified, click on the "HIV age distribution" tab at the top of the editor. This will bring you to the next screen, which looks like the one shown below.



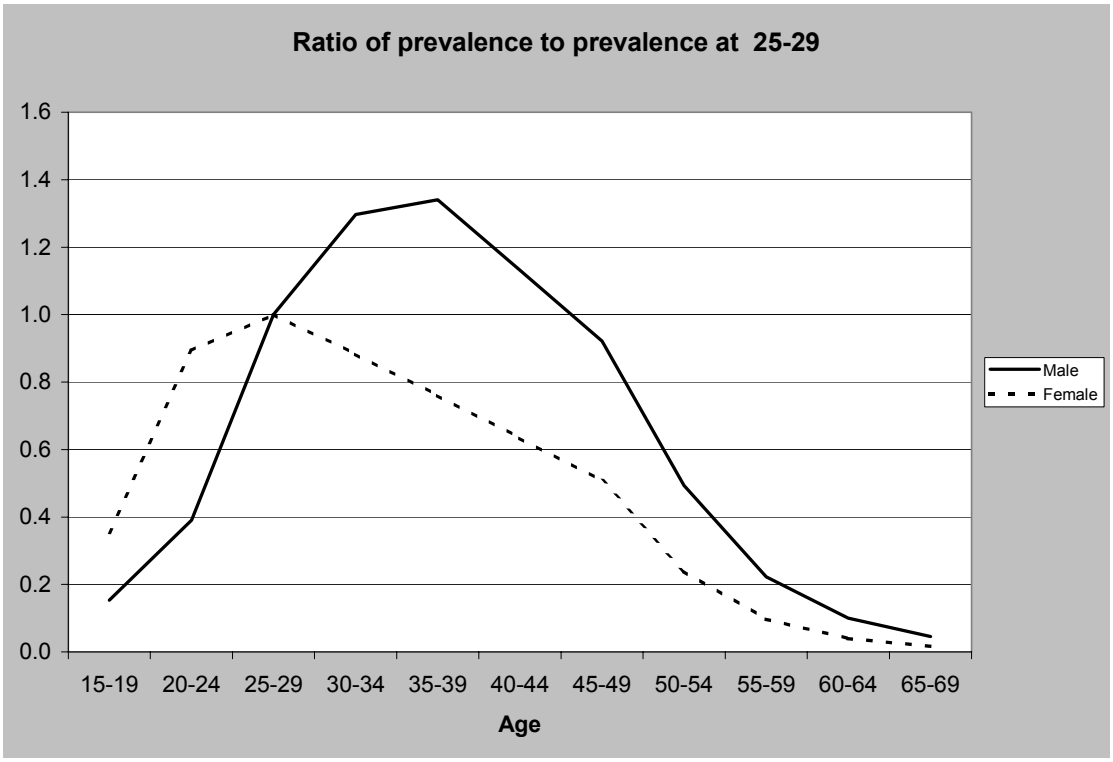
Age	1980	1981	1982	1983	1984	1985
0-4	0.00	0.00	0.00	0.00	0.00	0.00
5-9	0.00	0.00	0.00	0.00	0.00	0.00
10-14	0.00	0.00	0.00	0.00	0.00	0.00
15-19	0.22	0.22	0.22	0.22	0.22	0.22
20-24	0.60	0.60	0.60	0.60	0.60	0.60
25-29	1.00	1.00	1.00	1.00	1.00	1.00
30-34	1.20	1.20	1.20	1.20	1.20	1.20
35-39	1.15	1.15	1.15	1.15	1.15	1.15
40-44	1.03	1.03	1.03	1.03	1.03	1.03

To calculate HIV incidence from the prevalence input, AIM needs to have some information on the distribution of infection by age and sex. This information is provided through two editors, one for the ratio of female to male prevalence and one for the ratio of prevalence at each age group to prevalence in the 25-29 age group. In most epidemics, there are more male than female infections early in the epidemic. As the epidemic matures, the numbers become more equal and then, in heterosexual epidemics, there will eventually be more female than male infections. This pattern is especially noticeable in areas such as the Caribbean and Latin America, where the early infections were primarily among homosexual and bisexual men and the epidemic later spread to male and female heterosexuals. In many African countries today, female prevalence is significantly higher than male prevalence.

HIV surveillance surveys will usually provide estimates of prevalence by age. These figures can be used to calculate the ratio of prevalence in each five-year age group to prevalence in the 25-29 age group. If prevalence by age is not available, reported AIDS cases can be used to estimate these ratios, although AIDS cases refer more closely to HIV incidence than to prevalence. Although AIDS cases are usually underreported and female cases may be even more underreported than male cases, the reported cases may be useful for examining the distribution of cases by age within each sex, unless there is some reason to suspect strong age or sex biases in reported cases. Since AIDS cases are a reflection of infections that occurred 5 to 10 years earlier, it is necessary to adjust the figures for this time lag. Thus, the distribution of new AIDS cases reported in 1995 should be used to determine the distribution of prevalence in 1985.

AIM has a default patterns describing prevalence by age. This pattern is based on general population surveys from several African countries (Glynn, 2000; Wawer, 1997; Barongo, 1992; Kigadye, 1993; Fylkesnes, 2001; Fontanet, 1998, Zambia DHS 2001/02). The default distribution is shown in Figure 4.

Figure 4. Ratio of prevalence at any age to prevalence at 25-29

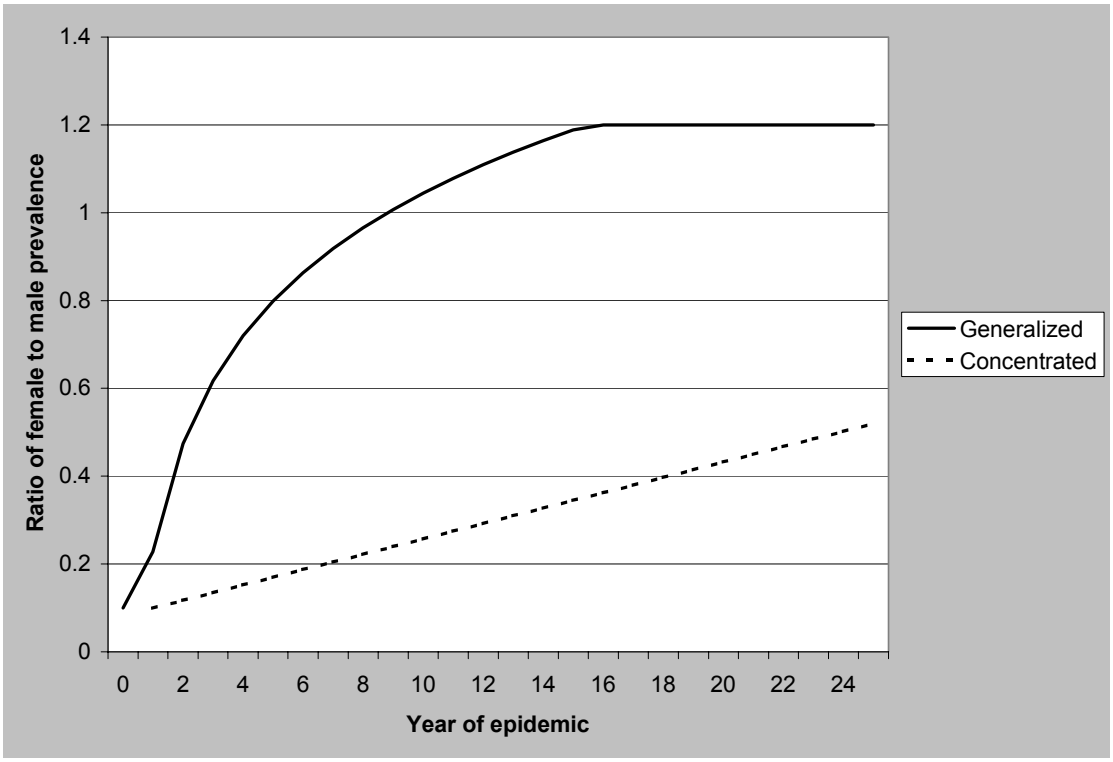


Sex ratio of HIV prevalence

AIM has two default patterns for the ratio of female to male prevalence. The pattern for heterosexual epidemics is based on the same population surveys mentioned above. The pattern for epidemics driven by transmission among men

who have sex with men and injecting drug users is based on the ratio of female to male reported AIDS cases in Central America. These patterns are shown in Figure 5 below.

Figure 5. Ratio of female to male prevalence



Mother-to-child transmission of HIV

The perinatal transmission rate is the percentage of babies born to HIV-infected mothers who are infected themselves. Studies have found that this percentage ranges from about 13 to 32 percent in industrialized countries and 25 to 48 percent in developing countries (Bryson, 1996; Dabis et al., 1993). The higher rates have generally been found in studies in Africa, where a significant amount of transmission through breastfeeding may take place, and the lower figures have been found in Western Europe. AIM uses a default value of 32 percent, typical of developing countries. If country-specific studies are available, this figure can be changed. It may also be changed for future years if the country implements programs to prevent mother-to-child transmission of HIV.

Fertility reduction due to HIV infection

It is not clear how the total fertility rate might be affected by an HIV/AIDS epidemic. Some women who find that they are infected with HIV may want to

have as many children as possible while they can, in order to leave descendants behind. Others may decide to stop childbearing upon learning that they are HIV positive in order to avoid leaving motherless children behind. Since the majority of people do not know if they are infected or not, knowledge of HIV infection is not likely to have a large effect on the desired fertility rate.

Age at marriage may also be affected and could, in turn, affect fertility rates. AIDS could lead to a lower age at marriage or first union if young women and their parents seek early marriage as a protection against the young woman having premarital sex with a number of different partners. This trend, in turn, could raise fertility rates if women are exposed longer to the possibility of pregnancy. Conversely, AIDS could lead to higher age at first intercourse as the dangers of unprotected sex become known. This trend would lead to lower fertility rates.

Gregson and colleagues have examined the question of the impact of HIV on fertility by examining potential changes in the proximate determinants of fertility (Gregson, 1994; Gregson et al., 1997). They found no clear evidence either way but concluded that the most likely result is that an HIV epidemic will slightly reduce fertility.

A study in Tanzania found weak evidence that adult mortality due to AIDS leads to reduced fertility rates (Ainsworth, Filmer and Semali,1995). Two studies in Uganda found that HIV-infected women had lower fertility rates than HIV-negative women. One of these, in rural Rakai district (Gray et al., 1997), found that age-specific fertility rates for HIV-infected women were 50 percent less than those for women who were not infected. Another study among a rural population in Masaka (Carpenter et al., 1997), found that fertility rates were 20 to 30 percent lower among HIV-infected women. Since most women did not know their sero-status, the reduced fertility rates were most likely due to biological rather than behavioral factors. This finding suggests that fertility might be 20 to 50 percent lower among HIV-infected women. In societies with substantial use of contraception, there might be a reduction in contraceptive use that would partially compensate for this effect. Fertility among young women who are HIV-positive is likely to be higher than for all women, since all HIV-positive women are sexually active but not all young women are sexually active.

The default value in AIM is that fertility among 15-19 year old women is 50 percent higher among HIV-positive women than HIV-negative women and that fertility among women 20-49 is 20 percent lower among HIV-positive women than HIV-negative women.

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