



# EpiDynamics

Models of  
Helminth  
Epidemiology



The Wellcome Trust Centre for the Epidemiology  
of Infectious Disease, University of Oxford

USER GUIDE

**EpiSchisto:**

A dynamic model of schistosomiasis control

**EpiFil:**

A dynamic model of lymphatic filariasis control

**EpiWorm:**

A dynamic model of intestinal helminth control

## EpiSchisto

**Development:** Man-Suen Chan and Don Bundy

**Programming:** Man-Suen Chan

Produced by the Partnership for Child Development and the World Health Organization Collaborating Centre for the Epidemiology of Intestinal Parasitic Infections.

Supported by the Edna McConnell Clark Foundation

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## EpiFil

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Produced in collaboration between the Wellcome Trust Centre for the Epidemiology of Infectious Disease, The Vector Control Research Centre (Pondicherry, India) and the University of Stirling.

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## EpiWorm

**Development:** Man-Suen Chan and Don Bundy

**Programming:** Man-Suen Chan

Produced by the Partnership for Child Development and the World Health Organization Collaborating Centre for the Epidemiology of Intestinal Parasitic Infections.

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## Acknowledgements

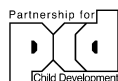
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## INTRODUCTION

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### What is EpiSchisto?

**EpiSchisto** is a computer program that enables control programme managers and others interested in schistosomiasis control to predict the impact of chemotherapy interventions. It is particularly intended for programmes in which children of school age are targeted. The program allows the user to specify the local epidemiological data and the programme of chemotherapy interventions and then the program will calculate predictions based on these data. Output is provided both as graphs on screen and as text files.

Embedded within the computer program is a quantitative framework, known as an epidemiological model, which predicts the transmission dynamics of schistosomiasis. Such epidemiological models are based on an understanding of the biological processes of infection and disease. These processes are described in terms of mathematical equations, which are then encoded as a computer program. Epidemiological models are an example of a wider class of models known as population dynamic models. In the field of infectious diseases, population dynamic models have been applied for measles and HIV, for example, as well as for the helminth infection, onchocerciasis. These models describe explicitly the biological processes of birth, death and infection and can be adapted for a wide range of applications.

The model used within **EpiSchisto**, which is based on a mathematical framework developed by Anderson and May (1985), has been developed specifically with the aim of applying it in a wide range of endemic situations. It has been in development since 1994 and the work has been published in the scientific literature (see bibliography).

The utility of a model will depend ultimately on its ability to predict the impact of interventions correctly. To this end, an essential part of model development is to compare the model prediction with data from past control programmes, a process known as model validation. The current model has been successfully validated against data from both *Schistosoma haematobium* and *S. mansoni* programmes in several African countries (Chan *et al.*, 1995; 1998).

### What can EpiSchisto do?

**EpiSchisto** can be used at many stages of a control programme. During the planning stage, **EpiSchisto** can be used to predict the decline in infection and disease prevalence and hence can be used when evaluating the benefits of intervention and setting reasonable targets. It can also be used to compare the potential effectiveness of different likely schedules of interventions. During the intervention phase of a programme, **EpiSchisto** can be of use to monitor the progress of the programme, to assess whether the programme is achieving its targets and also to adapt intervention schedules while the programme is running. **EpiSchisto** is also intended for educational use in developing understanding of the concepts of epidemiology and for training in the use of predictive methods.

## INSTALLATION

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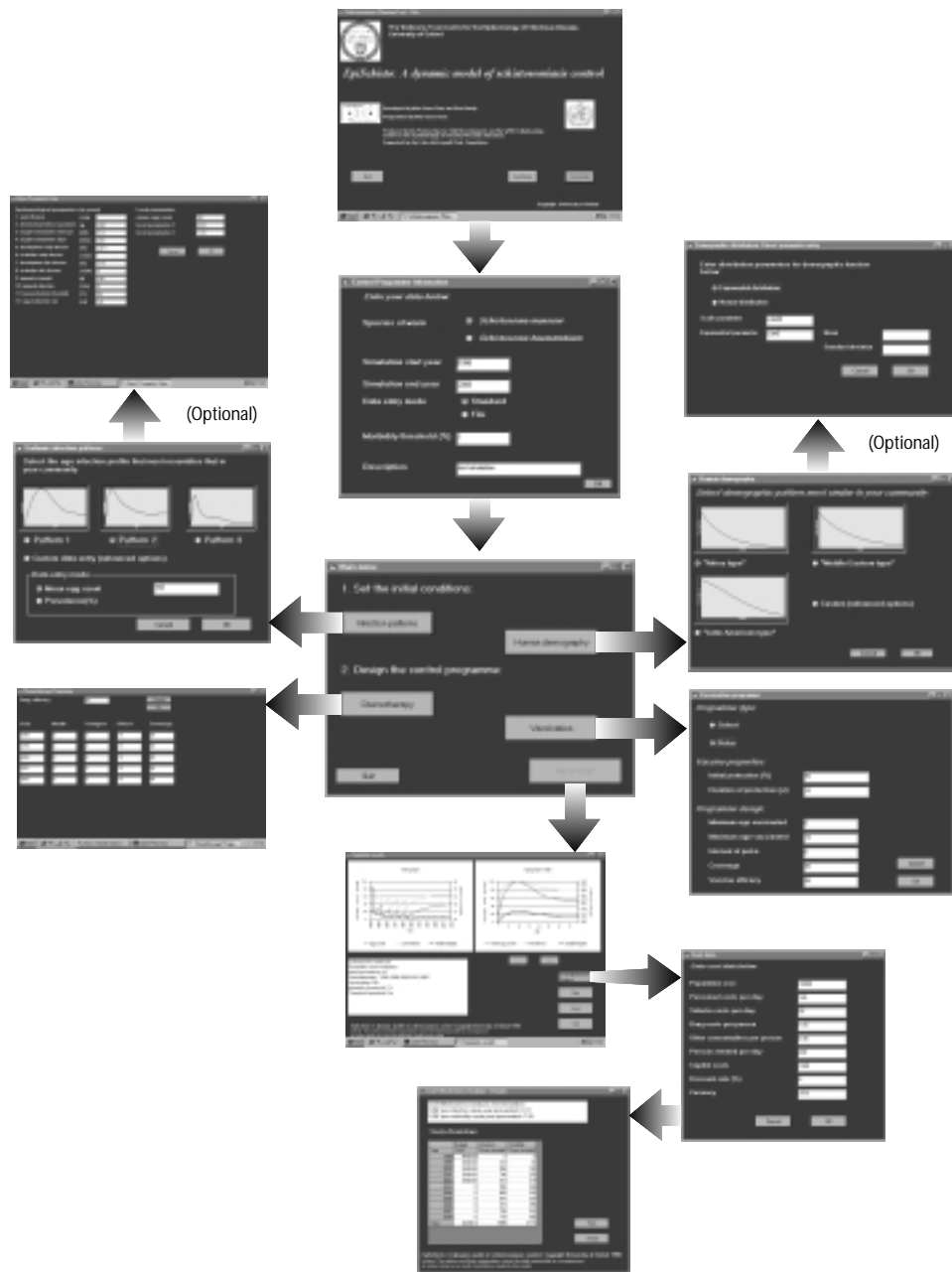
**EpiSchisto** can be installed on PCs with Windows 95/NT or higher.

To install **EpiSchisto**, use the customised **setup** program located in the **\package** folder of the distribution CD. This program will guide you through the various procedures necessary for setting up the program. You may need to reboot the machine during the setup procedure.

### Options on Title Screen

- |                  |   |
|------------------|---|
| <b>See Demo</b>  | runs a pre-loaded program file and goes straight to results |
| <b>Run Model</b> | goes into the parameter entry menus                         |
| <b>Quit</b>      | exits the program   |

## EPISCHISTO ROAD MAP



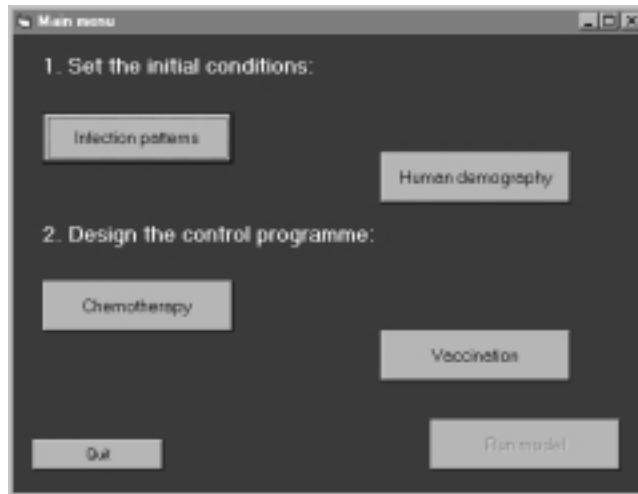
## PROGRAMME INFORMATION

The screenshot shows the 'Control Programme Information' dialog box. It contains the following fields and options:

- Species of worm:  *Schistosoma mansoni*,  *Schistosoma haematobium*
- Simulation start year: 1998
- Simulation end year: 2008
- Data entry mode:  Standard,  File
- Morbidity threshold (%): 1
- Description: Test simulation

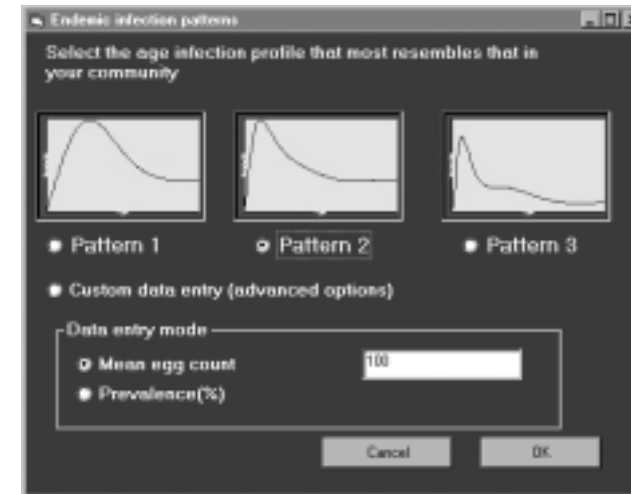
1. Select the species of schistosome. The 2 species have different parameters. *S.japonicum* is not yet included as it requires a model for the animal hosts.
2. Calendar years must be four digit numbers, *recommended simulation time 5-20 years*.
3. **Standard** data entry means you enter the data, **File** data entry data will be input from a file. *If you use Standard parameter entry the program does not 'remember' what you entered last time and will load the defaults.*
4. **Morbidity Threshold** (target level of morbidity, to be achieved by the control programme), in percent, should be quite low 1-10%.
5. **Description** is short text description, for your own use, which fits in the box
6. On pressing **OK**, if **File Entry** has been selected, a box will appear for you to select the input file. Simulation files of form \*.log in the \files subdirectory where you installed the program and any files you have saved yourself can be used. They contain the parameters to repeat a run of the model. *Note that Windows may produce other files of form \*.log which are not suitable (eg uninstall.log).*

## MAIN MENU



1. The **Main** menu is used to navigate around the various areas of parameter entry. Press each button in turn to enter parameter entry windows. After entry of parameters, you will return to the **Main** menu. The details of parameter entry are given in the next pages.
2. **Run Model** will not be enabled until parameters for both **Infection Patterns** and **Human Demography** are entered.
3. *If you have used File Entry only Chemotherapy and Vaccination can be changed.*
4. *If you do not enter any control parameters, the program will run but infection levels will not change.*
5. **Quit** will exit the program (you will be warned first).

## INFECTION PATTERNS (STANDARD ENTRY)



1. There are two **Infection Patterns** entry modes, (**Standard** and **Custom**) which are mutually exclusive. *Unless you know the model quite well you should use the **Standard** mode, patterns 1-3 on this menu.*
2. Select the **Age Infection Profile** that most resembles that in your community. Patterns 1-3 assume different levels of host immunity pattern 1= none, pattern 2=medium (default for *S. mansoni*) and pattern 3= high (default for *S. haematobium*).
3. Select **Mean Egg Count** (intensity in epg for *S. mansoni* or eggs per 10 ml for *S. haematobium*) or **Prevalence (%)** entry and *make sure the text box shows a sensible value.*
4. **OK** accepts the parameters, **Cancel** does not!

## ADVANCED EPIDEMIOLOGY (CUSTOM ENTRY)

Epidemiological parameters (in years)		Local parameters	
1. worm lifespan	[L] 1	mean egg count	100
2. density dependence parameter	[d] 0.001	local parameter 2	0.001
3. negative binomial 1 intercept	[k1] 11.11	local parameter 3	11.11
4. negative binomial 1 slope	[k1s] 0.001		
5. development early disease	[E] 0.001		
6. resolution early disease	[Lq1] 1		
7. development late disease	[E] 0.01		
8. resolution late disease	[Lq2] 11		
9. immunity strength	[R] 0.001		
10. immunity duration	[L] 11		
11. heavy infection threshold	[T] 10		
12. egg production rate	[e] 0.1		

1. *You are not recommended to change this unless you know what you are doing.* Changing the parameter values too much may result in errors. To return to **Standard** parameter entry press **Cancel**.
2. Use this menu to change the **Epidemiological Parameters**. The parameters are further described in the publications. The default values given when the screen is opened will give sensible results.
3. *None of the life span or duration type variables can be set to 0* since this will cause a 'divide by zero' error.
4. If **Direct Parameter Entry** is accepted, re-entry into **Infection Parameters** is disabled.

## HUMAN DEMOGRAPHY (STANDARD ENTRY)

Select demographic pattern most similar to your community:

"Africa type"  
 "Middle Eastern type"  
 "Latin American type"  
 Custom (advanced options)

1. You are recommended to accept one of the defaults, but can also enter your own values using the **Custom** option.
2. The regional names only refer to the demographic patterns and need not correspond to the actual geographical locations of the sites. They come from World Bank data.

## HUMAN DEMOGRAPHY — DIRECT PARAMETER ENTRY (CUSTOM ENTRY)

Demographic distribution: Direct parameter entry

Enter distribution parameters for demographic function below:

Exponential distribution

Normal distribution

Scale parameter: 0.0455

Exponential parameter: 0.045

Mean:

Standard deviation:

Cancel OK

1. To use this, you will need to fit your data to a negative exponential distribution or part of the curve of a Normal distribution. You will need to ensure that the distribution integrates to one over a reasonable age range. The program will not do this for you.
2. Note that the program assumes that the exponential distribution has a negative exponent so a minus sign is not needed.
3. On acceptance of these parameters, you will not be able to re-enter **Demography Parameter Entry**. To return to the preset defaults press **Cancel**.

## CHEMOTHERAPY

Chemotherapy Program

Drug efficacy: 10

Cancel OK

Year	Month	Youngest	Oldest	Coverage
1990	0	0	10	98
1991	0	0	10	98
1992	0	0	10	98
2001	0	0	10	98
2002	0	0	10	98

Taskbar: Start, Internet Explorer, Adobe Photoshop, Chemotherapy Progra..., 11:18

1. *In the message box, you can ask for up to 10 treatments.* Entry of invalid characters or 0 treatments would result in acceptance of the default (5 treatments).
2. Enter the **Drug Efficacy** as percentage reduction in egg count.
3. Each line of the table represents one treatment. Please enter for each round of treatment:
  - Calendar **Year** of treatment
  - **Month** of treatment where month refers to calendar month (1= January etc)
  - **Youngest** age treated (in years)
  - **Oldest** age treated (in years)
  - **Coverage** of treatment in percent of target age group
4. Please use integers for all entries in this table
5. *Do not enter 0 or 100 for Coverage or Drug Efficacy as this may give unreliable results.* (Use 1 or 99 instead)

## VACCINATION

**Vaccination program**

*Programme type:*

Cohort

Pulse

*Vaccine properties:*

Initial protection (%)

Duration of protection (yr)

*Programme design:*

Minimum age vaccinated

Maximum age vaccinated

Interval of pulse

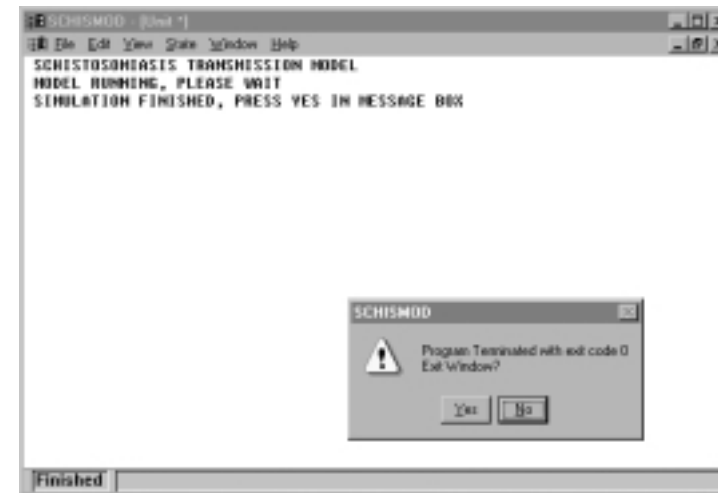
Coverage

Vaccine efficacy

Cancel OK

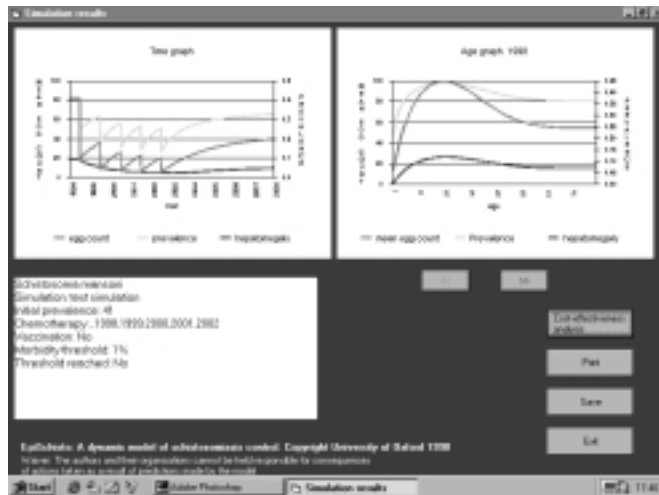
1. Vaccines are not yet available for schistosomiasis. However, this option is included in the software in order to allow you to assess the potential impact of vaccination programmes.
2. Select the type of vaccination programme. **Cohort** vaccination involves the vaccination of people as they reach a certain age. In **Pulse** vaccination a specified age group is vaccinated at intervals (of years).
3. Enter the **Vaccine Properties**. It is assumed that the vaccine has a certain **Initial** level of protection, which gradually decays. The **Duration** of protection is the 'half life' of this decay.
4. Note that **Cohort** vaccination has fewer parameters than **Pulse** vaccination, some labels and text boxes disappear when **Cohort** vaccination is selected.
5. *You are not recommended to enter 0 or 100 for Coverage, Vaccine Protection or Efficacy.*
6. **Duration of Protection** *must not be 0.*
7. **Vaccine Efficacy** refers to the percentage of vaccinations, which are protective.

## RUNNING THE MODEL



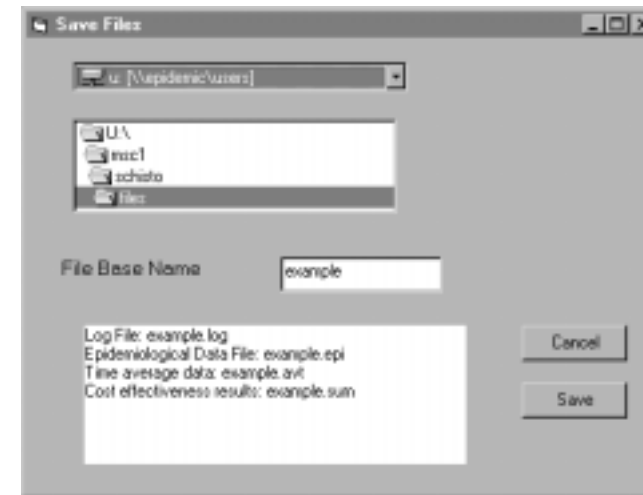
1. The actual calculation has been developed in FORTRAN whereas the front end menus have been developed in Visual Basic. When the model is run, a separate process is called. Only when the program window says it has finished has the program finished.
2. Please be patient, the model will take 1-2 minutes to complete. Do not interfere with the program window until the program tells you to do so.
3. If a run time error occurs, the program will stop and you will not be able to see the results. The program will exit. Such errors usually indicate you have selected unusual parameter combinations, which may not be valid.
4. In some circumstances, a calculation error may occur. In this case a message like 'error in c05azf, IFAIL=1' will be seen. You will be able to see some results but they may not be valid. If this happens, try running the program again with different parameters.
5. To avoid above errors, you are recommended to use parameters close to those suggested.

## SIMULATION RESULTS



1. **Time Graph** shows outputs for children only (6-15 yr)
2. Morbidity shown is hepatomegaly for *S. mansoni* and haematuria for *S. haematobium*
3. The **Age Graph** initially shows the starting age profiles of mean egg count, prevalence and morbidity. In order to see the age profiles in each year of the control programme, click on the forward (>>) button. To reverse the process, click on the reverse (<<) button.
4. The simulation report shows the schistosome species, the name of the simulation (which you entered on the **Control Programme Information** menu, the years chemotherapy occurs, the type of vaccination, the morbidity threshold and the years this threshold is reached.
5. In the report, threshold is reached only if over half of the entries in a given year are under the threshold (in children)
6. **Cost-Effectiveness Analysis** is available only for chemotherapy programmes (NOT for vaccination or combined chemotherapy and vaccination)
7. To print the results, press **Print**. The program will temporarily make the background white and hide the buttons while this is occurring to ensure a visually pleasing print out.

## SAVE FILES



1. To save the results to files, press the **Save** button in the **Results** screen
2. Save will save three files: **\*.epi** for epidemiological results, **\*.avt** for time averages (in children) and **\*.log** for the simulation log. If you have done **Cost-Effectiveness Analysis**, this will be saved in **\*.sum**. It is best to create your own folder to store your files. These files contain further information, not seen on screen which can be analysed in a spreadsheet.

## COST DATA — FOR COST-EFFECTIVENESS ANALYSIS

Cost data

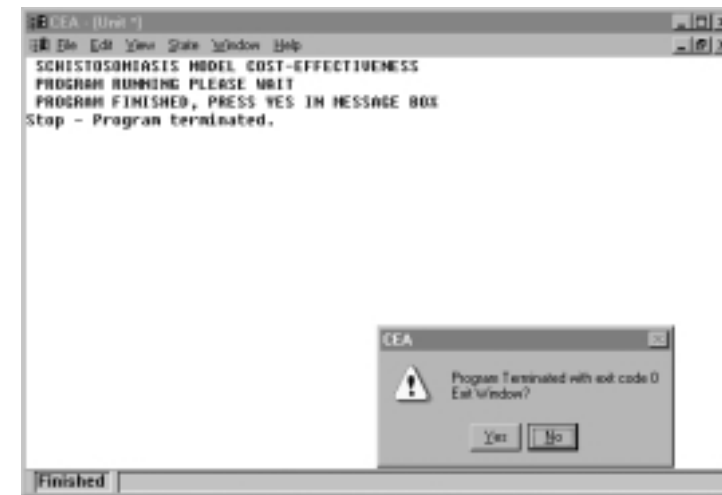
Enter cost data below:

Population size	1000
Personnel costs per day	100
Vehicle costs per day	50
Drug costs per person	1.00
Other consumables per person	0.30
Persons treated per day	400
Capital costs	1000
Discount rate (%)	5
Currency	US\$

Cancel OK

1. Note that the **Cost** menu is for a vertical treatment programme carried out by a mobile team. Therefore it may not be suitable for other types of programme designs.
2. Enter the total **Population** (adults and children) from which your treatment group are drawn. *The population should not be too large (up to 20,000).*
3. Enter **Personnel** and **Vehicle** costs per day.
4. Enter **Drug** costs and other **Consumable** costs per person.
5. *Enter Discount Rate in percent, which should not be 0*
4. The **Currency** is just a text description for your own use and does not need to follow any code. Note that if the currency unit is very small (< US\$0.01), the resulting calculation may result in numbers which are too high for the limits set for the program.
5. 10% wastage of consumables is automatically assumed in the calculation

## COST EFFECTIVENESS CALCULATION



1. This is also done in a separate program and *run time errors may occur if you use cost parameters very different from the defaults.* However, the calculation should be very quick.

## COST-EFFECTIVENESS ANALYSIS — RESULTS

Cost-effectiveness analysis: test simulation  
 USD per infection case/year prevented= 3.21  
 USD per morbidity case/year prevented= 7.59

Yearly observations

Year	Budget (USD)	Infection Cases averted	Morbidity Cases averted
1999	4342.00	8	8
1999	3040.00	373	87
2000	3040.00	598	132
2001	3040.00	748	259
2002	3040.00	673	215
2003	8	998	365
2004	8	665	302
2005	8	641	307
2006	8	615	306
2007	8	795	309
2008	8	778	305
2009	8	778	305
Total	20200.4	7655	2171

EpiSchisto: A dynamic model of schistosomiasis control. Copyright University of Oxford 1998  
 Warning: The authors and their organizations cannot be held responsible for consequences of actions taken as a result of predictions made by the model.

1. Scrollbars will appear if there are too many data, and these can be used to look around the data grid.
2. **Print** will only print what is visible on the screen but a saved file will contain all data.
3. The data in the table are absolute values whereas the overall cost-effectiveness ratios are calculated using discounted values.
4. <<**Back** takes you back to the **Results** page. *You will not be able to re-enter.*

## NOTES ON CONTENTS OF SAVED FILES

The files are saved as text files and can be imported into spreadsheets for further analysis.

1. **\*.log file.** This contains the parameters for the model and should only be used as input for the model
2. **\*.epi file.** This file contains the simulation results by age and time. It can be used to do custom plots and to investigate features not shown in the standard graphs. Each row of the file contains the following information (all prevalences are in proportions):
  - Year
  - Age
  - Mean egg count
  - Prevalence of infection
  - Prevalence of heavy infection (above defined threshold, defaults 250epg for *S. mansoni*, 50 e/10ml for *S. haematobium*)
  - Prevalence of early disease
  - Prevalence of late disease

Note that the 'morbidity' plotted in the graphs are equivalent to 'early disease' for *S. mansoni* and 'heavy infection' for *S. haematobium*.

3. **\*.avt file.** This file shows the average over children aged 5-16 years at 0.05 year intervals with the following fields: time in years since beginning of simulation, Mean egg count, Prevalence of infection, Prevalence of heavy infection, Prevalence of early disease, Prevalence of late disease.
4. **\*.sum file.** This shows the cost-effectiveness analysis results as follows: Species code (1=*S. mansoni*, 2=*S. haematobium*), Cases averted by year (infection and morbidity for all and for children), budget and economic (discounted) costs, cost-effectiveness ratios for all measures (1=infection, 2=morbidity).

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## INTRODUCTION

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### What is EpiFil?

**EpiFil** is a computer program that enables control programme managers and others interested in lymphatic filariasis control to predict the impact of chemotherapy interventions and vector control. The program allows the user to specify the local epidemiological data and the programme of chemotherapy interventions and then the program will calculate predictions based on these data. Output is provided both as graphs on screen and as text files.

Embedded within the computer program is a quantitative framework, known as an epidemiological model, which predicts the transmission dynamics of lymphatic filariasis. Such epidemiological models are based on an understanding of the biological processes of infection. These processes are described in terms of mathematical equations, which are then encoded as a computer program. Epidemiological models are an example of a wider class of models known as population dynamic models. In the field of infectious diseases, population dynamic models have been applied for measles and HIV, for example, as well as for the helminth infection, onchocerciasis. The essential common feature of these models is that they describe explicitly the biological processes of birth and death (and infection where applicable) and therefore the models can be adapted for a wide range of applications.

The model used within **EpiFil**, which is based on a mathematical framework developed by Anderson and May(1985), has been developed specifically with the aim of applying it in a wide range of endemic situations. It has been in development since 1996 and the work has been published in the scientific literature (see bibliography).

The utility of a model will depend ultimately on its ability to predict the impact of interventions correctly. To this end, an essential part of model development is to compare the model prediction with data from past control programmes, a process known as model validation. The current model has been successfully validated using data from India (Norman *et al.*, 1999).

## What can EpiFil do?

**EpiFil** can be used at many stages of a control programme. During the planning stage, **EpiFil** can be used to predict the decline in infection prevalence and intensity and hence can be used when evaluating the benefits of intervention and setting reasonable targets. Likewise, it can also be used to compare the potential effectiveness of different likely schedules of interventions. During the intervention phase of a programme, **EpiFil** can be of use to monitor the progress of the programme, to assess whether the programme is achieving its targets and also to adapt intervention schedules while the programme is running. **EpiFil** is also intended for educational use in developing understanding of the concepts of epidemiology and to train public health workers in the use of predictive methods.

## INSTALLATION

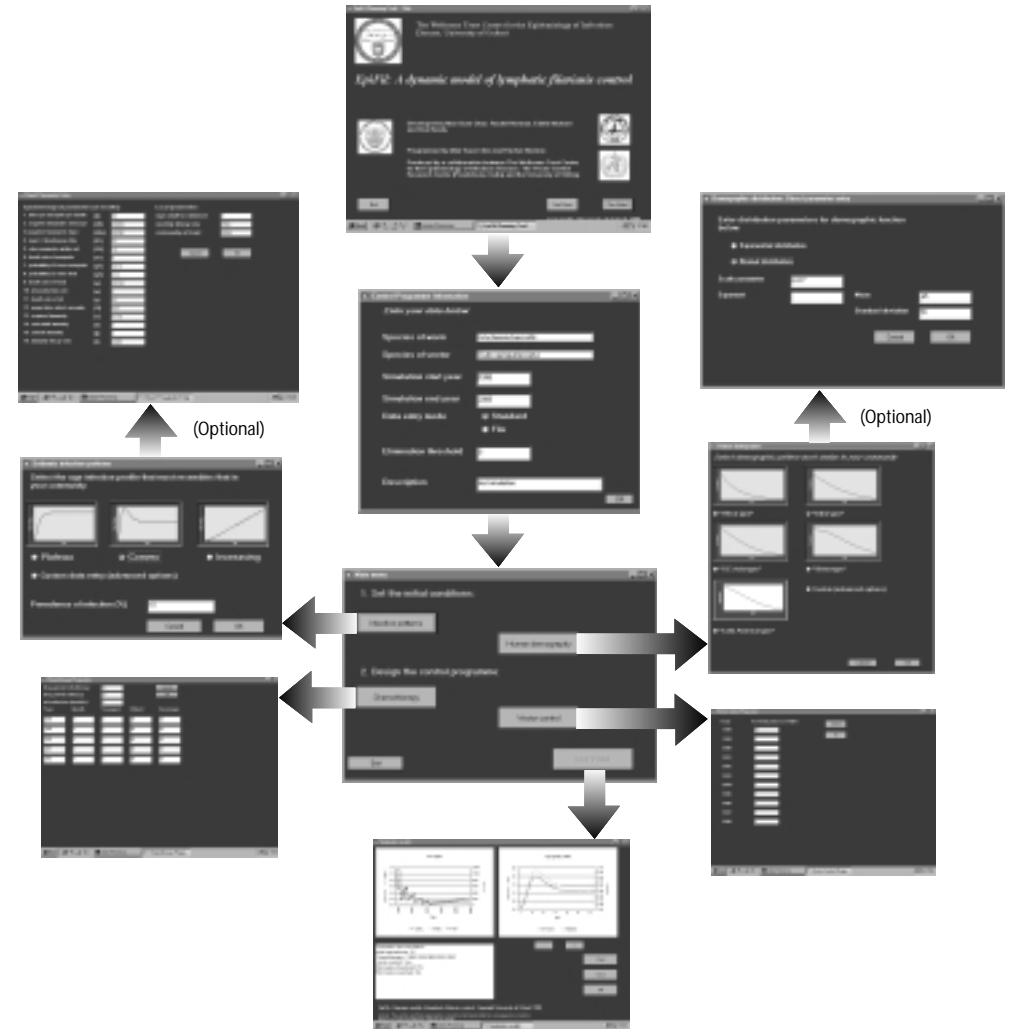
**EpiFil** can be installed on PCs with Windows 95/NT or higher.

To install **EpiFil**, use the customised **setup** program located in the **\package** folder of the distribution CD. This program will guide you through the various procedures necessary for setting up the program. You may need to reboot the machine during the setup procedure.

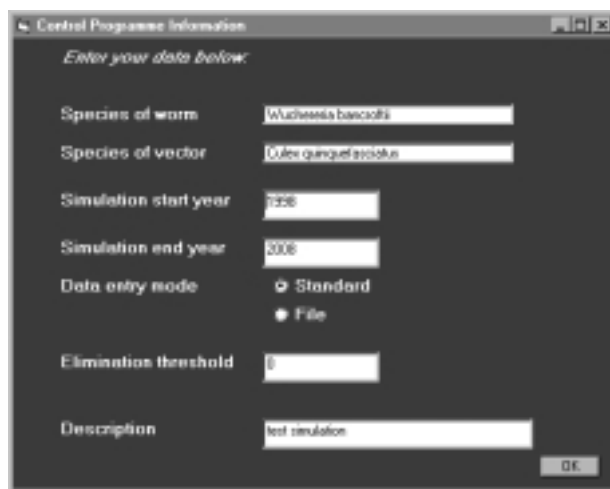
### Options on Title Screen

- See Demo** runs a pre-loaded program file and goes straight to results
- Run Model** goes into the parameter entry menus
- Quit** exits the program

## EPIFIL ROAD MAP

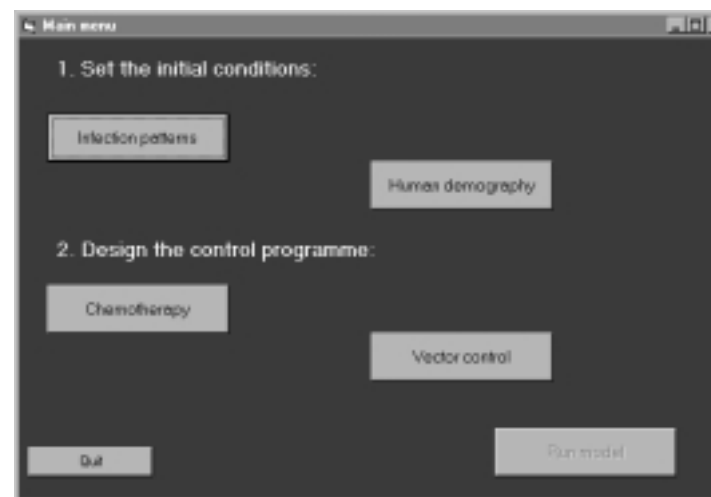


## PROGRAMME INFORMATION



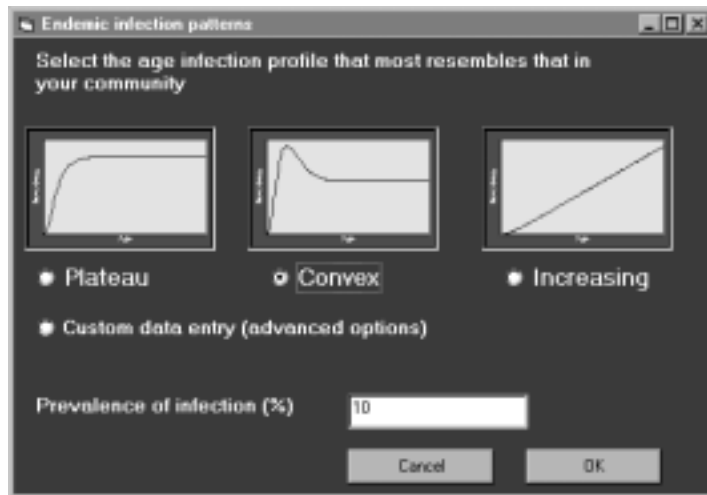
1. At present the model has only been validated for *bancrofti* transmitted by *Culex quinquefasciatus*. It is envisaged that in future it will be developed for other species of parasite and vector.
2. Calendar years must be four digit numbers, *recommended simulation time 5-20 years*.
3. **Standard** data entry means you enter the data, **File** data entry means data will be input from a file. *If you use Standard data entry the program does not 'remember' what you entered last time and will load the defaults.*
4. The **Elimination Threshold** is defined by the user. The program will tell you whether this is reached and sustained for five years. This does not necessarily imply that the infection is eliminated.
5. **Description** is short text description, which fits in the box, for your own use.
6. On pressing **OK**, if **File Data Entry** has been selected, a common dialog box will appear for you to select the input file. Simulation files of form **\*.log** in **\files** subdirectory where you installed the program and any files you have saved yourself can be used. They contain the parameters to repeat a run of the model. *Note that Windows may produce other files of form \*.log which are not suitable (eg uninstall.log).*

## MAIN MENU



1. The **Main** menu is used to navigate around the various areas of data entry. Press each button in turn to access data entry windows. After entry of data, you will return to the **Main** menu. The details of data entry are given on the next pages.
2. **Run Model** will not be enabled until parameters for both **Infection Patterns** and **Human Demography** are entered.
3. *If you have used File Data Entry only Chemotherapy and Vector Control can be changed.*
4. *If you do not enter any control data, the program will run but infection levels will not change*
5. **Quit** will exit the program (you will be warned first).

## INFECTION PATTERNS (STANDARD ENTRY)



1. There are two **Infection Patterns** entry modes, (**Standard** and **Custom**), which are mutually exclusive. *Unless you know the model quite well you should use the **Standard** mode which is patterns 1-3 (plateau, convex and increasing) on this menu.*
2. Select the age infection profile that most resembles that in your community. If the prevalence is moderate or high (>15%) you are recommended to use the plateau pattern.
3. Do not enter 0 or 100 for **Prevalence**.
4. **OK** accepts the parameters, **Cancel** does not!

## ADVANCED EPIDEMIOLOGY (CUSTOM ENTRY)



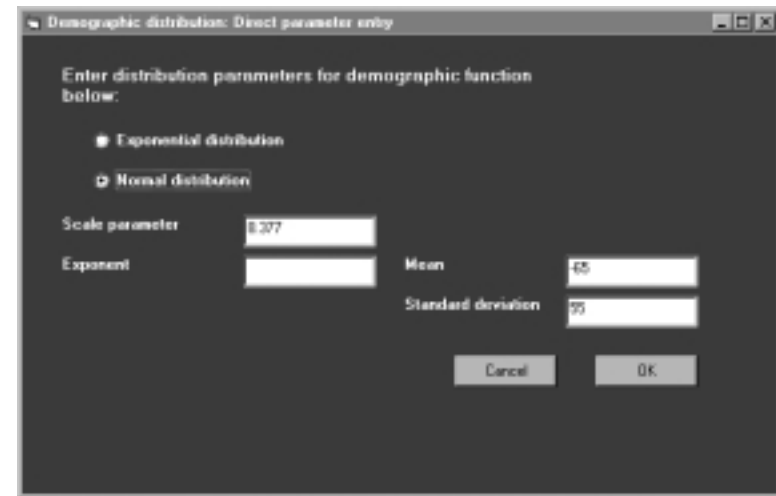
1. *You are not recommended to change this unless you know what you are doing.* Changing the data values too much may result in errors. To return to **Standard** data entry press **Cancel**.
2. Use this menu to change the **Epidemiological Parameters**. The parameters are further described in the publications. The default values given when the screen is opened will give sensible results.
3. All parameters are *in months*.
4. **Rate Parameters** are the inverse of the **Duration/Lifespan**.
5. If **Direct Parameter Entry** is accepted, re-entry into **Infection Parameters** is disabled.

## HUMAN DEMOGRAPHY (STANDARD ENTRY)



1. You are recommended to accept one of the defaults but can also enter your own values using the **Custom** option.
2. The regional names only refer to the demographic patterns and need not correspond to the actual geographical locations of the sites. They come from World Bank data.

## HUMAN DEMOGRAPHY (CUSTOM ENTRY)



1. To use this, you will need to fit your data to a *negative* exponential distribution or part of the curve of a Normal distribution. You will need to ensure that the distribution integrates to one over a reasonable age range. The program will not do this for you.
2. Note that the program assumes that the exponential distribution has a negative exponent so a minus sign is not needed.
3. On acceptance of these parameters, you will not be able to re-enter **Demography Parameter Entry**. To return to the preset defaults press **Cancel**

## CHEMOTHERAPY

Chemotherapy Program

Drug worm kill efficacy:

Drug mf kill efficacy:

of months (months):

Year	Month	Youngest	Oldest	Coverage
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>

1. In the message box, you can ask for up to 10 treatments. Entry of invalid characters or 0 treatments would result in acceptance of the default (5 treatments).
2. Enter the **Drug Efficacy** in terms of % adult worms killed, % mf killed (usually higher) and the number of months that mf production is reduced. Guide values for DEC are 50% worm kill, 90% mf kill for 6 months. Guide values for Ivermectin are 20% worm kill, 95% mf kill for 6 months.
3. Each line of the table represents one treatment. Please enter for each round of treatment:
  - Calendar **Year** of treatment
  - **Month** of treatment where month refers to calendar month (1=January etc)
  - **Youngest** age treated in years
  - **Oldest** age treated in years
  - **Coverage** of treatment in percent of target age group
4. Please use whole numbers for all entries in this table.
5. Do not enter 0 or 100 for **Coverage** or **Drug Efficacy** as this may give unreliable results (Use 1 or 99 instead).

## VECTOR CONTROL

Vector Control Program

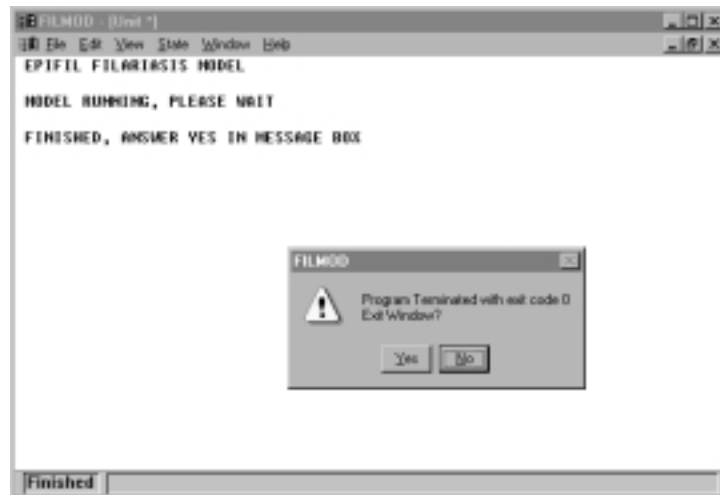
Year:

% Reduction in MBR:

Year	% Reduction in MBR
1998	<input type="text"/>
1999	<input type="text"/>
2000	<input type="text"/>
2001	<input type="text"/>
2002	<input type="text"/>
2003	<input type="text"/>
2004	<input type="text"/>
2005	<input type="text"/>
2006	<input type="text"/>
2007	<input type="text"/>
2008	<input type="text"/>

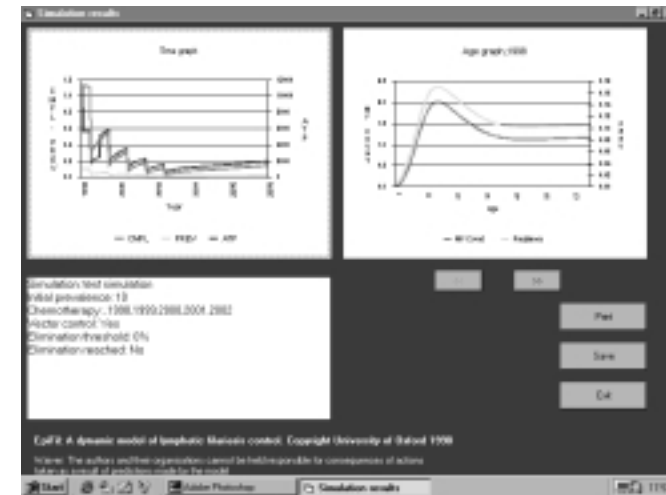
1. The program allows up to 11 years of **Vector Control**. In simulation runs longer than this, vector control occurs in the first 11 years.
2. For each year, vector control is defined as the percentage reduction in monthly biting rate of vectors achieved by the vector control programme.
3. Do not enter 100%.

## RUNNING THE MODEL



1. The actual calculation has been developed in FORTRAN whereas the front end menus have been developed in Visual Basic. When the model is run, a separate process is called. Only when the program window says it has finished has the program finished.
2. Please be patient, the model will take up to 1 minute to complete. Do not interfere with the program window until the program tells you to do so.
3. If a run time error occurs, the program will stop and you will not be able to see the results. The program will exit. Such errors usually indicate you have selected unusual parameter combinations, which may not be valid.
4. In some circumstances, a calculation error may occur. In this case a message like 'error in c05azf, IFAIL=1' will be seen. You will be able to see some results but they may not be valid. This may happen if the prevalence is high. If this happens, try running the program again with different parameters.
5. To avoid above errors, you are recommended to use parameters close to those suggested.

## SIMULATION RESULTS



1. **Time Graph** shows outputs for the whole population.
2. The **Time Graph** shows community microfilarial load (left axis), prevalence (*as proportion*, left axis) and annual transmission potential (right axis).
3. The **Age Graph** initially shows the starting age profiles of mean mf count (left axis), and prevalence (*as proportion*, right axis). In order to see the age profiles in each year of the control program, click on the forward (>>) button. To reverse the process, click on the reverse (<<) button.
4. The simulation report shows the name of the simulation, the years chemotherapy occurs, whether vector control occurred, the elimination threshold and the year this threshold is reached.
5. In the report, elimination is reported to be reached if it is maintained for 5 years. The simulation continues and may predict reinfection. The elimination threshold is user defined.
6. To print the results, press **Print**. The program will temporarily make the background white and hide the buttons while this is occurring to ensure a visually pleasing print out.

## SAVE FILES



1. To save the results to files, press the **Save** button in the results screen
2. **Save** will save three files: **\*.epi** for epidemiological results, **\*.avt** for time averages and **\*.log** for the simulation log. It is best to create your own folder to store your files. These files contain further information, not seen on screen, which can be analysed in a spreadsheet.

## NOTES ON CONTENTS OF SAVED FILES

The files are saved as text files and can be imported into spreadsheets for further analysis.

1. **\*.log file**. This contains the parameters for the model and should only be used as input for the model
2. **\*.epi file**. This file contains the simulation results by age and time. It can be used to do custom plots and to investigate features not shown in the standard graphs. Each row of the file contains the following information (all prevalences are in proportions):
  - Year
  - Age
  - Mean mf count
  - Prevalence of infection
3. **\*.avt file**. This file shows the average over the population at 1 month intervals with the following fields: time, Mean mf count, number of L3 per mosquito, annual transmission potential, prevalence of infection.

## BIBLIOGRAPHY

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Anderson, R. M. & May, R. M. (1985) Helminth infections of humans: mathematical models, population dynamics and control. *Advances in Parasitology*, **24**, 1-101.

Chan, M. S., Srividya, A., Norman, R. A., Pani, S. P., Ramaiah, K. D., Vanamail, P., Michael, E., Das, P. K. & Bundy, D. A. P. (1998) EPIFIL: A dynamic model of infection and disease in lymphatic filariasis. *American Journal of Tropical Medicine and Hygiene*, **59**, 606-614.

Norman, R. A., Chan, M. S., Srividya, A., Pani, S. P., Ramaiah, K. D., Vanamail, P., Michael, E., Das, P. K. & Bundy, D. A. P. (1999) The development of an age-structured model for lymphatic filariasis transmission dynamics and control and its validation for *Wuchereria bancroftii* transmitted by *Culex quinquefasciatus* in Pondicherry, South India. [Manuscript in preparation]

## EpiWorm

## INTRODUCTION

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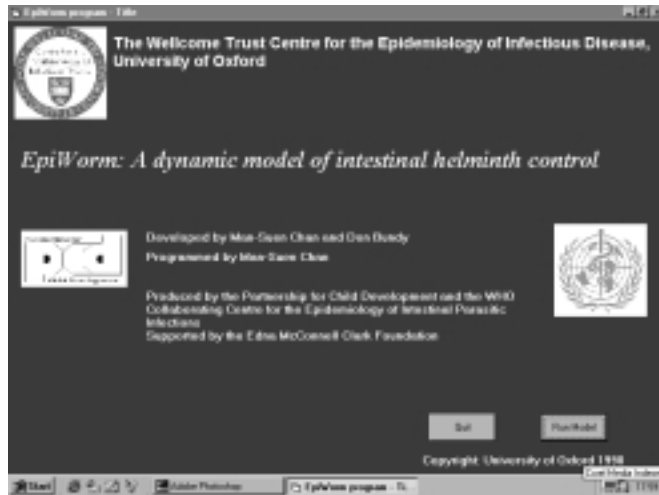
**EpiWorm** is a computer program that enables control programme managers and others interested in intestinal helminth control to predict the impact of chemotherapy interventions. It is particularly intended for programmes in which children of school age are targeted. The program allows the user to specify the local epidemiological data and the programme of chemotherapy interventions and then the program will calculate predictions based on these data. Output is provided both as graphs on screen and as text files.

Embedded within the computer program is a quantitative framework, known as an epidemiological model, which predicts the transmission dynamics of helminth infection. Such epidemiological models are based on an understanding of the biological processes of infection. These processes are described in terms of mathematical equations, which are then encoded as a computer program. Epidemiological models are an example of a wider class of models known as population dynamic models.

**EpiWorm** can be used at many stages of a control programme. During the planning stage, **EpiWorm** can be used to predict the decline in infection prevalence and other measures and hence can be used when evaluating the benefits of intervention and setting reasonable targets. It can also be used to compare the potential effectiveness of different schedules of interventions. During the intervention phase of a programme, **EpiWorm** can be of use to monitor the progress of the programme, to assess whether the programme is achieving its targets and also to adapt intervention schedules while the programme is running. **EpiWorm** is also intended for educational use in teaching students the concepts of epidemiology and to train public health workers in the use of predictive methods.

**EpiWorm** is a generic model, which can be used for more than one species of parasite. The current version can be used to provide information about the control of *Ascaris lumbricoides*, *Trichuris trichiura* and both species of hookworm.

## INSTALLATION

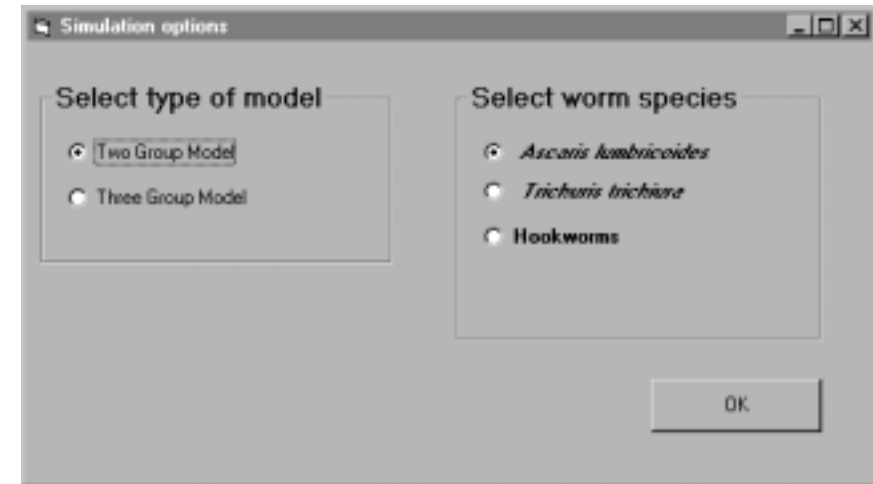


**EpiWorm** can be installed on PCs with Windows 95/NT or higher. To install **EpiWorm**, use the customised **setup** program located in the **\package** folder of the distribution CD. This program will guide you through the various procedures necessary for setting up the program. You may need to reboot the machine during the setup procedure.

### Options on Title Screen

- Run Model** goes into the parameter entry menus
- Quit** exits the program

## SIMULATION OPTIONS



1. Before you run the program you should select the type of model you want to run and the species of parasite.
2. The different types of model are based on the definition of different age groups. These age groups may have distinct infection patterns and can be targeted separately for treatment. For the **Two Group Model** Group 1 is children and Group 2 is adults. For the **Three Group Model**, Group 1 is schoolchildren, Group 2 is other children (these may be children not enrolled in school or pre-school children) and Group 3 is adults. The model you choose will be based on the structure of your data and whether you want to look specifically at distinct groups of children.
3. When you select the species, the model will automatically load the relevant parameters for that species. The hookworm parameters are based on a global analysis of mixed (species, *Necator americanus* and *Ancylostoma duodenale*) hookworm infections since data on each species are generally unavailable.

## EPIDEMIOLOGICAL PARAMETERS

Parameter	Group 1 Schoolchildren	Group 2 Adults
Worm Lifespan	1	
k of negative binomial	0.54	
Mean Worm Burden	18	5
Basic Reproductive Number	2	1.5
Proportion of Population	0.4	0.6
Morbidity Threshold	15	20

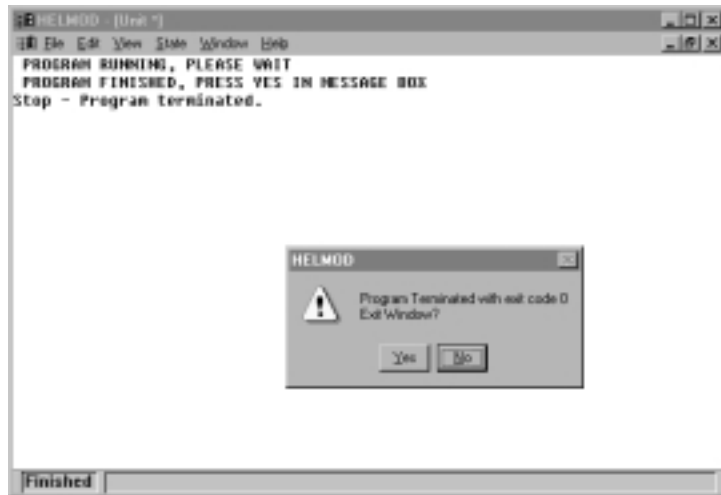
1. Note that **EpiWorm** is a 'generic' intestinal helminth model. The parameters automatically loaded for each species come from analysis of data sets from the literature and serve as guidelines only. There are no 'hidden' parameters; all the parameters used appear on screen and can be changed by the user.
2. The **Worm Lifespan** cannot be 0, this will cause an error.
3. The parameter **k of the Negative Binomial** is a measure of the aggregation of parasite distribution (lower k means more aggregation). The value is usually less than 1.
4. The group specific parameters loaded will give sensible results but you may wish to enter your own values. To vary the levels of transmission, vary the **Mean Worm Burdens**.
5. The **Basic Reproductive Number** is generally between 1 and 4. In any case the weighted average of basic reproductive numbers must be over 1 for a population of parasites to persist.
6. The **Proportion of the Population** in the 'last' group cannot be changed by the user, it is automatically updated by the program to add up to 1.
7. The **Morbidity Threshold** refers to the worm burden above which morbidity is observed in an individual.

## TREATMENT PROGRAMME

Interval of treatment (years)	1
Time of last treatment	5
Years to run model	10
Coverage Group 1	50
Coverage Group 2	0

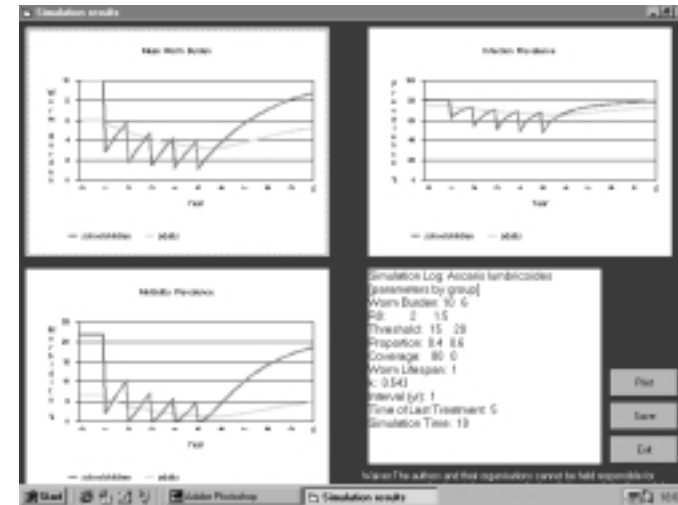
1. Treatment will occur at regular intervals defined by **Interval of Treatment** from year 1 until **Time of Last Treatment**. The simulation will stop after the number of years in the **Years to Run Model** input box.
2. If you want to treat more than once a year, enter the interval in decimal form (i.e. 0.5=6 months etc).
3. Enter **Coverage** for each age group in percent.

## RUNNING THE MODEL



1. The actual calculation has been developed in FORTRAN whereas the front end menus have been developed in Visual Basic. When the model is run, a separate process is called. Only when the program window says it has finished has the program finished.
2. Do not interfere with the program window until it tells you that the program has terminated.
3. If a run time error occurs, the program will stop and you will not be able to see the results. The program will exit. Such errors usually indicate you have selected unusual parameter combinations, which may not be valid.
4. In some circumstances, a calculation error may occur. In this case a message like 'error in c05azf, IFAIL=1' will be seen. You will be able to see some results but they may not be valid. If this happens, try running the program again, with different parameters.
5. To avoid above errors, you are recommended to use parameters close to those suggested.

## OUTPUT: SIMULATION RESULTS



1. The three graphs show **mean worm burden**, **prevalence (%)** and **prevalence of morbidity (%)** separately for each age group.
2. The simulation log shows the parameters you entered for the simulation.
3. To print the results (a picture of the whole results window), press **Print**. The colours will change temporarily to give a visually pleasing paper report.
4. To save the simulation results, press **Save**. Only the results are saved, not the simulation log. Therefore you should print the form in this case or make a note of the parameters.

## CONTENTS OF SAVED FILE

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1. The saved file is an ascii text file which can be imported into a spreadsheet for further analysis.
2. The file has the following columns:
  - Time (years)
  - Group
  - Mean Worm Burden
  - Prevalence (proportion)
  - Morbidity (proportion)
3. Note that if you ran a **Two Group Model**, the 'results' of an apparent third group in the saved file should be ignored, they are invalid.

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- Chan, M. S., Bradley, M. & Bundy, D. A. P. (1997) Transmission dynamics and the epidemiology of hookworm infection. *International Journal of Epidemiology*, **26**, 1392-1400