

INSIM A SIMULATION ENVIRONMENT FOR PEST FORECASTING AND SIMULATION OF PEST-NATURAL ENEMY INTERACTION.

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Keywords: Forecasting, simulation, phenological model, population model, apple pests.

Abstract

For the development of forecasting models a computer environment has been constructed which makes it possible to generate in a user friendly way a programme of the phenology and population development of an insect species. INSIM (INsect SIMulation) is menu driven and needs only the biological information of the insect species. INSIM generates age-structured models and therefore includes modules calculating number and development of insects by using of boxcars, to account for the relative dispersion of development. By means of tables all life-history data are read into the programme. For a simple phenological or population model the information needed is: life cycle, development rate and standard deviation of each insect stage, sex ratio, life expectancy of the adult and age dependent reproduction. In a spreadsheet the stages are coupled to each other which makes the program rather flexible. The weather data, the minimum and maximum daily temperature, are stored in an environment file. The temperature for each time step is calculated from a sinusoid through the minimum and maximum temperature. The output of the chosen variables can be presented graphically or numerically on the screen.

For the simulation of complicated predator- prey interactions specific programming is still needed but this is not too complicated as the program is written in Quick-Basic. Examples of simple phenological and population models and more complex pest-natural enemies models are presented.

1. Introduction

Apple growers have to deal with approximately 40 potential pest species, 15 of these may occasionally reach the pest status and 6 of them are an annually returning threat if no control measures are taken. To avoid problems these key pests are monitored each year by a specific trapping technique or by visual sampling to assess the presence or the number of a specific stage of a pest. Different life stages of a pest may have a different susceptibility for a pesticide. Therefore right timing of sampling and if necessary right timing of application of a selective chemical is essential for an optimal crop protection strategy. This will save time, labour, and pesticides and thus will save money and will be better for the environment. The use of forecasting models may be of great help in achieving this goal. To help the farmer or extension officers in pest forecasting, different models have been developed varying from statistical models to phenological and population models (Mols, 1992) some of them also including natural enemies (Nyrop & W. v.d. Werf, 1993). The most well known models used are the Temperature sum models. They have widely proven to be very effective for predicting the phenology of a specific stage of a pest. The T-sum can only be used for pests that have a linear relationship between rate of development and temperature. If that condition is not fulfilled forecasts have to be restricted for specific temperature ranges in the field for which the relationships approach linearity. Another problem is that for a proper use of

the T-sum model development thresholds of all the life stages have to be the same otherwise it becomes difficult to calculate the spread in the developmental stages.

As relationships between rate of development and temperature are seldom linear, in most cases they show an optimum curve, and because we wanted to predict in a proper way the spread of the life stages in the course of time, we decided for dynamic simulation models. In these models the flow of the individual insects from one stage to the next is taken into account by so called distributed-delay processes (de Wit and Goudriaan, 1978; Goudriaan & van Roermund, 1988). The dynamic models can also handle all kinds of relationships between rate of development and temperature.

Another condition was that it should be possible to implement biological data of different pest species with different life cycles in an user-friendly way, because to develop different models for each specific pest in the classic way would be too cumbersome. Therefore we developed an environment that could be used to generate in a simple way a model of a pest species without the need to program and without the expertise of a computer programmer.

2. The INSIM environment

2.1. The language

The INSIM environment is written in the programmers language Quick-Basic (including subroutines from QB professional). This language offers the advantage that it has both a very good editor and compiler and good debug facilities and the graphics are easy to program. For an overview of the structure of the program modules see appendix 1.

2.2. The menu structure

To make the program user-friendly it is made out of pull down menus as is the case in most of the computer programs nowadays. It contains menus for file handling, input and editing of data in specific spreadsheets (overview of the stages in the lifecycle arranged in boxcars and tables for the stage development-temperature relationships), arrangement of the output (numerical or graphical) and selection of variables and simulation options. For an overview of the menu structure see appendix 2.

2.3. Dispersion of development in the life stages.

The core of the program is the so-called fractional boxcar train which is used to mimic the dispersion of the individuals passing a life stage. Each life stage is represented by a boxcar train containing several subclasses (the boxes). The number of boxes depends on the relative dispersion of the development of a stage ($SD/Average$). Because temperatures change in the course of time so do the rates of development and their standard deviations. Therefore, these rates and their SD are the essential information needed in the program. Depending on the relative dispersion over the range of temperatures for each stage an optimal number of boxcars is calculated. This number remains constant during the simulation but the fraction by which the individuals shift in the train varies with changes in the relative dispersion (Goudriaan and Roermund, 1989). The number of life stages, the boxcar trains, determines the basic structure of the insect model. The interface between a boxcar train and the main program is composed of input variables (i.e. inflow, relative mortality, development rate, relative dispersion) and output variables (i.e. total mortality, total content of the boxcar, outflow). The user assigns a unique number to all the boxcar variables. Variable numbers are used to define the interface between various boxcar trains and the relation between boxcar variables and user specified intermediate variables. These variables are the basic units of the

program. They are defined in an INSIM-database. Five types of variables have been distinguished:

- Calculated variable: the variable is calculated by the program (e.g. the total content of a boxcar)
- Value: the variable is a constant
- AFGEN variable: the variable depends on another variable as specified in a user defined table. This table is defined in a spreadsheet. The program uses a linear interpolation scheme to calculate the value of the variable.
- Formula variable: a variable which depends on other variables as specified in a formula.
- Environmental variable: the value of the variable can be found in a climate data file.

2.4. Biological data needed for INSIM

2.4.1. The phenological model.

The biological data needed is: the number of life stages, the average duration of development of individuals throughout a life stage and its standard deviation. This information is obtained by rearing experiments under constant temperature conditions. To get a good relationship with temperature, observations from at least 5 temperatures are necessary. Thresholds of development can be found by extrapolation, although this remains the weak point. If the relationship is linear the threshold can be found by simple linear regression, but if a curvilinear relationship is involved other curvilinear models may be used to get an estimate (Logistic, LOGAN etc.) of the threshold. If enough field data is present even a simple trial and error method can be used for calibration of the development threshold.

2.4.2. The population model.

Besides information on duration of life stages and its SD, extra information is needed on reproduction and adult survival. The most accurate data are those where reproduction is related to the aging of the adult female. This can be implemented into the model by means of age classes. Therefore, for each temperature, the adult life time is divided into the same number of age classes. The form of the reproduction curve determines the number of classes which is appropriate to give a good description of the reproduction curve. The daily reproduction of each class is put into a spreadsheet from where the program takes its information for the calculation.

Natural occurring mortality related to temperature also has to be included for each stage and for the appropriate temperature range. This is also put into a table.

2.4.3. The predator/parasitoid - pest model

Besides the biological information on both pest insect and on the predator or parasitoid, extra information is needed about their interaction. This interaction section is not included in this version of INSIM . Therefore some extra programming has to be done. The interaction is by means of a Holling I or II curve for parasitoids or by means of temperature -feeding relationships for predators as has been implemented in the ERIOAPHE and THRIPSIM models (see examples)

3. Application of INSIM

With phenological models it is possible to predict the presence of a specific stage or the relative occurrence of the stages. They are very useful for determining the right time for monitoring or for spraying. They can also be used for optimisation procedures for control of pest complexes. They are very valuable when the economic injury level of the

pest species is low and when they are difficult to monitor. The models are relatively simple in structure and therefore easily to be changed. INSIM can be used to calculate a practical T-sum for species having curvi-linear relationships between development rate and temperature.

Population models are especially valuable when the pest species can be tolerated in higher numbers. They can be used to predict when the economic injury level will be exceeded. Therefore they need good initial data which are sometimes difficult to get. The simple population growth models are only accurate for relatively short periods as no natural enemies are included.

Predator/parasitoid- pest models are useful to make rough estimates of predator/parasitoid-pest ratios needed to control a pest or to fill in gaps in knowledge concerning the effect of interaction in the course of time. The phenology of the predator/parasitoid can be predicted offering the right moment for monitoring and improving the interpretation of the field data obtained.

4. Examples of models generated with INSIM

4.1. Phenological models

The green apple capsid (*Lygocoris pabulinus* L.)

The life cycle of the green apple capsid consists of egg, 5 larval stages and an adult stage. The input data are from Mols (1990). The model has been validated for several years and the results show a close agreement with field data. The model is used to predict the optimal moment for spraying which is between the first and third larval stage.

Tortricids (*Adoxophyes orana*, *Pandemis heperana* and *Cydia pomonella*)

Models have been developed for all the three species. Input data are from de Reede (1985) and from various authors respectively. The first two models were used to calculate the optimal practical T-sum for application of the growth regulator fenoxicarb at the beginning of the last larval stage. T-sum for the first flight of *C. pomonella* is as good as the model.

Clouded drab moth (*Orthosia incerta*). Forecasting of the flight of the Clouded drab moth for hanging out pheromone traps. Following phenology of eggs and the first two stages is of importance for timing of insecticide application when necessary. Input data of development stages are from Mols and v.d.Ende (in prep.)

Winter moth (*Operophtera brumata*). Forecasting of egg hatch and larval development. Data on egg development are from Embree (1970), on larval development from Mols (unpubl.)

Rosy apple leaf curling aphid (*Dysaphis devecta*). Forecasting of egg hatch. Data are from Znoar (unpubl.)

4.2. Population models

Rosy apple aphid (*Dysaphis plantaginea*, Pass.)

Breaking of diapause of winter eggs and the population growth in spring and summer of the rosy apple aphid (*D. plantaginea*) is simulated. Data concerning life cycle and development rates with SD are from Graf (1984) and Graf *et al.* (1985 a,b) in Switzerland. The results of the model show a good agreement with field data in the Netherlands.

Green peach aphid (*Myzus persicae*) on 2 cv of lettuce. The effect of partial resistance of 2 lettuce cv's on the population growth of the green peach aphid is shown. Data on development rate and reproduction are from Dieleman (pers. obs.)

INSIM-Mosquito

A specific version of INSIM has been written to model the phenology and population dynamics of mosquitos. Feeding and oviposition behaviour of adult mosquitos and their role as a vector for malaria is simulated. This version of INSIM has been connected to an

epidemiological malaria model (Takken *et al.*, in prep). It is used to calculate the spread of malaria mosquitos under different scenarios of the greenhouse effect.

4.3. Predator/Parasitoid- pest models

ERIOAPHE A model of Woolly apple aphid (*Eriosoma lanigerum*) and its natural enemies: the parasitoid *Aphelinus mali*, the earwig *Forficula auricularia* and the ladybird beetle *Exochomus quadripustulatus*. Input data of WAA are from Walker (1986), of *A.mali* from Evenhuis (1956), Trimble 1990 and Mueller *et al.* (1992), of earwig from Mueller *et al.* 1988 and Noppert *et al.*1987. Data on *E.quadripustulatus* are under elaboration in our department Mols (1993, and in prep.). The model aims at quantifying the role of natural enemies in controlling WAA. It predicts the right time for monitoring of WAA and *A.mali* parasitization, and the ratio's between WAA and its natural enemies necessary to control WAA.

THRIPSIM This is a model of the Western flower thrips *Frankiniella occidentalis* (Pergande) and the predatory mite *Amblyseius cucumeris* (Oudemans) to explore the dynamic behaviour of this prey -predator system on sweet peppers (*Capsicum annum*) in greenhouses. Data are from literature. The model is rather complex and includes the availability of flowers as refugia for the thrips and the availability of pollen as alternative food for both pest and predator (van Delden *et al.* 1995)

The model of *Frankiniella occidentalis* is also be coupled to the pirate bug *Orius laevigatus* (Mols and Burgio in prep.).

From *Thrips palmi* and the predator *Orius sauteri* data are implemented, but the model needs validation (Yano and Mols, in prep).

Acknowledgements

LEB-fonds Wageningen payed a part of the travel expenses to Avignon for wich I am very grateful.

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Appendix 1

Structure of the programme code.

The total code of the programme is divided into 5 modules:

1. The module for the menu library, consisting all the routines needed for the functioning of the items offered in the pull down menus.
2. The main module. Contains the code for reading parameters out of an array into the variables of the simulation programme
3. The declaration module. Contains declarations of the subroutines defined in the menu library
4. Controller module for the menu. Communication between user and simulation code
5. Simulation module. Contains the simulation code divided into subroutines

Modules 1-4 are used for making the INSIM environment user-friendly, like handling the pull down menus, input of variable names, organisation of the graphics on the screen etc., The simulation module is the core of the programme it contains the subroutines needed for the elaboration of the input by the user and the output on the screen.

The most important subroutines are:

The Boxcar and Fixbox subroutines. The first is used to mimic the spread and delays of the development stages of an insect (Goudriaan, Roermund,1989) by using the standard deviation of the average development of the stage. The fixbox is used to simulated age dependend reproduction.

The integrator subroutine. This routine is used to integrate at each time step the value of a variable with the product of rate of change of the variable and the time step. This so called rectilinear integration.

The AFGEN subroutine determines for each temperature by linear interpolation the value of a variable out of a table .

The Sinustemp subroutine calculates for each time of the day the actual temperature out of the daily minimum and maximum temperature.

The IMPULS subroutine. This is a switch that can have either the value 1 or 0 during one time step.

Appendix 2

Overview of the menu structure

The menu bar contains 5 main menus.

1. File menu (Contains 7 submenus)

- New file (Makes a new file with name untitled)
- Open file (Opens a file from a sub menu with a list of files)
- Save current file (Saves to a default name, to a run name or to a new namerun names are easy for sensitivity analysis)
- Delete a file
- Change drive/Directory
- Dos shell
- Exit

2. Input menu (Contains 5 submenus)

- Overview stages (Gives a spreadsheet with an overview of the stages, represented by boxcars. All the stages can be numbered and the boxcars can be coupled to each other by putting the number of a boxcar at the input column of another. Fractions of a boxcar can also be passed. This is needed when sex ratios have to be used.)
- Stage (Gives a menu of all the stages. Selecting one stage gives a table in which average development times with their SD have to be written for a range of temperatures. Relative mortality for each of the temperatures can be filled out here also.)
- Reproduction (The reproduction divided over age classes for a range of temperatures can be filled out here. The number of age classes has to be filled out in program parameters first)
- Program parameters (Contains all input values of the variables, the name of the environment file, the name of X and Y-axes and name above the graph.)
- Environment file (Contains the Min and Max daily temperatures.)
- Sort/Check data (To sort input temperature-development relationships at increasing temperature and calculate the optimal amount of substages in each boxcar, to get a good calculation.)

3 Output menu (Contains 6 submenus)

- Fix output (To fix the set of output variables and settings chosen in the output menu, this makes comparison of the output of different runs easier.)
- To screen (contains 3 submenus
 - Only time*: gives only last values of output on screen
 - Scroll output*: List of all output in text format
 - Graph output*: submenu to select range of axes and log transformation
- To other (To a printer or to an ascii file)

Variables	(To select variables for output on the screen from a menu)
Phenology	(To present the output of stages as a percentage of total number)
Eggs included	(Relative output with or without eggs, makes comparison with field data easier)

4 Simulation (Contains 3 submenus)

Start simulation	(Starts simulation of selected model and runs)
Activate run	(Changed models saved under a run number can be activated, 10 models can be run successively.)
From output file	(Previous simulations can be shown on the screen or send to a file or printer)

5 Help menu (under F1)

Gives in short information about moving and selecting in menus, about input of data from ascii files and writing of INSIM data to ascii files.