

Use of ROOT to build a software optimized for parameter estimation and simulations with Distributed Delay Model



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ABSTRACT

ROOT is a software package developed by a CERN project started in 1994 by René Brun for statistical analysis in high-energy physics. This software package can also be used in the field of protecting plants against pest insects. Indeed, for a long time there has been a significant use of the Distributed-Delay Model, but there is no specific software available to date that is useful for following the research from the first step to simulations and field validations.

This work, through ROOT's libraries, builds a series of macros that consent to do non-linear fits with functions such as Erlang PDF, linear-rate, Logan, Brière, Sharpe and De Michele, thereby giving support to the parameters-estimate step in laboratory sessions and then numerically solving the Distributed-Delay Model equations. This study supplies results both graphically and numerically.

1. Introduction

In Agricultural, Forest and Environmental Sciences, and especially in the context of risk management, modelling has become an important tool. In particular, entomologists started using several models to forecast pest insects' life cycles for two primary reasons: safeguarding human and environmental health, and because of the restrictive laws regarding pesticide use. The difference between a monitoring system and a forecasting system results from the possibility of having an idea of the risk situation of an agricultural field or an urban and peri-urban area (Speranza et al. 2007). There is a need to develop a control strategy different from the conventional one. Despite monitoring and forecast systems seeming similar, in reality there is a conspicuous difference between them. In the first case, data collected with traps placed in fields provides empirical information on insect presence. Capinera defines the term “*monitoring*” as “*careful observation of pest abundance and damage*” (Capinera 2001). The inconvenience is that monitoring provides no information about the future trends of the monitored population. On the other hand, a simulation could not report the exact field situation, but it is helpful to know the future development of the population. In other words, forecasting is “*the process of making predictions based on past and present data*”. These predictions can support a series of research projects that involve using natural enemies such as predators, parasitoids, entomopathogenic fungi and bacteria for the

control of insect pests. Indeed, natural enemy complex plays a pre-eminent role in controlling invasive and autochthonous species in different environmental contexts. For example, the entomopathogenic fungus *Entomophaga maimaiga* in areas where it has been introduced is effective against the gipsy moth *Lymantria dispar* (Lepidoptera: Erebididae) populations (Pilarska et al., 2006), encouraging further experimentation aimed at diffusing this pathogen in new areas across the world (Contarini et al. 2016). In the agronomic context, the biological control applications of the entomopathogenic bacteria *Bacillus thuringiensis* (Alsaedi et al. 2017; González-Cabrera et al. 2011) or the predator *Zelus obscuridorsis* (Hemiptera: Heteroptera: Reduviidae) (Speranza et al. 2014) in the tomato leaf miner, *Tuta absoluta* (Lepidoptera: Gelechiidae) might be mentioned. The inconvenience of this type of control is that it requires highly qualified technicians, quick response and accurate knowledge of the most susceptible life stage of the insect pest if one is to maximize the efficacy of the use of biological control. On the other hand, if it is impossible to apply a biological control strategy, to know the pests' population trends helps one perform chemical control to reduce the quantity of the pesticide in question. One of the widely used models is the Distributed Delay Model (DDM).

Beginning with its introduction by Manetsch (1976), the DDM has garnished interest from entomologists and environmental scientists to describe the life cycle of poikilothermic organisms. One of the strengths concerns the possibility of linking environmental and species'

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parameters to the description of a population dynamics. Several applications have shown the DDM's adaptability to different pest insect species (Alilla et al. 2007; Blythe et al. 1985; Galeano-Vasco et al. 2013; Limonta et al. 2009; Pucci and Spanedda 2006; Schaalje and van der Vaart 1989; Severini 2004; Speranza et al. 2007; Wang et al. 1977). A typical application of the DDM for a species with a poorly known biological cycle starts with a series of constant-temperature laboratory rearing. This is the first phase or "laboratory session": entomologists build cohorts of insects (all laid on the same day) and put them in climatic cells. Researchers follow each cohort's individual day by day during its life cycle, collecting data of the duration of each stage. There were similar observations for other insect pests belonging to different orders, including the beetles (Coleoptera) *Rhynchophorus ferrugineus* (Dryophthoridae) and *Anthonomus eugenii* (Curculionidae) (Li et al. 2010; Toapanta et al. 2005), the butterflies (Lepidoptera) *Lobesia botrana* (Tortricidae), *Corcyra cephalonica* (Pyralidae), and *Tuta absoluta* (Gelechiidae) (Moshtaghi Maleki et al. 2016; Osman et al. 1984; Özgökçe et al. 2016), the wasp (Hymenoptera) *Diadegma anurum* (Ichneumonidae) (Golizadeh et al. 2008), and the true bug (Hemiptera) *Halyomorpha halys* (Pentatomidae) (Nielsen et al. 2008).

Life tables are important because of the description of the relationship between the temperature (the main environmental driving variable for poikilothermic organisms) and the average developmental time, $D[T]$, for each stage composing the life cycle. It is common in practical cases to convert the mean developmental time $D[T]$ in mean development rate $R[T]$, (specific for each temperature), by the expression (Liu et al. 1995; Severini and Gilioli 2002).

$$R[T] = \frac{1}{D[T]} \tag{1}$$

The reason behind this choice is the trend reported in a plot rate-temperature. In fact, with this conversion, one can obtain an increasing-decreasing profile which highlights the thermal optimum for the species as well as its lower and upper thermal thresholds. The second phase of a simulation process concerns the simulation: all the estimated parameters are inserted in a model together with the measured average daily temperature. This obtains the forecasted population dynamics. Subsequently, a validation is made comparing the results of a simulation, with data collected via in-field monitoring. Despite wide application, one of the main problems reported by the insiders is the lack of a specific software that allows researchers to collect data during each step of the project. This current work introduces a new application of the ROOT software as a base to build a helpful tool for all simulation processes with DDM. More specifically, ROOT is "a modular scientific software framework. It provides all the functionalities needed to deal with big data processing, statistical analysis, visualization and storage. It is mainly written in C++ but integrated with other languages such as Python and R." (<http://root.cern.ch>) (Brun and Rademakers 1997). The following sections describe the specifics of each operation and the corresponding ROOT's macro developed to manage all the required calculations.

2. Materials and methods

Manetsch first introduced DDM, though Vansickle (Vansickle 1977a) performed it for the first time one year afterward, at the same time introducing the mortality coefficient as attrition. More specifically, Vansickle's improvements concern comparing the mortality to a friction force: in his work he considered that for each life stage there is a specific mortality coefficient (such as the attrition coefficient in physics) which is directly proportional to population density. Accordingly, the rate of dead is higher as the population density increases. In the case of insects, it is possible to indicate the entire life cycle with a series of chained boxes, each of which is described by an ordinary differential equation. If we call $Q_i(t)$ the number of individuals in the i -th stage, $D[T(t)]$ the average developmental time (depending on the temperature),

and h the number of steps for each prediction. The mathematical expression of Manetsch's model is the following:

$$\begin{cases} \frac{d}{dt}Q_1(t) = \frac{h}{D[T(t)]} [Q_0(t) - Q_1(t)] \\ \frac{d}{dt}Q_2(t) = \frac{h}{D[T(t)]} [Q_1(t) - Q_2(t)] \\ \vdots \\ \frac{d}{dt}Q_h(t) = \frac{h}{D[T(t)]} [Q_{h-1}(t) - Q_h(t)] \end{cases} \tag{2}$$

The system (2) can be solved analytically for constant temperatures rearing in the case of a Dirac delta function $\delta(t)$ as input function $Q_0(t)$. In the most general case, indicated in the system (2), temperature is variable over time, so to assert that it is constant leads one to consider $D[T]$ instead of $D[T(t)]$. This is a mathematical means of representing a cohort of individuals that join the process at the same time, as well as what is done to build life tables with constant temperature rearing. The analytical solution is represented by the Erlang Probability Density Function (Erlang PDF) (Manetsch 1976; Severini et al. 1990; Vansickle 1977a):

$$f(t) = N \cdot \left(\frac{h}{D[T]} \right)^h \frac{t^{h-1}}{(h-1)!} e^{-\frac{h}{D}t} \tag{3}$$

Several works (Alilla et al. 2005; Plant and Wilson 1986; Schaub et al. 2017; Severini et al. 1990) have shown that the development over time for a cohort is well described from the expression (3) in which N is a normalization constant considered as the number of initial individuals in a cohort. In fact, the temperature causes variations in development time of a poikilothermic organism, making it directly linked to the average development time $D[T]$. Expression (3) is helpful in the laboratory phase: since the emerging time follows an Erlang PDF trend, it is possible to do a non-linear fit operation to estimate the parameters h , $D[T]$ and N . In particular, $D[T]$ is the most important as it represents the expected value of the emerging time; it can be converted into development rate through the expression (1). A series of pairs of points ($T_b, R[T_b]$) is obtainable by repeating rearing with different constant temperatures. This mathematical description inspired the development of the first two macros using the ROOT's libraries: *graph2Dpunti*. This was done to plot experimental points as well as *fiterlang* to work out the non-linear fit operations with the Erlang PDF.

The series of experimental pairs of points ($T_b, R[T_b]$) is useful for building the development rate function (Curry and Feldman 1987; Damos and Savopoulou-Soultani 2012). This function represents a driving function for the development through stages, at the same time providing the corresponding rate for each temperature. For a simulation process, the role of the development rate function is crucial in that it links the population dynamics to the environmental parameters. In other words, it represents a driving function for the development through the stages and provides the corresponding rate (or time, if converted with the expression (1)) for each temperature measured in the open field. In fact, the open field is definable as the environment in which the mean daily temperature is variable, $T(t)$. The typical trend reported in life tables starts from a lower temperature threshold, T_L , under which the development rate is equal to zero. There is then an increasing range until it reaches a maximum peak that represents the optimal temperature for development. On the right of the maximum a decreasing trend is until a maximum threshold value T_M ; after that, the development rate is equal to zero. Fig. 2 presents the case of *A. eugenii* as an example (Toapanta et al. 2005).

One of the main problems of the development rate function is the lack of points: in fact, the build of the life tables requires significant time and a conspicuous number of individuals to compose the cohort. Furthermore, one of the hardest parts is the rearing of insects at temperatures close to the upper and lower thresholds. The number of

individuals for the starting cohort in this case have to be higher than the other cases (e.g. rearing near the optimum temperature) because of high mortality. Significant errors thereby affect data from the “laboratory phase” owing to the genetic variability of the population, as well as other systematic errors due to the instrumentation, to the insiders' expertise, and to diet (artificial or natural).

To date there is no preferred mathematical expression to describe the relationship between rate and temperature, but over the course of time scientists have reported several functions that insiders have used widely on the basis of the available life tables. The most common are:

- the linear rate function (Damos and Savopoulou-Soultani 2012; Severini and Gilioli 2002)

$$R[T] = aT + b \quad (4)$$

with a and b the empirical parameters;

- the Brière rate function (Briere et al. 1999)

$$R[T] = a \cdot T(T - T_0)(T_L - T)^{1/m} \quad (5)$$

with a and m empirical parameters, T_0 the lower development threshold, T_L the upper development threshold.

- the Logan rate function (Logan et al. 1976)

$$R[T] = \psi \left[\exp(\rho T) - \exp\left(\rho T_M - \frac{T_M - T}{\Delta T}\right) \right] \quad (6)$$

with ψ and ρ empirical parameters, T_M the maximum threshold and ΔT the distance between the maximum peak of the function and T_M .

- the Sharpe and De Michele rate function (Sharpe and DeMichele 1977):

$$R[T] = \frac{T \cdot \exp\left(A - \frac{B}{T}\right)}{1 + \exp\left(C - \frac{D}{T}\right) + \exp\left(E - \frac{F}{T}\right)} \quad (7)$$

in which A, B, C, D, E, F are parameters related to the enzyme's kinetics.

Other than the linear rate function (4), the other functions all have more than two parameters to estimate through the non-linear fit model method. The proposed macro named *fitasso*, makes this operation simpler. The idea is that the experimenter inserts his/her life tables and executes the non-linear fitting operations using the preferred development rate function between the listed above. To determine which is the best expression related to the experimental data, it is necessary to cross check between the R^2 and χ^2 -values, and their calculation is therefore an obliged request for the related macro. The second phase concerns the simulation, and using Manetsch's model estimates all parameters and other inputs discussed afterwards that forecast the insects' life cycle (2). The first problem encountered is related to the lack of an analytical function that exactly describes the daily average temperature trend. Simulations can usually be used while inserting theoretical or measured temperature data, but an analytical function would not describe both cases. Theoretical values generate on the basis of historical data or meteorological models as a series of pairs of points $[t, T(t)]$. In the context of applications in the field of entomology, measuring this data through the use of a meteorological station or a datalogger placed in required in a specific point of interest for the simulation if one is to predict the populations of the insect pests to be controlled. Furthermore, to perform the simulations, it is possible to insert forecasted temperatures for the following in according with a weather forecasting system. All this implies it is impossible to solve the system (2) in an analytical form (because of the varying daily temperature) – a numerical solution is needed. The developed simulator uses the finite difference method to obtain a discrete form of the DDM (Severini et al. 2005). One of the inputs needed for the simulation, is the mean

development time value for the specific daily average temperature measured. Performing this operation requires a macro with the task to input all the estimated parameters related to the development rate function, the daily temperature, as well as to provide the corresponding development rate as output. Moreover, to complete the operation, it is necessary to convert this result in development time, $D[T]$, using the expression (1). A dedicated macro to work out this process has been developed: *functioncalculator*. The need to have a fast screening to determine the average development time on the basis of recent temperatures drives the decision to exclude this result from the simulator. In this way the simulation software has only one input that encloses all the results of the laboratory and acquisition data phase. At this point, the simulation process involves only the numerical solutions for the system (2). Typical research concerning the use of a modelling approach to forecast insects' life cycle ends with a validation process. It is necessary to compare the series of simulated curves provided by the simulator with field data, monitoring the results. Determining the individuation of which is the most faithful simulated curve to the experimental data is difficult, and manual realization takes a long time. To optimize time and resources, this study developed a conclusive macro. In the results section, we show the details of each developed macro.

3. Results

More macros that are organized by the experimental guidelines articulate the “DSimulator” (Delay Simulator). The logical succession represents every step followed by an entomologist while estimating parameters, simulations and validations with field data. One of the advantages of using ROOT's libraries is to develop every macro independently with respect to one another. Each can be launched and used independently through ROOT's command line. In addition, this study developed a main interface that collects all of these tools to permit multiple actions when all data are available.

Even if ROOT is not difficult to use, a little knowledge is required with regards to ROOT's basic commands, such as “.x DSimulator.c” to load and run macros. A peculiarity of this software is its speed in reaching results: every output and input file becomes available to all tools that need such information. Users can report their data in specific .txt files, then at the end of every process, they can find results in a clear way printed in .txt output files, in ROOT's shell, and in a “canvas” with charts. To better understand the capabilities of this structure, we show every single macro in detail:

- *graph2Dpunti*: this is the first and the simplest macro built, and it is very close to ROOT's basic functions. This is a solution to a typical need during experimental trials: creating charts with acquired points and corresponding error bars. The user can report data in a file named “graph.txt,” dividing them into four ordered columns which represent x-axis, y-axis, x-values errors and y-values errors. Launching this tool also creates a “canvas” containing the corresponding chart. Some ROOT's operations are available through the toolbar, such as linear, gauss, polynomial and exponential fitting. One can change the plotted points and adjust them by selecting different styles. There is finally a possibility to export the graph as a .pdf file.
- *fitlang*: after a cohort of insects ended its lifecycle in climatic cells, it is possible to estimate the corresponding developmental time. The easiest thing to do is to calculate the average value and its corresponding standard deviation. A procedure like this is often justified because big data is relatively unavailable, and the point's shape seems to be a normal distribution. Nevertheless, many publications (Bellagamba et al. 1987; Di Cola and Gilioli 1996; Severini et al. 1990; Wermelinger et al. 1991) have shown that the Erlang PDF-function (3) is more appropriate for describing the exit times of an insect population whose individuals all started their lifecycle in the

same day. The approach considered introduces greater precision in experimental results but complicates the calculation operations. With ROOT it is possible to build a macro in which scientists can input a .txt file called “erl.txt” containing four columns ordered as described above for the “*graph2Dpunti*” tool: time-values, number of individuals, and their corresponding errors. It is complicated to give an estimation of the error for the number of individuals, so it is common to consider only time as a variable, which varies with respect to the sampling rate. After macro's launch, there is a possibility to choose between a no mortality Erlang function (Manetsch 1976) and a mortality Erlang function (Vansickle 1977a, 1977b). The main difference is that the first is like (3), with three parameters to estimate, whereas the second has a similar shape but contains another parameter, AR, which represents the mortality coefficient meant as an attrition:

$$f(t) = N \cdot \left(\frac{h}{D}\right)^h \frac{t^{h-1}}{(h-1)!} e^{-\left(AR + \frac{h}{D}\right)t} \quad (8)$$

Given “erl.txt” in input, “*fiterlang*” tool returns a .txt file named “Erl_fitris.txt” containing the initial values chosen to start the fitting process, the best fit parameters value with their corresponding errors, the χ^2 -value, the adjusted R^2 -value, and the number of degrees of freedom. The correlation matrix is shown only on ROOT's console. Another output is a canvas containing a double chart, with the possibility to export it: only the experimental points are plotted on the left, and the right represents the fit results (points, best fit function and a resume of the values).

- *fitasso*: it operates in the same way as “*fiterlang*” described above. There are many input files based on the type of function with which users want to operate: “LSDM.txt” is specific for Logan and Sharpe - De Michele development rate-function, while “briere.txt” and “tas-solin.txt” are dedicated respectively to Brière and linear development rate-functions. When macro is loaded, it is possible to choose which kind of fit is necessary, thereby obtaining results in .txt files (“LSDM_fitris.txt”, “fitlin_ris.txt”, “Logan_fitris.txt”). This indicates the initial values for the fitting process, the best fit parameters with their errors and, lastly, χ^2 -value, adjusted R^2 -value, and the number of degrees of freedom (Fig. 1).

Additional helpful information includes the coordinate ($T_{max}, R[T]_{max}$) related to the maximum of each function discussed. Information such as this is important because it indicates the optimal temperature for a species' development. In addition, the associated errors are reported.

Two charts containing a canvas provides a graphical view (Fig. 2), available in the same way as through the “*fiterlang*” tool.

- *fitlineare*: linear regression is one of the most common operations when working with data. Even if ROOT has a specific tool for linear fitting, and even we also added a function of this type in the last macro, we deem it appropriate to include a tool on the logic line of the others. In a .txt file named “fitlin.txt”, it is possible to insert the x-values, y-values, and their respective errors into four columns. The outputs are a canvas with two charts and a .txt file, “lin_fitris.txt”, with the same list mentioned in “*fitasso*”.
- *functioncalculator*: a development rate-function is needed for a simulation, because when recording the daily temperature, it is possible to know the daily development-rate (or the daily mean development-time). The task of this tool as follows: it takes for its input the daily average-temperature and evaluates the rate function of these points. The input file is called “dailytemp.txt,” and it is composed of two columns. The first accounts for days, and the second reports the corresponding average temperature. After launch, the user can choose which kind of development rate-function to use

before inserting the corresponding best-fit parameters (evaluated with “*fitasso*” macro). A final question is whether the user wants only to calculate rates and average times, or to also visualize the results in a chart (Fig. 3). Results can be found in two .txt files, “DailyRate.txt” and “MeanDevelopTime.txt”. A specific control in the code eliminates temperatures greater or less than the development thresholds for the analysed species so as to reduce distortions in simulation due to abnormal values.

- *Simulatore 1.0*: one of the needs introduced is to solve the system (2) numerically, and now, with previous tools, we have all the input files we need. The time-scale is daily, and it corresponds to each step in Euler's method (Pesolillo et al. 2004). All the equations are located in columns, then incremented row by row. A configuration of this type means that every row corresponds to the daily value for each h-th equation. There are different input files that merit discussion here: the first is the “cohort.txt” file, which reports the initial population if the information is available. If such information is not available, there is a “standard” file that concentrates a cohort on the day zero, meaning that the other days have 0 (zero) values. A configuration of this type causes results to be read as probability densities values. The peaks will therefore represent the most probable developmental period. The second input is “MeanDevelopTime.txt”, the output from “*functioncalculator*”, which provides the corresponding daily-value of the mean development time, $D[T(t)]$, shown in the system (2). Because of how “*functioncalculator*” is built, there are many “MeanDevelopTime.txt” files that are ordered in different folders. When the user loads “*simulatore*”, the program asks them which kind of developmental rate-function is preferable, thereby ensuring the right one is used. Outputs in this case are different. A folder stores a series of .txt files called “h = number.txt” in which “number” is indicated by the corresponding equation's number. Each file is composed of two columns, one relative to the number of days, and the other to the corresponding Erlang's value, calculated numerically. Before the end of the process, it is possible to choose which files to represent in a canvas composed of four charts (hence must be chosen four h-values), and then which files to represent in a single chart (Fig. 4).

The guideline to have numerical and graphical results is maintained here. In addition, between the outputs there is a last file named “simulergang.txt” in which all the single h-files are gathered into columns.

Before the calibration, it is difficult to understand which is the most correct file, but afterward the user has the “best h-value” available.

- *calibratore*: in the previous section we indicated there is a need to know which h-value corresponds to reality. The Euler's method application to Manetsch's equations has the inconvenience of needing to solve all equations because it lacks a formula that relates the experimental h-value with the h-th system equation. To resolve this problem, there is “*calibratore*”, which takes as its input “obserlang.txt”, a file containing field validation data organized in two columns: days and the number of individuals. The sum of the standard deviation between each point and the nearest h-value is printed on the ROOT's console serve to compare every h-file resulting from “*simulatore*”. That value is the one to read in every future simulation.
- *DS terminal interface*: a primary interface collects and presents all macros described above. The user can choose what they intend to use by typing the corresponding letter. In that way, it is possible to save more time between operations.

4. Discussion and conclusions

In the context of entomological modelling, several studies have discussed building software using one of the existing programming

Briere FIT FUNCTION: fit a Briere function of the type $R[T] = [a]*T*(T-[T_0])*pow((T_L-T), (1/[m]))$

Initial value setted for a = 1.0e-03
 Initial value setted for T_0 = 1.2e+01
 Initial value setted for T_L = 3.4e+01
 Initial value setted for m = 3.0e+00

FIT RESULTS:

```
*****
a =      8.2469e-05  +/-  7.8687e-06
T_0 =    5.6576e+00  +/-  2.3766e+00
T_L =    3.3390e+01  +/-  8.9511e-01
m =      4.9002e+00  +/-  1.9167e+00

ChiSquared = 8.790
Coefficient of determination (R^2) = 0.985
Adjusted coefficient of determination (R^2_adj) = 0.955
Degrees of freedom = 3
```

Optimal temperature:

T_opt = 31.659366 +/- 1.436632

Optimal rate value R[T_opt]:

R[T_opt] = 0.997120 +/- 0.014256

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Fig. 1. Example of non-linear fit using “fittasso” macro. This is a screenshot from the .txt file in output, corresponding to the graph in Fig. 2. Data for the calculation are from Toapanta et al. (Toapanta et al. 2005).

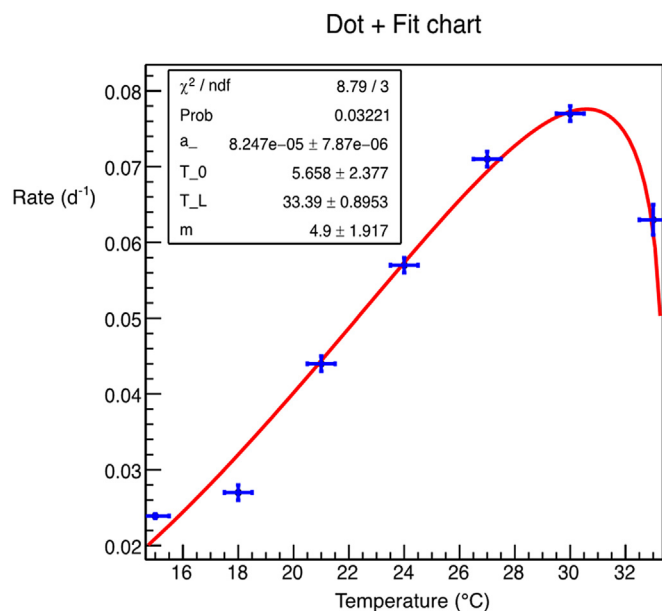


Fig. 2. Example of non-linear fit using “fittasso” macro, which is the most important of the two charts. This is a Briere fit function with data for the calculation from Toapanta et al. (Toapanta et al. 2005). The results are provided in graphical mode.

languages, as well as which among the languages is most adaptable. The operation presented in this article, if entrusted to a software company, can absorb many economic resources (i.e. to pay developers or software licenses (Jorgensen and Shepperd 2007)). Furthermore, a common problem is that there are communication difficulties between users and software developers – typically belonging to different scientific fields. Misunderstandings are often responsible for time delays due to software adjustments (Grudin 1991; Von Hippel 2001). The economic aspects, together with the possible but not immediate availability of the professional roles required, penalizes small scientific groups, above all in developing countries (Câmara and Fonseca 2007). With this work, we present an application in the field of entomology of an existing and powerful open-source software that does not require a deep knowledge of programming language. This current development is only an early version, and future developments are likely to include several additional functions, such as mortality and fecundity rates, as well as an estimation of the errors beginning from the firsts steps until the simulation. It is important to indicate that this study has not considered two aspects: the mortality and fecundity rate. However, these represent a simple modification to add in future works without making major changes in what we have illustrated. An additional modification would be integration with other common models used in population dynamics, such as the Von Foerster equation (Von Foerster 1959) and other models based on Markov chains (Bellagamba et al. 1987; Liénard et al. 2015; Strigul et al. 2012). The user in this way could have a broader choice so as to align with their needs. An improvement of this kind would be an extension of software usefulness in ecology. Last but

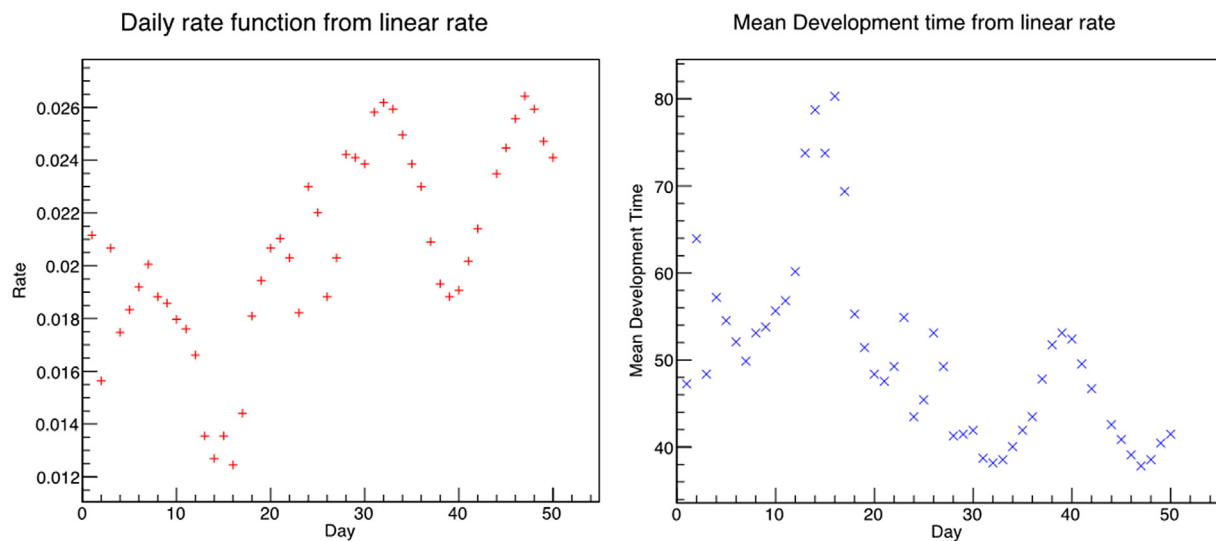


Fig. 3. Daily rate function (left) and daily mean development time (right) from linear rate function, worked out with “*functioncalculator*” macro. A linear rate function has been calculated with data from Toapanta et al. (Toapanta et al. 2005). The rate is relative to the daily temperature registered during a period of 50 days, the information for which a meteorological station provides.

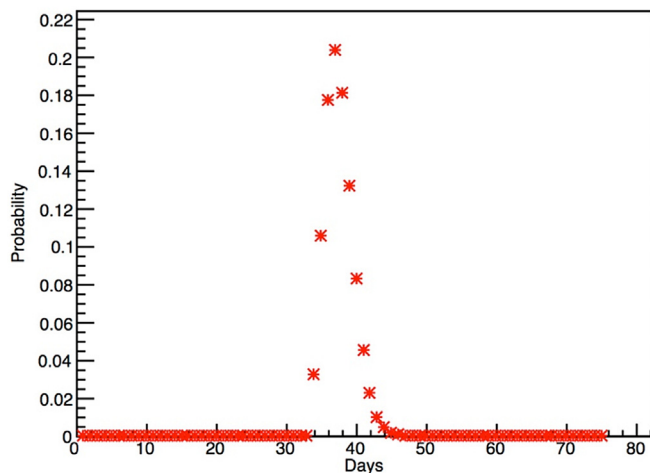


Fig. 4. A simulation output from the “*simulatore*” macro. Data relate to the lifecycle of *Anthonomus eugenii* at constant temperature (24 °C), with a Brière rate function in input. Data for the Brière's rate function parameter estimation are from Toapanta et al. (Toapanta et al. 2005) (Fig. 1).

not least is the will to transform the “*DS terminal interface*” into a graphic one that is simple to use and that can allow management of more operations. ROOT represents a good basis for our aims. It poses wide documentation and a large community of users, and it covers all the most common mathematical operations through its various functions (Brun and Rademakers 2007). The importance of modelling approaches in Integrated Pest Management has been increasing. A good forecast is important as a Decision Support System to show to Agronomists and Technicians which is the better moment for chemical treatments, and for the launch of natural enemies in the case of biological control. Furthermore, Gutierrez and colleagues, in their recent works (Gutierrez et al. 2017, 2012, 2009) illustrated that modelling in agriculture is important also for projections of the risks in the case of an increase of temperatures due to climate change (Estay et al. 2014). This aspect has great importance in the twenty-first century; in plant protection it enforces the role of simulations, but it is also important in relation to the problem of invasive species. Such alien species establishing and spreading are the consequences of increased human mobility and global trade (Hulme 2009), and this problem's prevalence is evidence of the

far-reaching effects of global warming (Robinet et al. 2012; Walther et al. 2009) that has exponentially sped up (Hill et al. 2016; Roques et al. 2016). The introduction of invasive species represents a threat for composition and processes of ecosystems, causing a decrease of native species abundance and richness (Mooney and Cleland 2001). This also leads to an increase of costs associated with their management and damage (Pimentel 2011). Simulations are of crucial interest to provide a quick response to scientists, farmers and technicians to plan an eradication or control strategy of the non-indigenous species. This study uses applications of the described ROOT's libraries in the case of two alien species to Italy (*A. eugenii* and *T. absoluta*), and they will be the object of further publications.

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