

ILCYM – Insect Life Cycle Modeling 4.0



A software package for developing temperature-based insect phenology models with applications to regional and global analysis of insect population and mapping

Marc Sporleder

Pablo Carhuapoma

Henry S. Juarez

Heidy Gamarra

Reinhard Simon

Jürgen Kroschel

**Agroecology/IPM
Integrated Crop
Management Division**

Insect Life Cycle Modeling (ILCYM, Version 4.0): A software package for developing temperature-based insect phenology models with applications for local, regional and global analysis of insect population and mapping

ILCYM Version 4.0

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International Potato Center, 2017
La Molina Ave. 1895, La Molina
Apartado 1558, Lima 12, Perú
cip@cgiar.org • www.cipotato.org

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Preface to the new edition

Preface to the previous editions

The International Potato Center (CIP) seeks to reduce poverty and achieve food security on a sustained basis in developing countries through scientific research and related activities on potato (*Solanum tuberosum* L.), sweetpotato (*Ipomoea batatas* L. Poir.) and other root and tuber crops, and on the improved management of natural resources in the Andes and other mountain areas. The origin of the potato is the High Andes in South America. Its global distribution began about three hundred years ago, first to Europe and then to other parts of the world. Many potato pests have evolved in the center of origin of the potato. Andean potato weevils of the genus *Premnotrypes* (Coleoptera: Curculionidae) are major problems for potato growers in the Andean region from Venezuela to Bolivia but have fortunately not spread to other potato growing regions outside the Andes. Instead, the potato tuber moth (*Phthorimaea operculella* (Zeller) [Lepidoptera: Gelechiidae]) or the leafminer fly (*Liriomyza huidobrensis* (Blanchard) [Diptera: Agromyzidae]) have become invasive in many tropical, subtropical or temperate regions. The potato tuber moth is today reported in more than 90 countries and is considered the most damaging potato pest in the developing world. The leafminer fly, which is highly polyphagous, is reported in 66 countries.

In its global pest management research effort CIP's Agroecology/IPM team is interested in better understanding pest biology and ecology in order to find out why some species are more invasive than others. We also aim to predict the potential pest population development in different agroecological zones as well as to determine critical infestation periods for better targeting pests during the cropping season. Phenology models for potato pests based on temperature have become important analytical tools in CIP's research program for predicting, evaluating and understanding their population dynamics in agroecosystems under a variety of environmental conditions. At the beginning a temperature-driven phenology model for the potato tuber moth was developed and validated through field and laboratory data which, successfully predicted life-table parameters for different agroecological zones. It was then used to predict the establishment risk and potential pest activity in specific agroecologies according to temperature records. It has also been used to estimate the population structure under given temperatures and allows for performance simulations of field applications and to determine field application rates and frequencies. Further possible applications of these models are manifold.

The approach used to develop and implement the potato tuber moth model can be principally used for other insect species. The strong collaboration between CIP's Agroecology/IPM team and the Research Informatics Unit made it possible to develop the software program Insect Life Cycle Modeling (ILCYM version 4.0) with the objective of facilitating the development of further insect phenology models and to provide

analytical tools for studying insects' population ecology. It is hoped that the ILCYM software will benefit researchers from national and international agricultural research institutes and universities who either intend to start with insect modeling or want to apply advanced modeling techniques without having the requisite mathematical knowledge or being experts in the field. Ultimately, the application of ILCYM software and modeling results should provide a better understanding of insect's biology and ecology and in the long-term should support a rational decision making process in pest management and improving farmers' food security and daily lives.

Dr. Jürgen Kroschel
Head Agroecology/IPM
International Potato Center
Lima, Peru

Acknowledgment

The Insect Life Cycle Modeling software described here has been jointly developed by staff members of the Integrated Crop Management Division (ICM Division) and the Research Informatics Unit (RIU) of the International Potato Center (CIP).

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I. INTRODUCTION

Interest in models to predict the environmental suitability for invasive insect pest species has grown radically in the last two decades. In particular, the need to understand the impact of climate change on the potential distribution of pests has accelerated the demand for tools to estimate the potential risk of their invading new environments and agricultural regions. For this purpose, maps are becoming important means of communication using different spatial scales, from local, regional to worldwide to visualize the potential risk of pest distribution and the economic damage it may inflict on crops. Thus, maps are used to inform policy and management in this field to aid in strategic pest management decisions, such as restrictions on the importation of certain crops in international trade, implementation of quarantine measures, the design of pest surveys, etc. (Baker, 1996; Baker *et al.*, 2000; Braasch *et al.*, 1996; McKenney *et al.*, 2003).

Two distinct approaches prevalent in the modelling of insect pests and the risk of establishment and expansion; these can be described as a) “inductive” and b) “deductive”. The “inductive” approach combines through statistical or machine learning methods the known occurrence records of insect species with digital layers of environmental variables. It uses minimal data sets and simple functions to describe the species’ response to temperature and other climatic factors. Generally, presence/absence data or occurrence data only from different locations are sufficient for creating risk maps. The combination of occurrence records and environmental variables can be performed through the application of climate match functions that seek out the establishment potential of an invasive species to new areas by comparing the long-term meteorological data for each selected location where the species is absent with the same data for the location of origin or locations where the species prevails (Sutherst *et al.*, 2000; Sutherst and Maywald, 1991). For applying this approach, computer-aided tools such as CLIMEX (Peacock and Worner, 2006; Vanhanen *et al.*, 2008a; Vanhanen *et al.*, 2008b; Wilmot Senaratne *et al.*, 2006) and BIOCLIM (Kohlmann *et al.*, 1988; Steinbauer *et al.*, 2002) have been developed and used to predict insect species’ demography for pest risk analysis (Rafoss, 2003; Sutherst, 1991; Zalucki and

Furlong, 2005) and possible climate change effects (Sutherst and Maywald, 1990).

The “inductive” modelling approach has made considerable advances and a great number of computer programs, including BioMOD, GARP, HABITAT, etc., have been developed (reviewed by Venette *et al.*, 2010). This modelling approach showed advantages where detailed information about insect species is not available; however, critical limitations are the failure to consider the species’ biological characteristics in the modelling framework (Venette *et al.*, 2010). Hence, resulting risk maps may inform about potential establishment, but they do not provide information on the species population growth and damage potential or temporal population change within a cropping season or year in a given region. By contrast, the “deductive” approach uses a process-based climatic response model (i.e., phenology model) for a particular insect species of interest. Phenology models are analytical tools for the evaluation, understanding and prediction of the dynamics of insect populations in ecosystems under a variety of environmental conditions and management practices, and more recently they are also being used in phytosanitary risk assessments (Baker, 1991; Jarvis and Baker, 2001a,b). The development of insects, as in other ectothermic organisms, depends on the ambient temperature. This temperature dependency can be applied in a process-oriented framework; forecasting the potential distribution of insect species is completely independent of observed occurrences, and this approach is therefore referred to as “deductive”.

Degree-day models are often used to describe the linear development of insects using the accumulation of temperature above the minimum temperature threshold (Allen, 1976); see Nietschke *et al.* (2007). However, due to the non-linearity of the development curve, especially when temperature deviates from the intrinsic optimal temperature of a species, degree-day models are poor predictors of insect development. This method works well for intermediate temperatures, but produces errors, i.e. significant deviations from the real development, when daily temperature fluctuates to extremes (Stinner *et al.*, 1974; Worner, 1992). Modern, more progressive models use non-linear functions of

higher biological significance (i.e. Logan *et al.*, 1976; Sharpe and DeMichele, 1977, etc.), and include stochastic functions for variability in development times among individuals within a population (Sharpe *et al.*, 1981; Wagner *et al.*, 1984).

Computer-aided modelling packages such as DYMEX (Kriticos *et al.*, 2003), NAPPFAST (Nietschke *et al.*, 2008), ECAMON (Trnka *et al.*, 2007) or ILCYM (Sporleder *et al.*, 2007; Sporleder *et al.*, 2009) support the development of process-oriented temperature-driven and age-stage structured insect phenology/population models. The latter, ILCYM (Insect Life Cycle Modeling software, version 3.0), has recently been developed by the International Potato Center (CIP), Lima, Peru and is freely available at <http://www.cipotato.org/ilcym/>.

Insect Life Cycle Modeling (ILCYM) software has been developed to support the development of process-oriented temperature-driven and age-stage structured insect phenology/population models by the International Potato Center (CIP), Lima, Peru. Improving the software is an ongoing process. Now version 4 is available that can be freely downloaded from the web at <http://www.cipotato.org/ilcym/>.

This book describes the application of ILCYM software, which supports the development of process-oriented temperature-driven and age-stage structured insect phenology/population models. ILCYM interactively leads the user through the steps for developing insect phenology models, for conducting simulations, and for producing potential population distribution and risk mapping under current or future temperature (climate change) scenarios. The objective of the present document is to explain how the developed modeling approach works; what type of data need to be generated to develop an insect phenology model, what type of data need to be generated to validate a, how are implemented, and what type of insect population analysis will be provided. With the current version of ILCYM the authors intend to share the knowledge gained in insect pest population modeling research at the Agroecology/IPM unit at CIP and provide an open-source computer aided tool, especially for researcher in developing countries,

that facilitates the development of own using advanced modeling techniques without being experts in the field.

1.1 The modeling approach applied in ILCYM

Modeling of insect populations is for some reasons more complicate than modeling populations of other organisms. Insects pass through different stage before reaching maturity, within these immature stages they may die, and when mature they reproduce. Some species have seasonality (that means different life-stages of the insects are only found during specific seasons of the year), while others reproduce continuously throughout the year. Populations of the latter are heterogeneous in their age-stage structure with overlapping generations. Even so, the development of insects is always strongly determined by temperature. The approach used in ILCYM is to define temperature-dependent sub-models describing development and mortality in each immature life-stage, adult senescence and reproduction of the species, as well as distribution functions that describe variation in these parameters among the individuals in a population. These sub-models are based on experimental data obtained through temperature experiments. The reproduction model might include functions for different processes depending on the insect species under study, that is, for example, due to changing sex ratio in adults with changing temperature, age-dependent reproduction frequencies, temperature-dependent reproduction frequencies, etc. The overall approach is factor-process based, while temperature is the principle driver (factor) of these processes.

Nevertheless, insects species that show seasonality generally have an overwintering stage in which the insect hibernates or diapauses. The factors which are responsible to reactivate hibernating insects are often not temperature alone. Temperature might be an indirect factor in breaking hibernation but for modeling considering temperature alone might not explain this process in its totality. Therefore, ILCYM's approach is more adequate for insect species that do not hibernate and hence do not show seasonality in its development. However, many components of ILCYM might be used for such species as well.

ILCYM's compiles the established function into a general (generic) phenology model that uses rate summation and a cohort up-dating approach for simulating populations. The cohort up-dating algorithm is based on scheme proposed by Curry *et al.* (1978a) that was further described by Wagner *et al.* (1985) and Logan (1988). In published articles, there is not so much discussion on including temperature-induced mortality in immature life stages and recruitment. Both are necessary for more realistic simulation and both are included in ILCYM. Development, reproduction, and survival in insect species describe primarily insect demography; however, for understanding population dynamics additional knowledge about dispersal and migration, as well as the influence of other biotic or abiotic factors affecting the insects' survival are necessary. The cohort up-dating algorithm calculates population number (size); Thus it also provides information about the quantitative biology of the insect species under study. Let us note that the resulting simulated population increase only represents the potential population growth of the species at a given temperature regime. Real population increase might be limited due to additional biotic and abiotic factors that affect populations in a given environment. Including such factors in the simulation would introduce much more complexity into the algorithm, which is not provided in this version of ILCYM. However, when a temperature-driven model for a given species is developed it can directly be applied in ILCYM-GIS environment for spatial analysis; based on real or simulated/interpolated daily temperature data, ILCYM's simulates the potential population increase over time and calculates risk indices that are used to visualize the pest distribution potential in maps. If host plant/land covers data are available these shape files can be used as filters for the simulation or for analyzing potential climate change impacts on the crop due to alterations in pest abundance.

The steps of developing a model with ILCYM are principally four:

- 1) Collect the data through conducting temperature experiments or, if available, from the literature.
- 2) Define the functions describing the temperature-driven processes in insect development using ILCYM's "Model builder"; when all submodels

required to describe the species life cycle are determined, the final overall life cycle model will be compiled automatically.

- 3) Validate the model using additional data that were not included for developing the model (generally this data is from experiments conducted under fluctuating temperatures).
- 4) Use the life cycle model with ILCYM:s “Simulation modules”.

Before and during the development of IPhM, be aware of the following steps and questions:

- 1) What is the species you are interested in (think first: is the ILCYM approach the right one? How you want to use the model? Modeling is not the purpose itself, there should be another aim why you want to have a model (the purpose might be to learn about the insect biology alone. In any case, researchers who start with the experiments described here will learn something about the species population biology. The knowledge gained can be applied latter for many different purposes).
- 2) Collect literature on the species for which you want to make a model; what has been done so far? Are literature data available that can be used for modeling or model validation?
- 3) Define hypothesis! Finally, you are working on a piece of science, and science requires hypothesis.
- 4) Design and plan your experiment: what do you need (insect rearing facilities, incubators, thermometers or loggers, what are the temperatures you want to test, plan for precision, etc.)? Use dummy data: you may use the dummy data provided in ILCYM to get familiar with the analysis and learn about the approach. You might also create own dummy data with different numbers of temperatures and with different numbers of insects in the experiment for learning about the statistical precision of your planed experiment. Decide about the type of data you want to collect (see chapter on data collection: life-table data versus cohort studies or mixed – advantages and disadvantages, for your purposes you should know before designing the experiment), and finally adaptation to interval format.

- 5) Collect the data. Bear in mind that the data collection might take a long time. At cold temperatures development times of test individuals might be quite long; the whole life cycle might last more than one year. In such conditions the cohort approach for collecting the data might be better than establishing a life table where a whole life-cycle of one generation need to be monitored. As a role, developing a model should not take longer than one year.
- 6) Use the “model builder” of ILCYM defining all sub-models for the overall phenology model: at this stage you might start writing a report on results obtained. (What to report?)
- 7) Once all sub-models are selected, they are compiled to obtain the overall phenology model (ILCYM compiles the overall model automatically according to your initial (interactive) statements you have made when starting a new project). It is recommended that users have some level of familiarity with the structure of the overall phenology model and the modeling approach of ILCYM before starting serious analysis with the software.
- 8) Conduct sensitivity analysis and validate the model through comparing simulation results with the data from fluctuating temperature experiments or data published in the literature (ILCYM provides tools for that). At this stage you might finalize the report about your model developed.
- 9) Employ the model for your purposes. You might apply the new model for “pest risk mapping”, which is the third module of ILCYM (i.e. generate maps that indicate the potential population growth of the species you are studying within a given region of interest.

1.2 The conceptual basis of ILCYM

Phenology models predict time of events in an organism's development. Development of many organisms that cannot internally regulate their own temperature (poikilothermic organisms, ectothermic organisms) is dependent on temperatures to which they are exposed in the environment. Plants and invertebrates, including insects and nematodes, require a certain amount of heat

to develop from one point in their life-cycle to another, e.g., from eggs to larvae. Because of yearly variations in weather, calendar dates are not a good basis for making management decisions. Measuring the amount of heat accumulated over time provides a physiological time scale that is biologically more accurate than calendar days.

Phenology models for insect species based on temperature are important analytical tools for predicting, evaluating, and understanding the dynamics of populations in ecosystems under a variety of environmental conditions. The International Potato center (CIP) initially developed a temperature-driven phenology model for the potato tuber moth, *Phthorimaea operculella* Zeller (Lepidoptera: Gelechiidae), which well predicted the life-table parameters in different agro-ecological zones. This model was validated through field and laboratory data. It was used to predict the establishment risk and potential pest activity in specific agro-ecologies according to temperature records. Linked with geographic information systems (GIS) and atmospheric temperature the model allowed simulation of three risk indices on a worldwide scale and was also used to predict potential future changes in these indices that may be caused by global warming.

The success of the approach used on developing and implementing the *P. operculella* model stimulated the extension to other insect species. CIP therefore, developed the Insect Life Cycle Software (ILCYM) version 4.0 presented in this manual. The main goal of the software is to facilitate the development of insect phenology models and provide analytical tools for studying insect population ecology.

The authors are aware that a single modeling approach does not fit to every insect species of interest and that it cannot meet every purpose for which a model needs to be developed. However, it is believing that the approach presented here might be a model applicable to many insect species and in many circumstances for which insect phenology models are developed. An important issue in integrated pest management (IPM) research is to evaluate the potential effects of certain pest management strategies. Parasitoid life tables can be analyzed in

the ILCYM “Modeling” and parasitoid phenology models obtained, then applied in ILCYM-GIS “Simulation” component to identify regions in which the parasitoid can potentially establish and control its host (an insect pest). This is an important analysis for planning classical biological control and identifying potential parasitoid release sites. For the development of a two-species interaction model, a parasitism rate function is used for linking the parasitoid and the host (pest) phenology models through a deterministic simulation procedure under constant and varying temperature conditions. This process uses the predicted temperature-dependent development times and parasitoid fertility rates for simulations of the host population growth and development.

1.3 Data

ILCYM analyzes data of different types. The question in modeling the effects of temperature on insect population development is not so much a question of “what data should be collected”, but rather “how these data should be used”. Therefore, ILCYM allows the use of a type of experimental data as input information for developing a pest phenology model; however, the data should allow modeling of the species whole life cycle and should be arranged in a manner to meet certain criteria employed within the software. Data collection and its arrangement to be used as input data in ILCYM is the topic of this section.

1.4 Life table data

Studying insect population ecology is often based on life table studies. A life table is conducted by following a population of $n = x$ individuals from its birth up to the birth of all progeny of these individuals. Events like death or reproduction are monitored in equal time interval (hours, days, years, etc., depending on the organism under study). This methodology is used for populations of many organisms, including humans and other animal populations, to describe the life expectancy of individuals (life insurance companies use this to estimate the probability of death of a person of certain age) and their reproduction capacity. Specific statistics were developed to calculate “life table parameters”, describing the population growth according to the Malthusian law of population increase. Life table analysis is broadly employed in studying populations; however, since the life cycle is more complicated in insects (due to different

immature life stages) than in other animals several modifications were made in ILCYM software.

For constructing a life-table for an insect cohort (i.e. a group of individual of the same age), the experiment generally starts from "eggs" that were all laid within the same time period; p.e. within the last 12 or 24 hours. The number of eggs used should be at least $n \geq 100$ because during each life stage holds certain proportion of the insects that might die and the number of individuals entering each subsequent life stage will be hence reduced. Then the number of individuals observed might be insufficient for the last life stages or the number of females might be insufficient to assess well fecundity. It would be recommendable to have at least 30 surviving females in the experiment for assessment of fecundity. Especially, the number of insects used for constructing a life table at extreme high and low temperatures, where mortality is generally high, should be increased because of the expected increased mortality during immature life stages. The number of individual used for life tables at different temperatures need not to be balanced. Analysis of these data will include weights that account for differences in numbers of individuals that entered a certain life stage at a given temperature. Life tables can be repeated at the same temperatures with another batch of individuals (cohort) from the population. Also the number of life tables in each temperature does not need to be balanced. In the analysis data from the same temperature (replications) can be pooled or used separately when fitting models for describing temperature effects on insect development or fecundity; however, if the temperature for repeated life tables deviated by more than 1°C the data should not be pooled but submitted separately to the analysis.

1.4.1 Data records for “complete life tables”

Data for each life table can be arranged in an ordinary spreadsheet. The life stage of each individual of the cohort is traced in one column (i.e. number of columns = n). The state of each individual is noted in rows for each evaluation time (generally one day) until the last individual of the cohort has died. An example is given in Figure 1. For each individual surviving the development stage, which is in the example given “egg”, “larva”, or “pupa”, is recorded for each evaluation

time (indicated in the spreadsheet as “E” = egg, ”L” = larva, and “P” = pupa). The evaluation interval is generally one day; however, the evaluation time might be changed; for example 12 h, 8 h, etc.; however, the interval should be constant throughout the experiment and always the same in all life tables constructed at different constant temperatures that enter the analysis for developing the phenology model in ILCYM. The number of life stages to be evaluated depends on the species under study and needs to be chosen by the investigator. Letters for indicating each life stage can be freely chosen. Non-survivors are marked always as "dead". Emergence of male adults will be recorded as "M" while for living female adults the number of eggs laid per female during the evaluation interval is noted.

Excuse: Notes on the evaluation interval: Since at high temperatures the development is faster than at low temperatures it could be that the interval of one day might be too broad for determining well the variation in insect development to the next stage. In the example given (Figure 1) all eggs remained egg at the 4th evaluation and had developed into larvae at the 5th evaluation. Therefore, these data would not provide good information to assess the distribution curve for the development from eggs into larva. The median development time would be expected to be between 4 and 5 days but its real value and the slope of the distribution curve cannot be assessed. In this case it would be helpful to reduce the interval time to 8 or 12 hours for obtaining at least one data point in which the proportion of subjects developed into larvae is higher than 0% and lower than 100%. For lower temperatures, such a shallow evaluation interval probably would be not necessary because the development time increases significantly and the development time distribution curve could be well established even when a broader evaluation interval would have been used; for example of 2 days. The evaluation interval could be differently chosen specifically to each temperature evaluated; however, in the data spreadsheets used for developing IPhM in ILCYM the interval (rows) needs to be the same in all life tables (temperatures). Therefore, even if the interval used for one life table was for example 2 days and the interval used for the life table at the highest temperature was 12 hours all spreadsheets need to be filled using an 8-hour interval.

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	E	E	E	E	E	E	E	E	E	E	E	E
2	E	E	E	E	E	E	E	E	E	E	E	E
3	E	E	E	E	E	E	E	E	E	E	E	E
4	E	E	E	E	E	E	E	E	E	E	E	E
5	L	L	L	L	L	L	L	L	L	L	L	L
6	L	L	L	L	L	L	L	L	L	L	L	L
7	L	L	L	L	L	L	L	L	L	L	L	L
8	L	L	L	L	L	L	L	L	L	L	L	L
9	L	L	L	L	L	L	L	L	L	L	L	L
10	L	L	L	L	L	L	L	L	L	L	L	L
11	L	L	L	L	L	L	L	L	L	L	L	L
12	L	L	L	L	L	L	L	L	L	L	L	L
13	L	L	L	L	L	L	L	L	L	L	L	L
14	P	P	dead	P	P	P	P	L	L	L	L	L
15	P	P	dead	P	P	P	P	P	P	P	P	P
16	P	P	dead	P	P	P	P	P	P	P	P	P
17	P	P	dead	P	P	P	P	P	P	P	P	P
18	P	P	dead	P	P	P	P	P	P	P	P	P
19	P	M	dead	P	P	P	P	P	P	P	P	P
20	M	M	dead	18	13	M	14	P	P	P	P	dead
21	M	M	dead	25	17	M	18	4	5	M	M	dead
22	M	M	dead	21	13	M	17	22	20	M	M	dead
23	M	M	dead	11	4	M	4	13	20	M	M	dead
24	M	M	dead	6	6	M	6	10	12	M	M	dead
25	M	M	dead	3	2	M	3	6	6	M	M	dead
26	M	M	dead	2	1	M	2	4	4	M	M	dead
27	M	M	dead	1	2	M	1	1	1	M	M	dead
28	M	M	dead	1	1	M	1	1	1	M	M	dead
29	M	M	dead	dead	dead	M	dead	0	1	M	M	dead
30	M	dead	dead	dead	dead	dead	dead	dead	0	M	M	dead
31	dead	dead	dead	dead	dead	dead	dead	dead	dead	M	M	dead
32	dead	dead	dead	dead	dead	dead	dead	dead	dead	dead	dead	dead

Figure 1: Example for recording life table data in a spreadsheet. Each column represents an individual and its state (life stage) is recorded in a constant time interval (generally one day) until its death. Different development stages of the species are recorded by using stage-specific letters. Adult males are marked as “M” and for surviving females the number of eggs laid per evaluation interval is recorded. For further explanations see the text.

For subjects that remained in the same stage as in the 2-day earlier evaluation the state of subject is clear for the missing time intervals and can be filled; however, if a subject developed within this 2-day interval into the next stage then the state is unclear for the missing intervals. In that case missing values need to be filled. ILCYM will handle these data as “interval censored data” (i.e. development between interval “x” and interval “x-2 days”. For further information on this merit see section “data analysis”.

Transforming spreadsheet data into the format for analysis in ILCYM

ILCYM software only run data in text formats. Data organized in a spreadsheet need to transform in test format with the extension .txt (see. Figure). For easy identification of the data it is recommended to include the following identifiers in the document’s name: Species name, evaluated temperature (and optionally a number that indicates the replication at a given temperature), and the interval;

p.e. "Phthorimaea-operculella_28-1_1d"; that is, *Phthorimaea operculella* was the species used in this experiment, incubation temperature was constantly 28°C and it was the first life table constructed at this temperature, and the evaluation interval between rows in the document is one day.

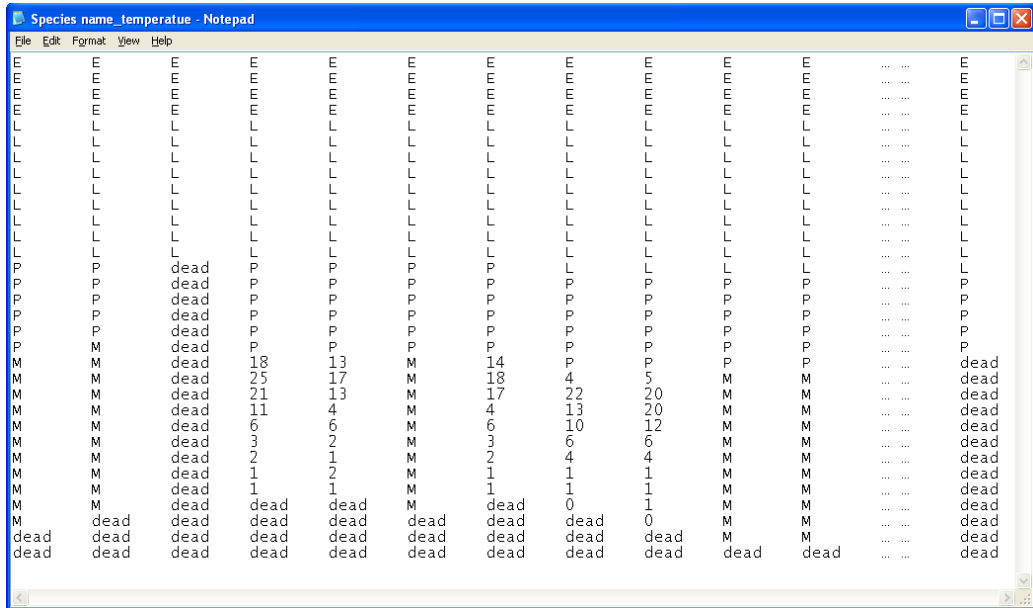


Figure 2: Life table data text file generated by saving the above spreadsheet as txt-file (tab-delimited) for use in ILCYM. The file name should indicate the species name studied and the temperature at which the life table was constructed.

If the female rate in the progeny is expected to be variable:

In case that the female rate in the progeny is not constant but possibly affected by temperature or female age all eggs need to be further reared in batches (the eggs from each individual female during one evaluation interval can be reared jointly) to adult stage and their sex determined. The data can be arranged as shown in Figure 3 for analysis in ILCYM.

A

Oviposition: Male - Notepad

14	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead
20	4																
20	5																
20	8																
20	11																
20	12																
20	0																
20	10																
20	0																
20	3																
20	7																
20	0																
25	5																
25	2																
25	4																
25	4																
25	3																
25	4																
25	5																
25	4																
25	3																
25	5																
25	4																
25	3																
28	5																
28	4																
28	3																
28	6																
28	7																
28	3																
28	2																
28	5																
28	4																
28	5																
30	7																
30	0																
30	0																
30	7																
30	0																
30	4																
30	0																

B

Oviposition: Female - Notepad

14	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead
20	6																
20	7																
20	2																
20	6																
20	0																
20	3																
20	11																
20	0																
20	1																
20	12																
20	4																
20	11																
20	4																
25	10																
25	4																
25	3																
25	9																
25	7																
25	4																
25	7																
25	8																
25	7																
25	9																
25	1																
28	2																
28	4																
28	2																
28	2																
28	3																
28	3																
28	3																
28	2																
28	2																
28	1																
28	2																
30	0																
30	3																
30	0																
30	1																
30	1																

Figure 3: Example for arranging the data in text file for differentiating between female and male individuals in the progeny; above (A): data for males reproduced, below (B): data for reproduced females. In both data files, the first column represents the temperature and the subsequent columns represent number of egg laid by the individual in a constant time interval (generally one day) until its death.

If only temperature is expected to affect the female rate in the progeny but not female age the eggs obtained from each temperature tested can be reared together (pooled) because then the effect of female age will not be analyzed; in

that case the female rate is considered to be constant throughout the life-span of female adult.

1.4.2 Data records for “incomplete life tables”

The life-tables would be incomplete if the cohorts’ history were followed-up until insects have reached the adult stage. Data recording would be the same as for “complete” life tables but only the event of male and female emergences would be indicated. After adult emergence the survival time of adults would not be further monitored and hence the columns can be indicated as “dead” in the subsequent cells of the row. Data for a single life table would look as shown in Figure 2. Reproduction would be assessed with other subjects in additional experiments at the same temperatures and adult survival time would be retrieved from these experiments.

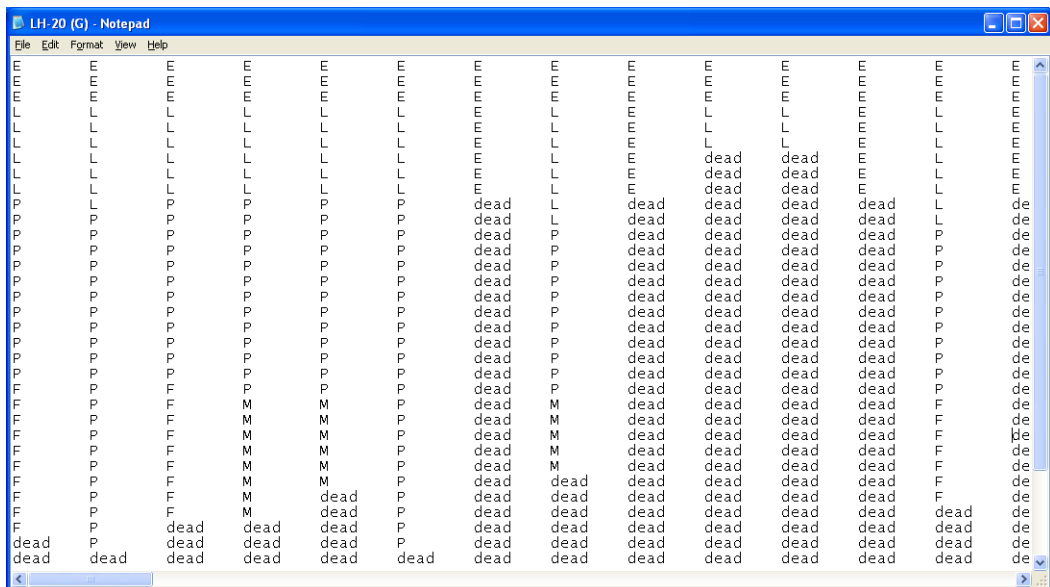


Figure 4 Example for recording “incomplete” life table data at constant temperature (20°C) in a text file. As for “complete” life table each column represents an individual and its state (life stage) is recorded in a constant time interval (generally one day) until its death or development into adult. Survival time of adults is not monitored further because adult survival time will be assessed in an additional experiment for determining adult survival time and oviposition; however, emergence of males (“M”) and females (“F”) is recorded.

The oviposition-file for each temperature would look as shown in Figure 3; either a single file if the female rate is constant over all temperatures or two files, one

for reproduced males and one for reproduced females, if the female rate is expected to be variable.

1.4.3 Cohort studies

In cohort studies, the structure of data for the analysis in ILCYM is different. Survival time and mortality is assessed in the same way as for “life tables” but for a single life stage only. Data are arranged by specific life stages; i.e. there is one data file for each life stage in the life history of the insect under study. For example, if the life history of the species comprises three immature life stages, i.e. egg, larva, and pupa, five files are required, that is one for “Egg”, one for “Larva”, one for “Pupa” stages, and one for “Female adults” and “Male adults” survival each. In addition, one or two oviposition-files are required depending if the female rate in the species is constantly the same across temperatures or if the female rate needs to be evaluated from the data (variable rate). The latter is when temperature affects the “female rate” or if the female rate is expected to change with female adult age. Data on oviposition need to be retrieved from the same cohort of adults (“female adults”) used to establish the overall model. Researcher can freely chose the number of life stages according to their choices or requirement; for example the larva-stage can be separated by specific larval instars (L₁, L₂ L₃, etc.), or a “prepupal” stage could be includes. Important is that the whole life cycle is covered and that there is no overlapping when assessing the development/survival time of individual life stages/instars. There should be a clear definition when each single life stage/instar is completed and the insects used to initiate a cohort study should be of this specific physiological age.

An example for arranging the data is given in Figure 5. The data file contains 4 columns of which the first column represents the temperature used (in the example a total of 7 temperatures were evaluated), second column indicates the evaluation time after experiment set-up (records should start from the evaluation before first development was observed) here measured as “days-after-experiment set-up”), third column indicates the number of insects used in each temperature, and the forth column indicates the number of individual that had developed to the next stage on each evaluation date. In “life table” studies the

evaluation interval needs to be always the same for calculating life table parameters. Such condition is not needed with “cohort study” however, missing evaluations should not be included in file (for example, if the cohort was evaluated after 3 days and again after 5 days, and in day 4 no evaluation was conducted, day 4 should not appear in the records).

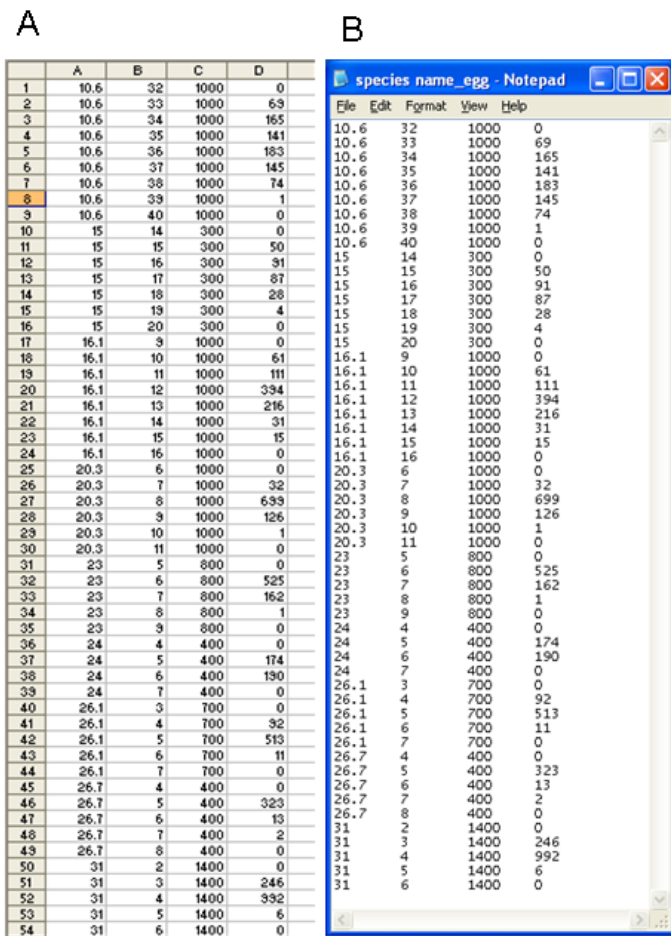


Figure 5: Example for recording “cohort study” data in a spreadsheet (A) and the same data saved as a txt-file (tab-delimited) (B) for use in ILCYM. The first column indicates the temperature evaluated (here a total of 7 temperatures were tested), second column indicates the evaluation intervals number (here measured as “days-after-experiment set-up”), third column indicates the number of insects used in each temperature, and the forth column indicates the number of individual that had developed to the next stage on each evaluation date. For further explication see the text.

ILCYM handle such data as “interval censored data” and retrieves the interval limits from the previous row (i.e. development between day “3” and day “5” after experiment set-up. The recording should be continued until the last individual of

the cohort developed to the next stage or died. ILCYM retrieves the mortality rate in each life stage for each temperature from the number of individuals used and the number of individuals that developed to the next stage (survivors). Evaluations that resulted in “zero” observations (change of stage) need to be included in the record; otherwise ILCYM would not determine well the time span in which the individuals developed to the next stage.

Data for adults (survival time of males and females) are recorded in the same manner. The difference is that adults do not develop into another stage but die. Hence the number of insects tested (column 3) should be equal to the sum of individuals that were recorded as dead over all evaluation for a single temperature. No additional mortality rate is calculated as for the immature life stages. The oviposition data are recorded as described above for “life table” data. The number of eggs oviposited should be retrieved for the cohort of females included in this experiment.

Data type dealing with only female population

ILCYM authors recommend two-sex life table to be used as input data to the software as described above. This is because most insect species (Lepidoptera, Coleoptera, Orthoptera, and Diptera) are bisexual having both males and females, and both sexes may cause economical loss or be vectors of disease. In addition, there is variation in developmental rate among individual and between sexes in natural population. However traditional way of collecting life table Lotka (1907) only deal with female population and ignore the raisons mentioned earlier.

For complete life table data arrangement are similar as explained above where life stage of each individual is traced in one column and the state of each individual is noted in rows for each evaluation time until the last individual of the group has died. The main difference here is the absence of male progeny.

For cohort study, the data arrangement is identical to the description provided above; only that male file is omitted. Below is an example file for complete life table at a given temperature.

Figure 6: Life table data file dealing with only female. The main difference here to Figure 3 is that all individual that evolved and became male are not accounted for, the file only shows immature life stage (“egg”, “larva”, or “pupa”, is recorded for each evaluation time.

1.4.4 Interval Type

ILCYM 4.0 interface only works with intervals type, however all types shown above could be adapted to interval type using R codes prepared to do this, otherwise contact us for support to p.carhuapoma@cgiar.org or ilcym.support@cgiar.org.

Those type of records are used extensively to examine the temperature effects on event times in censored data applying models about accelerated failure time (AFT). The columns description:

- **Column 1:** Batch or replication for the same constant temperature.

- **Column 2:** Constant temperature defined.
- **Column 3:** Day whenever start the event (according the Interval of the days that insect has developed or oviposited).
- **Column 4:** Day whenever end the event defined above.
- **Column 5:** The sample size according the temperature.

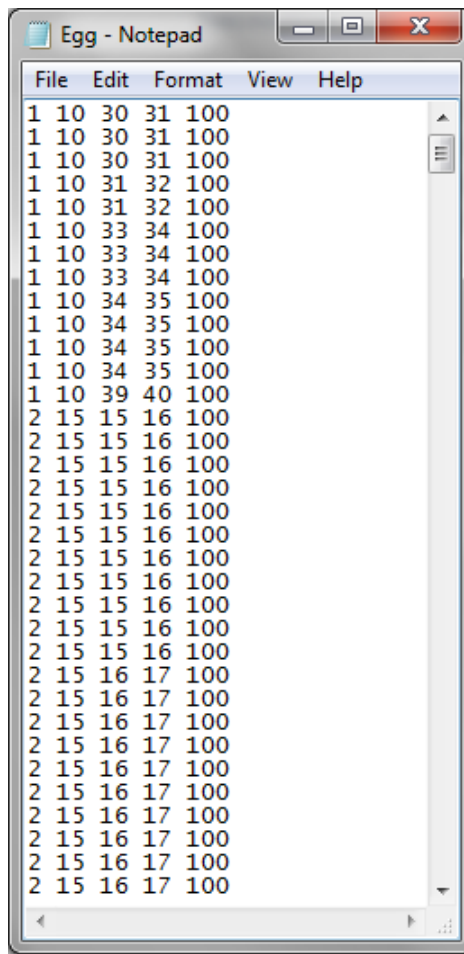


Figure 7: AFT format data. The main difference with Figure 5 is that all individual shows the evaluation time as interval (start and end) for each row and is not a count.

II. ILCYM DOWNLOADED

2.1 Full version

To be able to run ILCYM software you need to copy the compressed file “ILCYM 4.0-portable.zip”. All packages and programs required by ILCYM are included in

the zipfile and may be downloaded from the website below.
<https://research.cip.cgiar.org/confluence/display/ilcym/Downloads>

In case you have downloaded the software, make sure you unzip the file and place the full folder (called ILCYM 4.0) on your desktop.

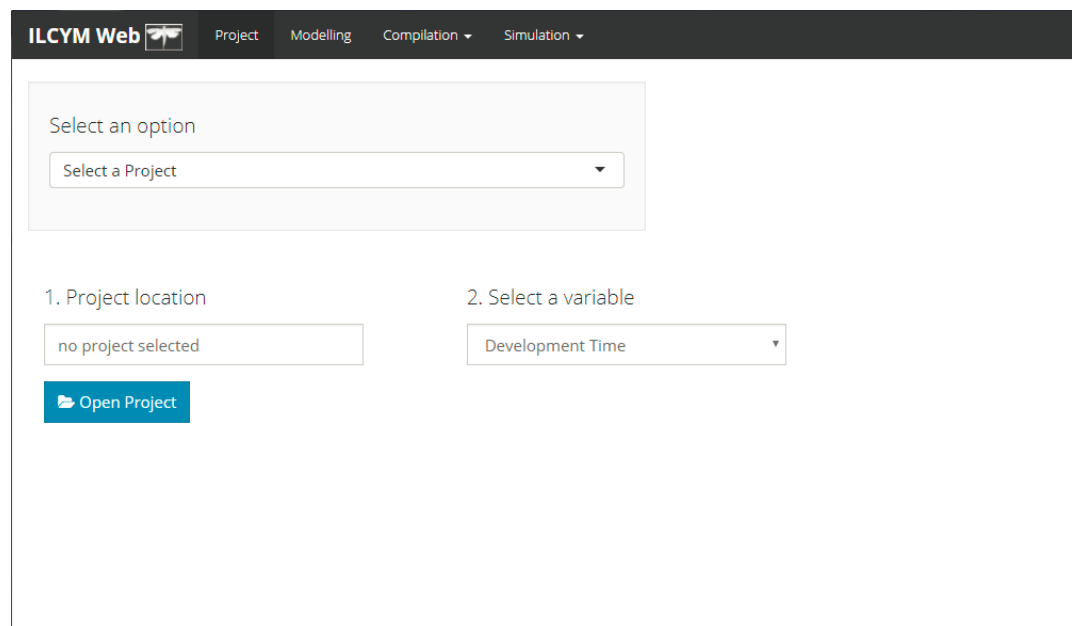
2.2 Installing ILCYM

2.2.1. Windows XP, Vista, 7 and above for computer with 32 bytes

To install ILCYM software in this operating system, the following steps need to be executed.

1. Copy the file "ILCYM 4.0 portable.zip". in anywhere (Could be in **D:**).
2. Extract the file and should appear a folder with name "ILCYM 4.0" (do double click in the file "run.bat").

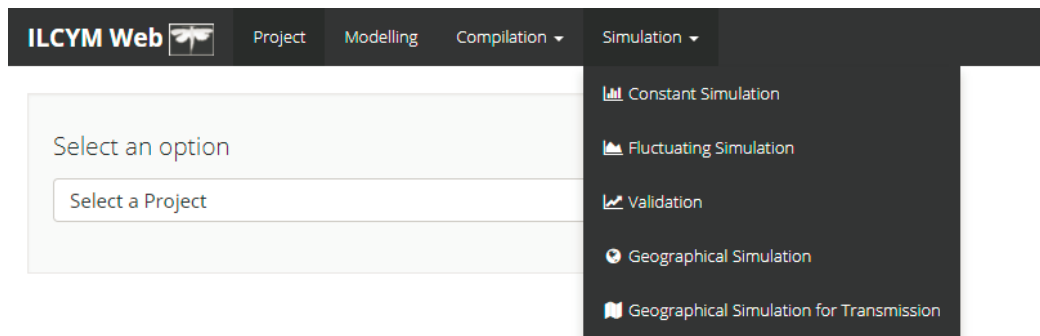
Once the application has been installed, you will see the following window:



III. ILCYM'S DESIGN

This latest version of ILCYM software is developed under an interactive web platform offered by the "Shiny" package which connects with the "R" statistical software to perform all the processing.. ILCYM 4.0 contains 4 modules: **Project**,

Modeling, Compilation and Simulation. To access the outlook of a module, go to the main **Window** -> **Select** the module you want to use.



3.1 Project and Modeling

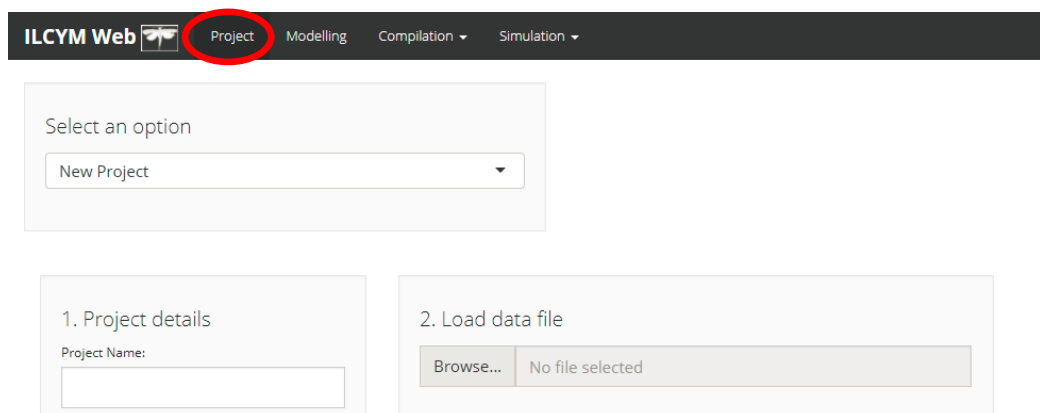
3.1.1 Creating new project and uploading data

Before you start with an evaluation of data for developing an insect phenology model, you need to create and register a new project. All data, evaluation outputs, maps, etc. that are used or created during project development are managed within a single “ILCYM’s project”.

Therefore, for each insect species you want to develop a model, a new project needs to be created. To create a project follows the steps below:

Go to **Project** -> **Select an option** -> **New project**.

There are 2 steps: “1. Project details” and “2. Load data file”



The image shows a web form with the following fields and elements:

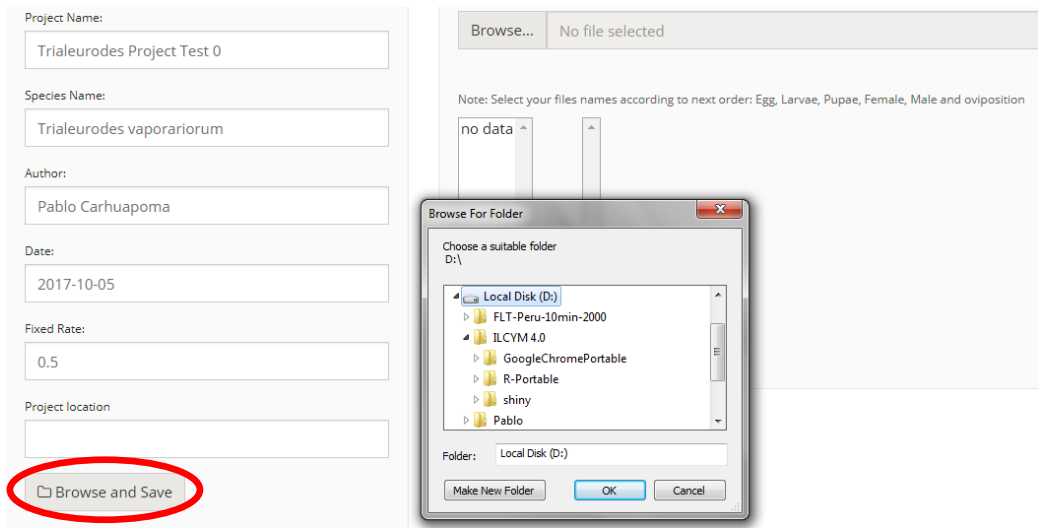
- Species Name:** An empty text input field.
- Author:** An empty text input field.
- Date:** A text input field containing "2017-10-05".
- Fixed Rate:** A text input field containing "0.5".
- Project location:** A text input field containing "C:\Users\pcarhuapoma\Document".
- Buttons:** A "Browse and Save" button at the bottom of the form, and an "Upload" button in the adjacent panel.
- Adjacent Panel:** Contains a note: "Note: Select your files names according to next order: Egg, Larvae, Pupae, Female, Male and oviposition". Below the note is a list area with "no data" at the top and two circular arrows (right and left) for navigation.

The “Project details” step is well described below.

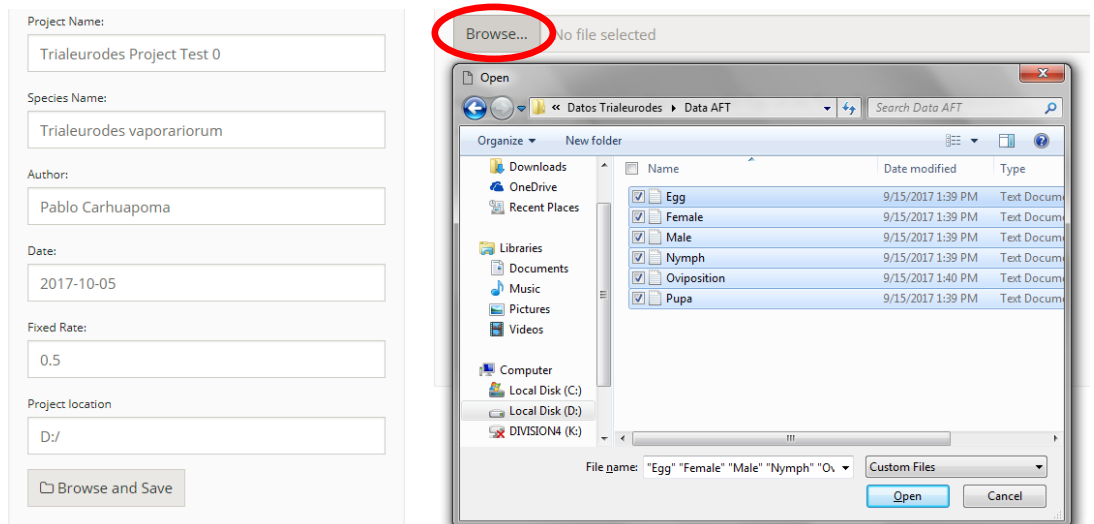
- **Project Name**, Name of the Project.
- **Species Name**, Write the name of the species
- **Author**, Name of the person creating the project.
- **Date**, Date of the project creation (it appears automatically).
- **Fixed Rate**, If the female rate is expected to be constant, i.e. independent of the temperature and female age, or any other parameter, mark this button and indicate the value of female rate, usually 0.5.

The female rate in the progeny is going to be constant over all temperatures, and independent from the age of ovipositing females.

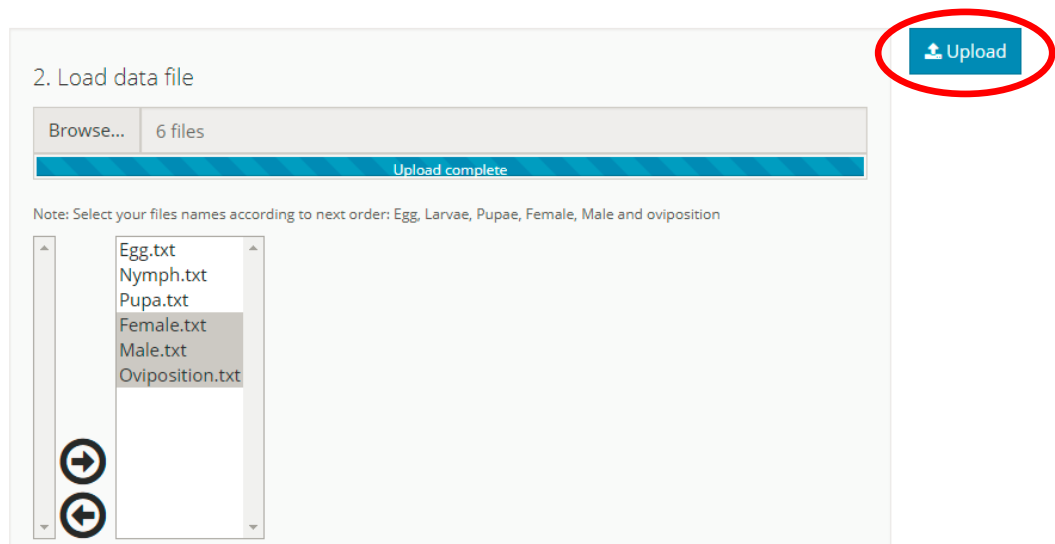
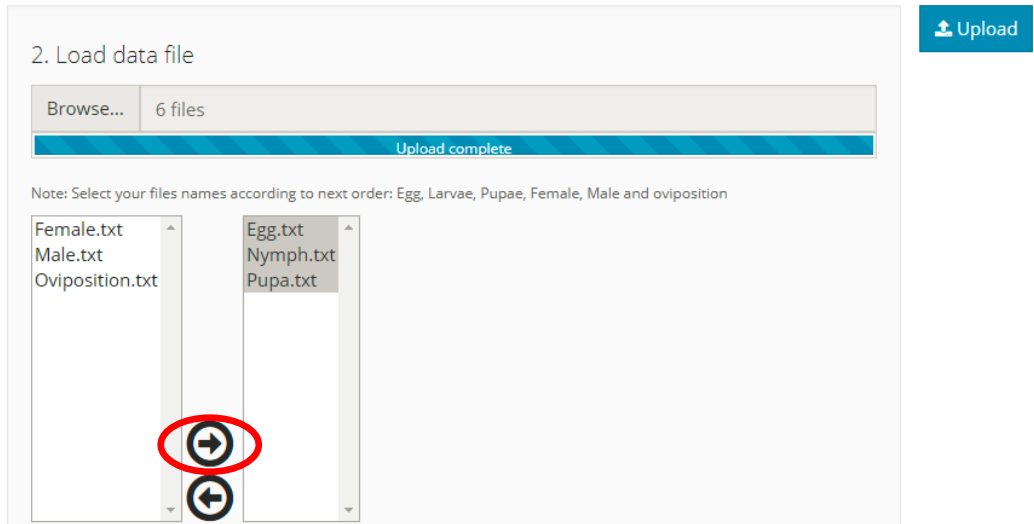
All projects will be saved when the button “Browse and Save” is used and appears the follow window:



Therefore, the new project will have created automatically in the path selected, but before you need to load the input data (life table data adapted as intervals format):



Finally, select your files names according to next order: Egg, Larvae, Pupae, Female, Male and oviposition, then is following a natural stage order (use the right arrow to select):

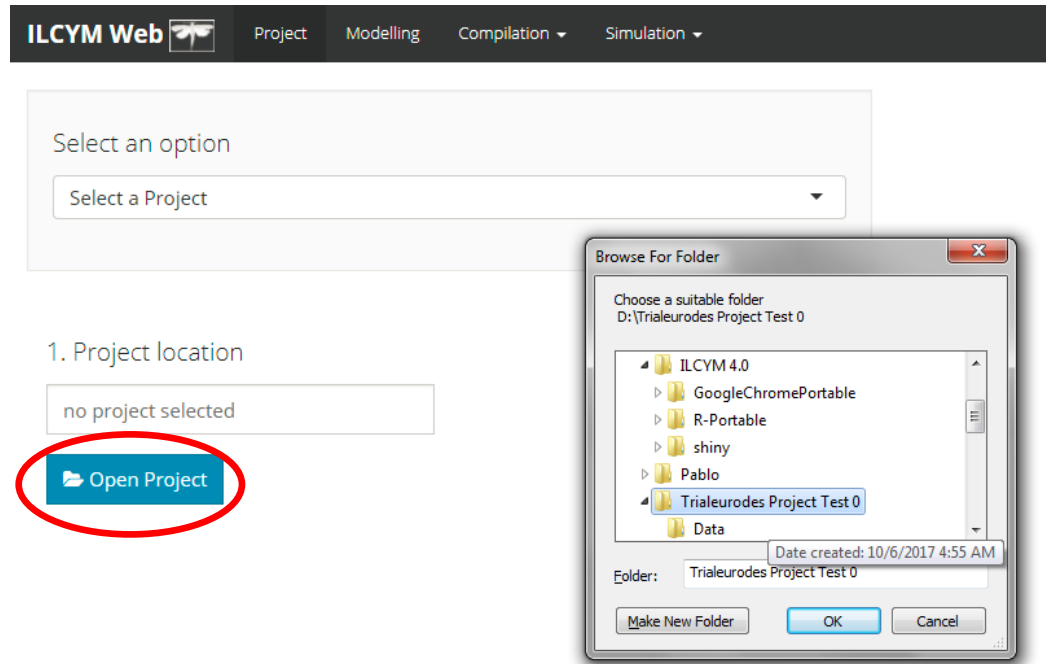


And finally, do click on "Upload" (Go to your project path and check it)

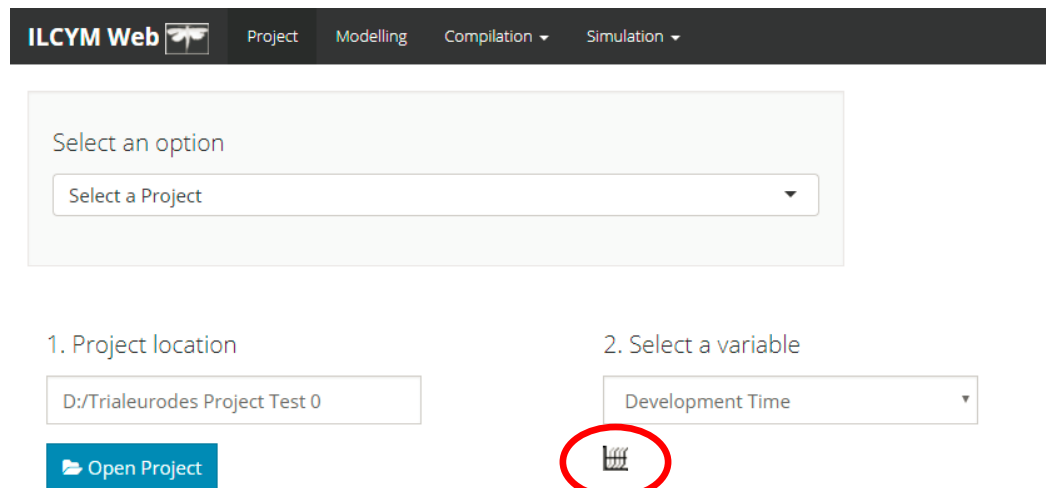
3.1.2 Importing project

If you have created a project and you want to display or work on it in another computer, the complete project should be selected into the ILCYM.

To import the project right click in **Project** and click on **Select an option** and choice the option **Select a Project**. When appears more fields do click in **Open Project**. (therefore, appears a new window where should select your project)

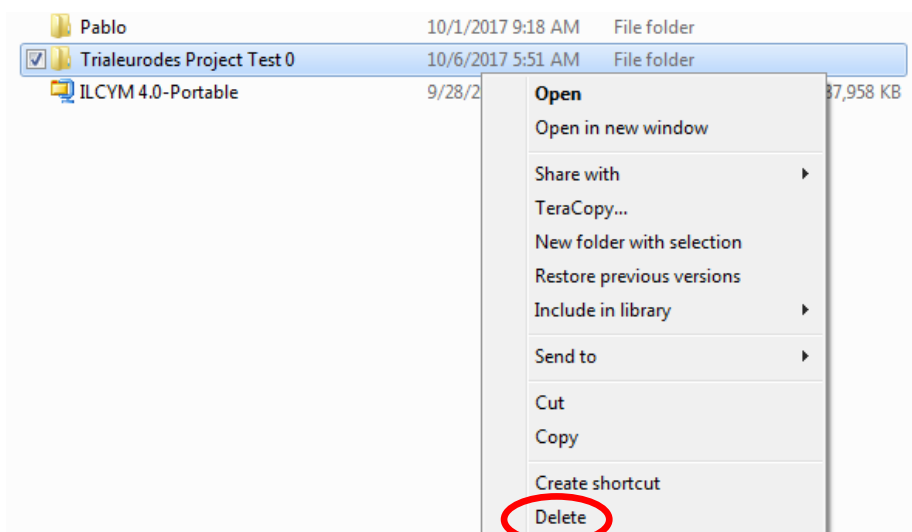


If all components of the project are ok, then appears an icon for the phenological variable.



3.1.3 Deleting project

During project creation, if the user has forgotten some life-stages and desire to delete the project and create a new project with the same name or another, just close ILCYM 4.0 and go to the project path and delete like any file.



3.1.6 Developing the overall phenology

To obtain a full phenology of a particular species, the seven (7) evaluations below are performed in subsequent order.

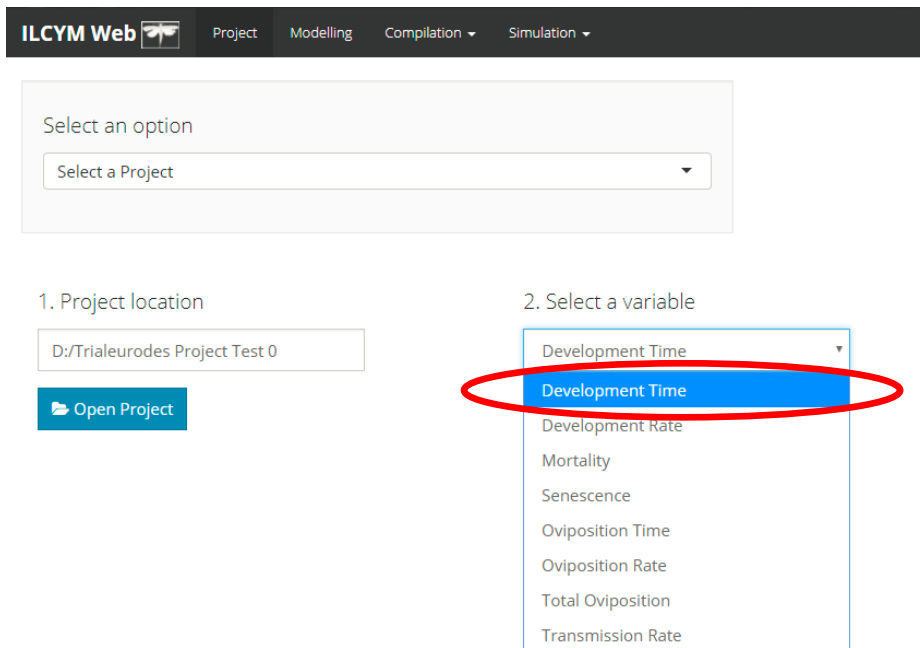
Name	Description
1. Development time and its variation	Fits the development curve in a parallel line assay to accumulated development frequencies of each constant temperature tested. The application delivers an estimate of the median development time (days) with the standard error (SE) at 95% Confidence Limits for each temperature, and a parameter describing the variation in development times between individuals.
2. Development rate	This parameter is obtained through fitting of various functions that describe the relationship between temperature and the development rate.

3. Senescence The fitting of various functions that describe the relationship between temperature and the adults' senescence.
4. Mortality The fitting of functions that describe temperature-dependent mortality is done and with the help of some statistical criteria, best model is selected.
5. Total oviposition The total oviposition is obtained by fitting functions that describe temperature-dependent total oviposition per female.
6. Oviposition Time Fit a function to describe the temperature-dependent cumulated oviposition time curves.
7. Oviposition Rate This parameter is obtained through fitting of various functions that describe the relationship between temperature and the oviposition rate.

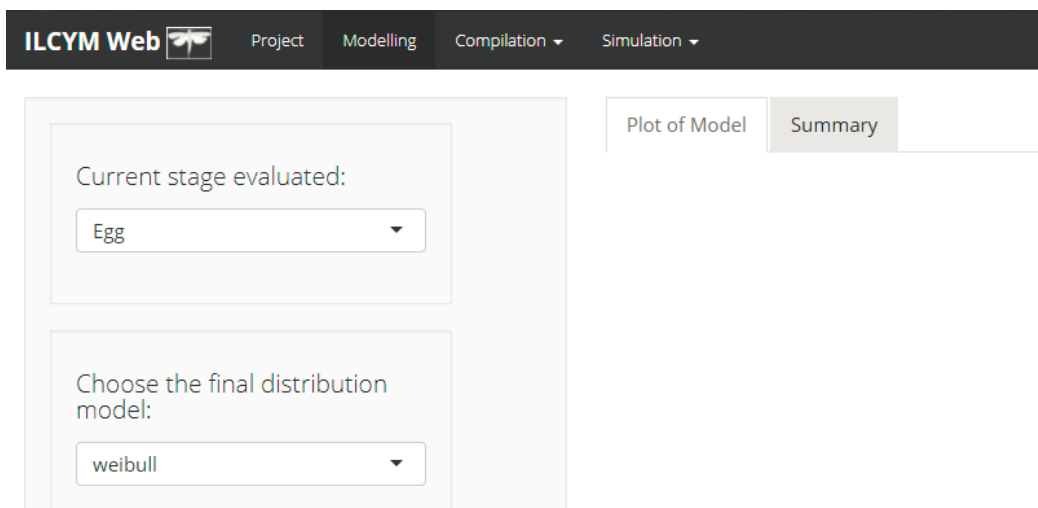
a) Development time

For conducting this evaluation, the data are fit to three distribution models (Weibull, Lognormal, and Loglogistic). The user selects the best model based on added selection criterion such as the Akaike's selection criterion (AIC). On the base of the selected function the "median development times" with 95% confidence limits are estimated (output statistics are explained on subsequent pages).

The window below displays how development time is estimated in ILCYM. Under **Project** select **Development Time**:



Then go **Modeling** to choose one of the options for each field (as the below image) and then proceed with your analysis.



The user is requested to select the insect life stage and the distribution model, then the analysis will start automatically when do click in **OK** and this will provide a statistical output, a list of indicators and a figure showing the data points entered in the analysis and the resulting development time frequency curves for each temperature.

ILCYM Web Project Modelling Compilation Simulation

1 Current stage evaluated: Egg

Choose the final distribution model: weibull

Range of the x axis: 0 4 10

Range of the y axis: 0 100

2 accumulated development frequency

3 List of indicators

Model	AIC	Deviance	LogLik
weibull	2225.15	1211.68	-1109.58
lognormal	1552.40	NA	-773.20
loglogistic	1373.50	704.37	-683.75

4 Summary

Plot of Model

```

Call:
survreg(formula = Surv(start, stop, type = "interval2") ~ Group,
data = dat, dist = modelo)

      Value Std. Error      z      p
(Intercept)  3.516    0.0531  66.2  0.00e+00
Group15-2    -0.655    0.0565 -11.6  4.70e-31
Group18-3    -1.243    0.0566 -22.0  5.58e-107
Group20-4    -1.264    0.0566 -22.3  1.76e-110
Group25-5    -1.833    0.0568 -32.3  1.09e-228
Group28-6    -1.873    0.0568 -33.0  1.97e-238
Group32-7    -1.230    0.0613 -20.1  1.23e-89
Log(scale)   -1.653    0.0317 -52.1  0.00e+00

Scale= 0.191

Weibull distribution
Loglik(model)= -1109.6  Loglik(intercept only)= -1757.1
  Chisq= 1295.15 on 6 degrees of freedom, p= 0
Number of Newton-Raphson Iterations: 6
n= 589

```

List of indicators

Model	AIC	Deviance	LogLik
weibull	2225.15	1211.68	-1109.58
lognormal	1552.40	NA	-773.20
loglogistic	1373.50	704.37	-683.75

OK Save

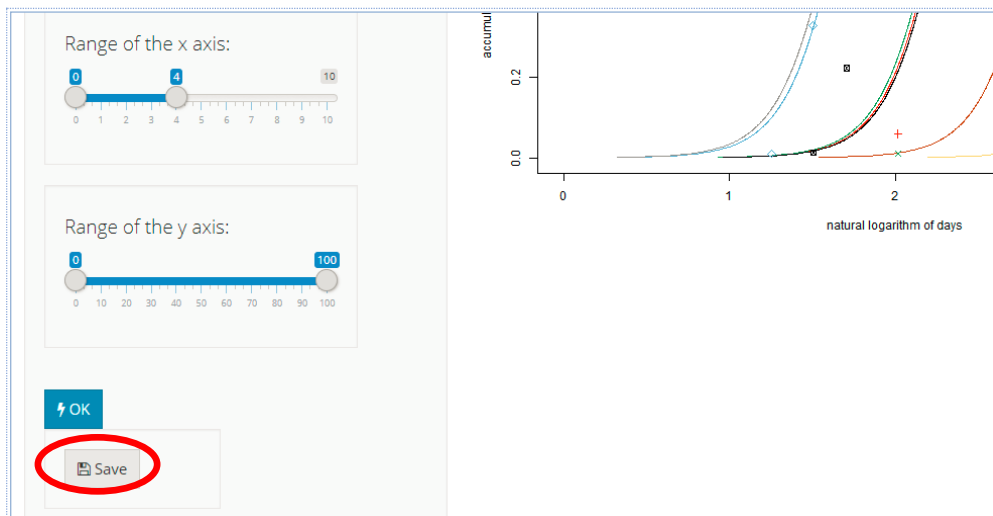
Red box 1: show the options (state, model, axis and buttons)

Red box 2: indicates adjusted model family

Red box 3: indicates the best-fitted model

Red box 4: indicates the summary of the fitted model

This window will show below of all options a button called **Save**, then do click on this button only if you agree to the selected function or select other model distribution based on the model selection criteria.



Block of lines below Red box 4: Intercepts for each temperature, standard error (SE), z-values, and the probability. The last line of the block shows the common estimated slope, these parameters all describe variation of the development time at different temperatures.

Selection criteria

Lists of criteria used to select one out of many provided functions or models. The most important are the AIC that demonstrates the deviations between observed and predicted data and the R^2 that explains how the model captures the variability within the data.

To modify the scales, legend's coordinates of the graphs, modify on the left side menu of the module and to visualize the changes **click** on the "**OK**" button.

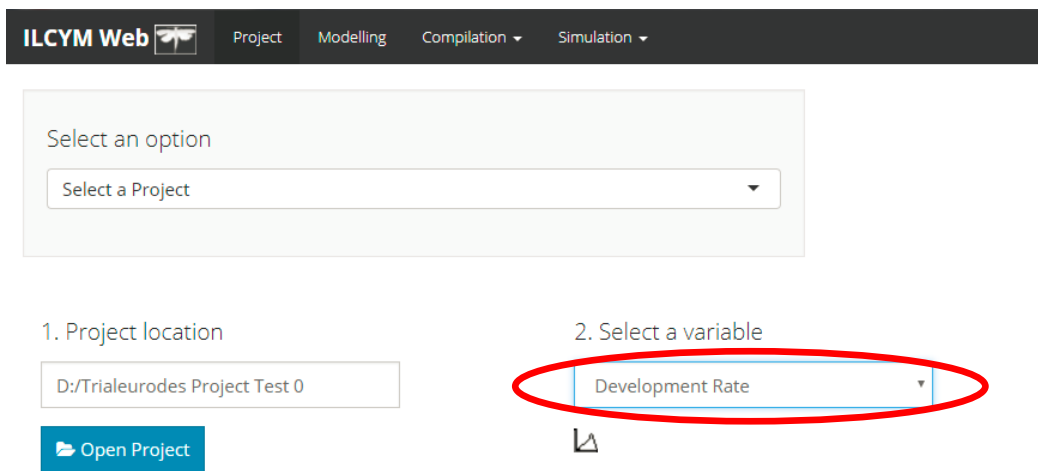
b) Development rate

The inverse of the median time ($1/\text{median time}$), calculated by the estimated function of the development distribution is the development rate due to temperature. This evaluation in ILCYM complements the evaluation of the development time; here you fit a model that describes the temperature-dependent development rate for each particular life stage. ILCYM provides several models that might describe well the development curve of insects. ILCYM

does not check the appropriateness of each model automatically. You might test several models and select the best one according to the selection criteria AIC, R^2 and P-Value.

The window below displays how development rate is estimated in ILCYM.

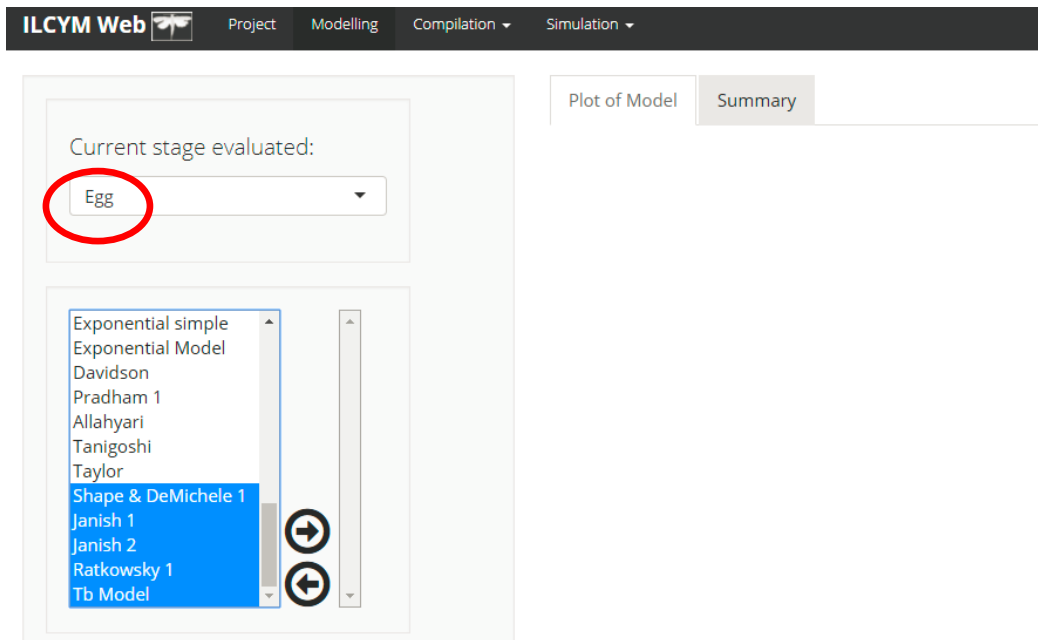
Under **Project** select **Development Rate**:



The screenshot shows the ILCYM Web interface. At the top, there is a dark navigation bar with the ILCYM Web logo and menu items: Project, Modelling, Compilation, and Simulation. Below the navigation bar, there is a light gray box containing a dropdown menu labeled 'Select an option' with the text 'Select a Project' and a downward arrow. Below this, there are two numbered steps: '1. Project location' and '2. Select a variable'. Under '1. Project location', there is a text input field containing 'D:/Trialeurodes Project Test 0' and a blue button labeled 'Open Project'. Under '2. Select a variable', there is a dropdown menu with 'Development Rate' selected, which is circled in red. Below the dropdown menu is a small icon of a document with a pencil.

ILCYM contains different models for development rate; these models are represented by the name of the first authors who first developed the equation i.e Shape De Michelle, Deva, Logan etc... Under the name of each author, there are series of models developed from the original equations marked by number i.e Shape De Michelle 1, Logan 2 etc.

Then go **Modeling** to choose one of the options for each field (as the below image) and then proceed with your analysis.



The first left part of the module displays the insect state that the user will evaluate (**change to evaluate other state**) as well as options to select the best model, either by comparing various sub-models or all at once or separately by choosing a sub-model (use CTRL).

In this menu, you can operate multiple selections or single selection **Multiple selections**

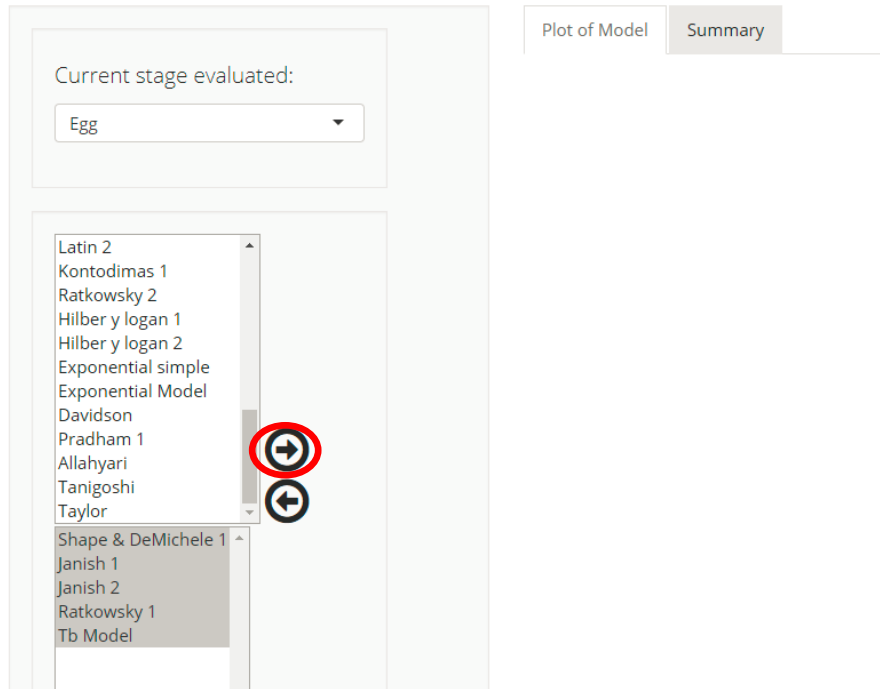
i) Select all sub-models and click in at once and choose the best fitted sub-model using inbuilt selection criteria.



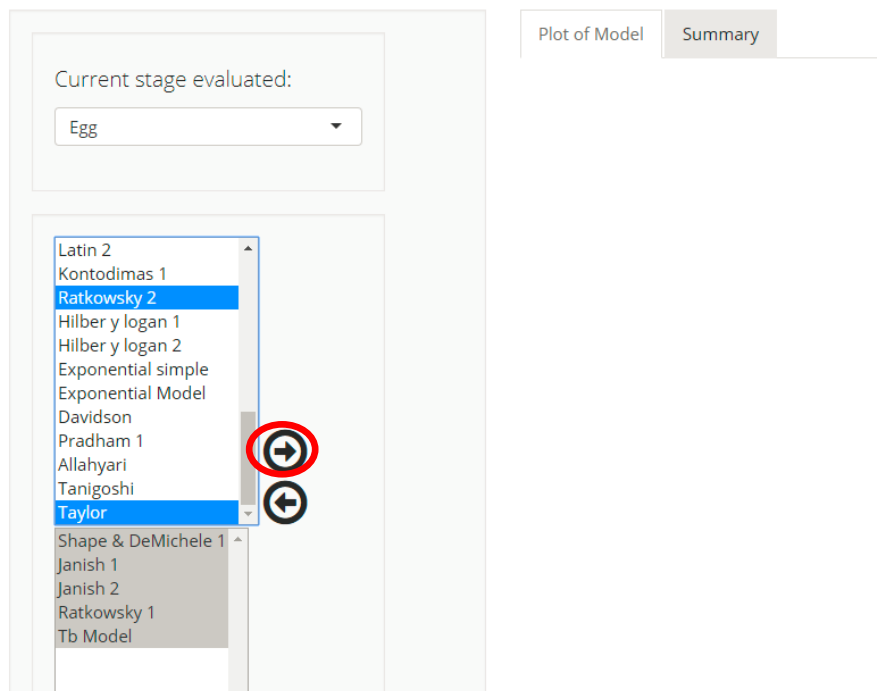
Means "right arrow " to select any model or models.



Means "left arrow" to deselect any model or models.



ii) If need select other group of sub-models use right arrow.



then the analysis will start automatically when do click in **OK** and this will provide a statistical output, a list of indicators and a figure showing the data points entered in the analysis and the resulting development rate curve according the temperature.

Below is ILCYM's window for seven sub-model selections (use the scroll bar to see the other model charts selected):

The screenshot shows the ILCYM Web interface with the following components:

- Red box 1:** A dropdown menu for 'Current stage evaluated:' set to 'Egg', and a scrollable list of models including Stinner 3, Stinner 4, Latin 2, Kontodimas 1, Hilber y logan 1, Hilber y logan 2, Exponential simple, Exponential Model, Davidson, Pradham 1, Allahyari, Tanigoshi, Shape & DeMichele 1, Janish 1, Janish 2, Ratkowsky 1, Tb Model, Ratkowsky 2, and Taylor.
- Red box 2:** A plot titled 'Shape & DeMichele 1' showing development rate (1/day) vs temperature (°C) with multiple data series and a dashed red trend line.
- Red box 3:** A table titled 'List of indicators' with columns for Model, AIC, R2, and Pvalue.
- Red box 4:** A 'Summary' tab for the selected model.

Model	AIC	R2	Pvalue
Shape & DeMichele 1	-40.494	0.991	0.018
Janish 1	-44.493	0.991	0
Janish 2	-42.524	0.991	0.001
Ratkowsky 1	-23.382	0.758	0.011
Tb Model	-41.698	0.99	0.002
Ratkowsky 2	-30.277	0.949	0.019
Taylor	-38.45	0.979	0

Red box 1: show the options (state, model, axis and buttons)

Red box 2: indicates the adjusted nonlinear model (all models selected)

Red box 3: indicates the best-fitted model (as list)

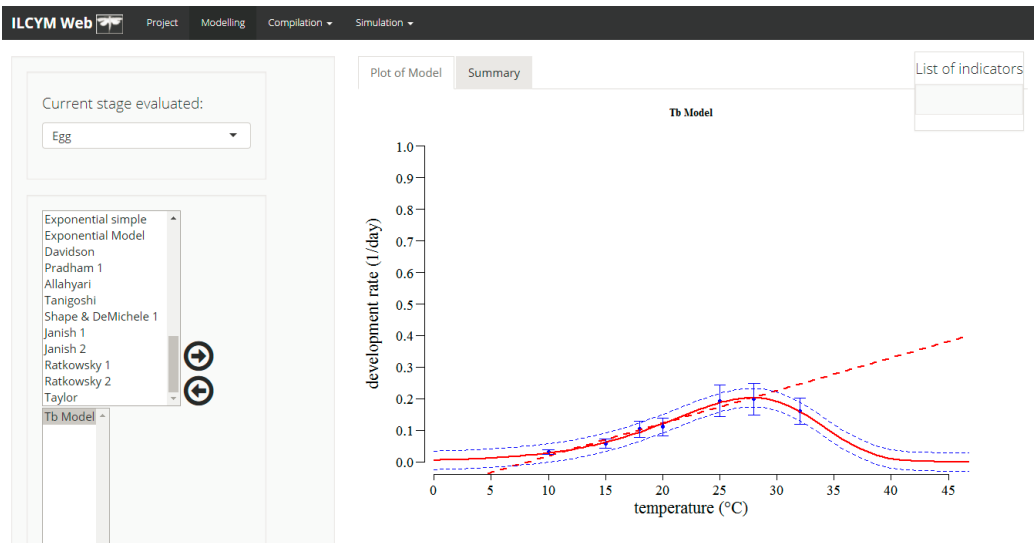
Red box 4: indicates the summary of the fitted model (only when one model is selected)

You can choose all models and compare, such case several charst will appear with the modeling result and a unique window for indicators comparison (red box 3).

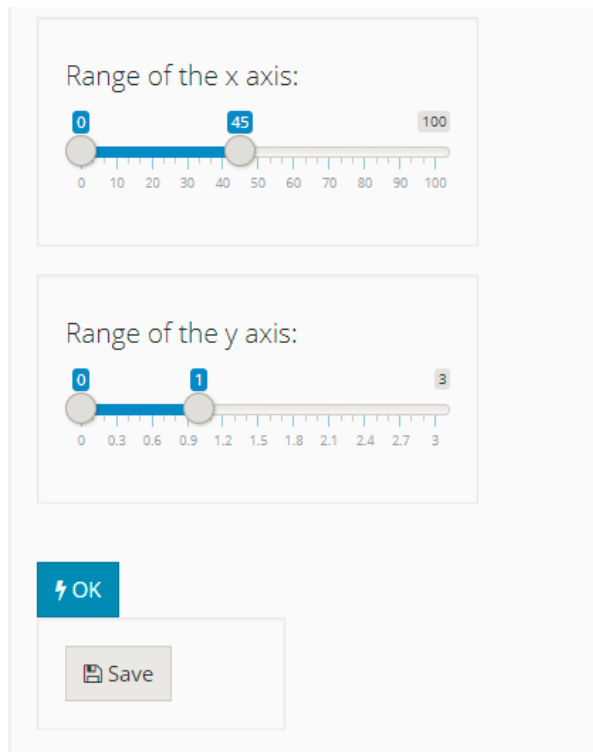
So, the statistical criteria for selecting best sub-model will appear (red box 4) and the best model should be selected using the best criteria and the best realistic chart.

List of indicators

Model	AIC	R2	Pvalue
Shape & DeMichele 1	-40.494	0.991	0.018
Janish 1	-44.493	0.991	0
Janish 2	-42.524	0.991	0.001
Ratkowsky 1	-23.382	0.758	0.011
Tb Model	-41.698	0.99	0.002
Ratkowsky 2	-30.277	0.949	0.019
Taylor	-38.45	0.979	0



To modify the scales, legend's coordinates of the graphs, modify on the left side menu of the module and to visualize the changes **click** on the "OK" button.



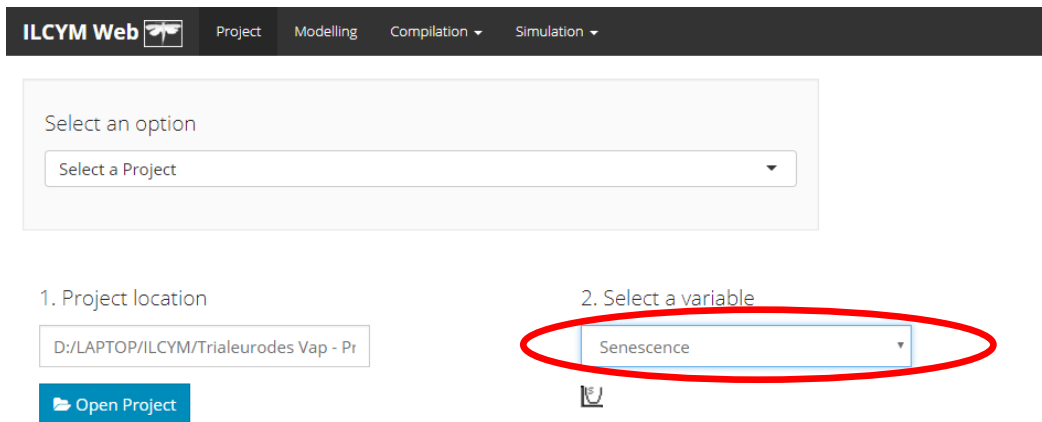
This window will show below of all options a button called **Save** (*only appears when there is one model selected*), then do click on this button only if you agree to the selected function or select other model distribution based on the model selection criteria.

c) Senescence

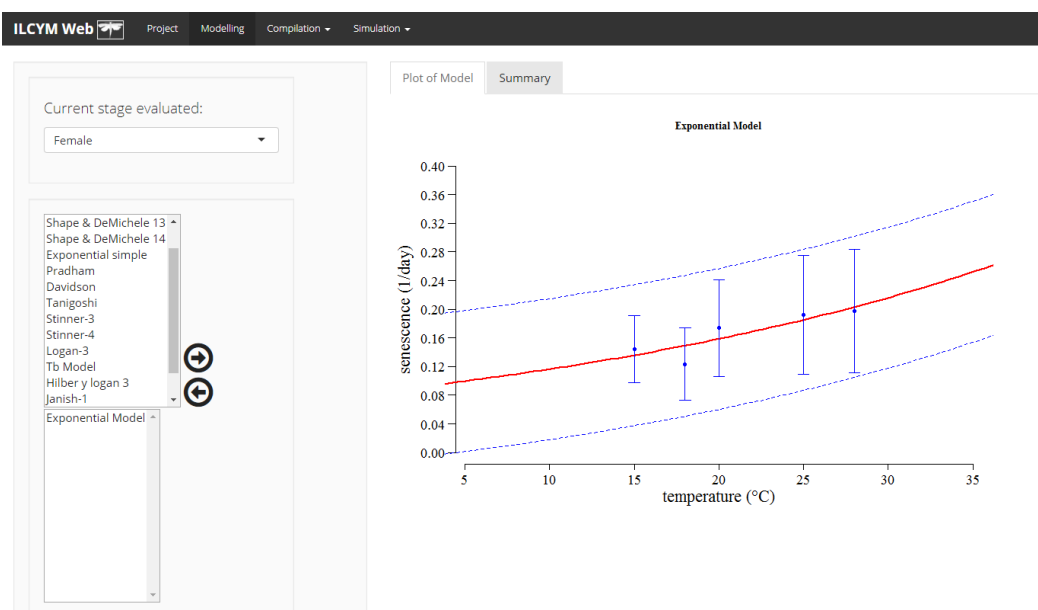
At adult stages ("males" and "female"), because the insects die instead of developing to a next stage, the sub-model in this section describes the temperature-dependent senescence rate. ILCYM software provides several sub-models just as for development rate that can be used for describing temperature-dependent senescence rate. The process of model selection is identical as on developmental rate.

The window below displays how development rate is estimated in ILCYM.

Under **Project** select **Senescence**:



So, the statistical criteria for selecting best sub-model and using the best realistic chart.

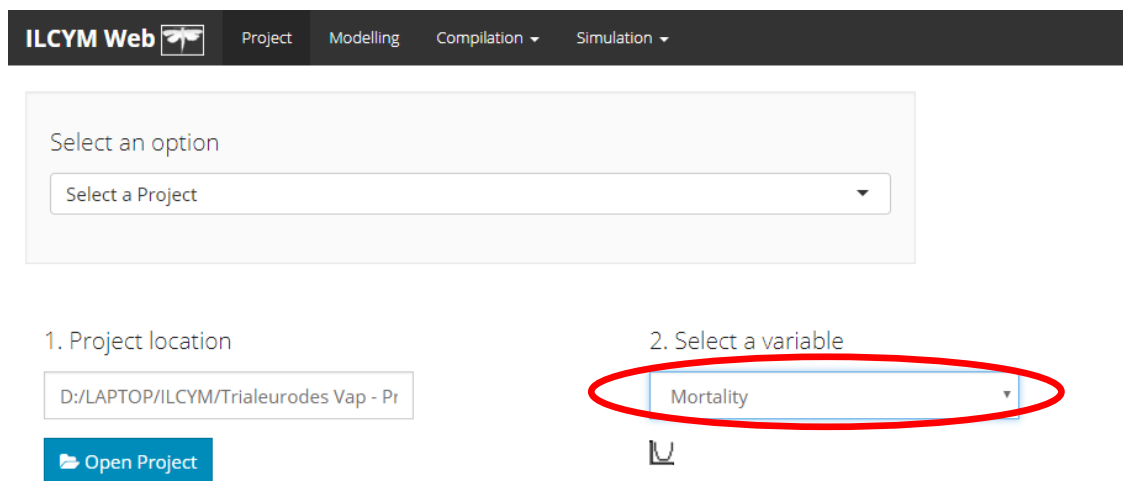


d) Mortality

Mortality is another important process in an insect life cycle that is affected by temperature. ILCYM's quantify the effect of temperature on the immature stages (egg, larva, and pupa) of the insect life-cycle. Many non-linear models that can best describe the mortality induced by temperature (low mortality near an optimal temperature and mortality increase with the deviation from the optimal temperature) are given in this program.

The best sub-model can be selected based on the available statistic just like in the previous life stages.

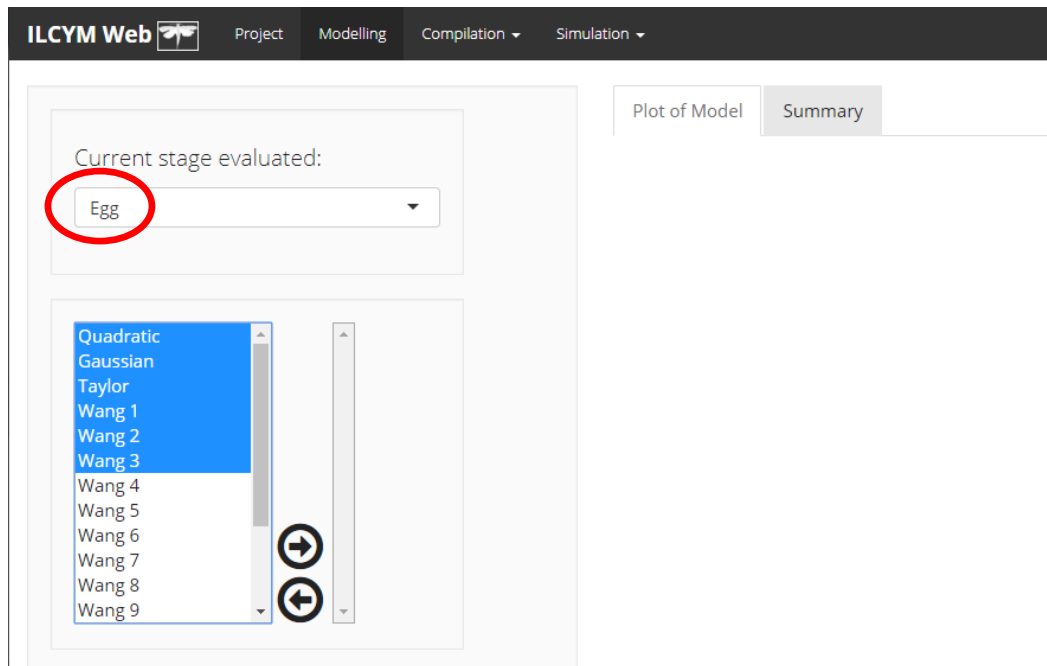
The window below displays how mortality is estimated in ILCYM. Under **Project** select **Mortality**:



The screenshot shows the ILCYM Web interface. At the top, there is a dark navigation bar with the text 'ILCYM Web' and a logo, followed by menu items: 'Project', 'Modelling', 'Compilation', and 'Simulation'. Below this is a large light gray box containing a dropdown menu labeled 'Select an option' with the text 'Select a Project' inside. Below this box are two columns of input fields. The first column is labeled '1. Project location' and contains a text input field with the path 'D:/LAPTOP/ILCYM/Trialeurodes Vap - Pr' and a blue 'Open Project' button. The second column is labeled '2. Select a variable' and contains a dropdown menu with 'Mortality' selected. This dropdown menu is circled in red. Below the dropdown menu is a small icon of a person.

ILCYM contains different models for mortality; these models are represented by the name of the first authors who first developed the equation i.e. Taylor, Whang, etc. or common name. There are series of models developed from the original equations.

Then go **Modeling** to choose one of the options for each field (as the below image) and then proceed with your analysis.



The first left part of the module displays the insect state that the user will evaluate (**change to evaluate other state**) as well as options to select the best model, either by comparing various sub-models or all at once or separately by choosing a sub-model (use CTRL).

In this menu, you can operate multiple selections or single selection **Multiple selections**

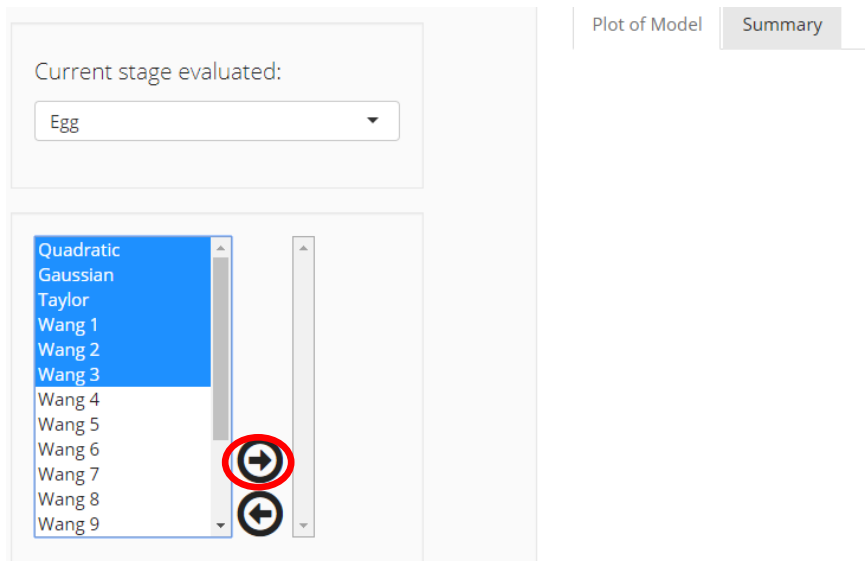
i) Select all sub-models and click in at once and choose the best fitted sub-model using inbuilt selection criteria.



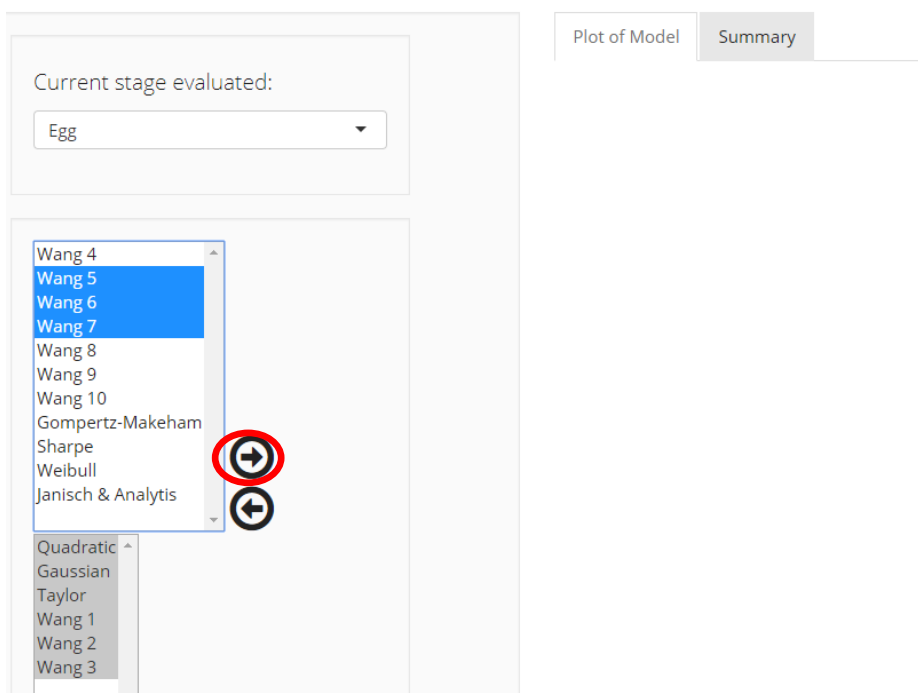
Means "right arrow" to select any model or models.



Means "left arrow" to deselect any model or models.

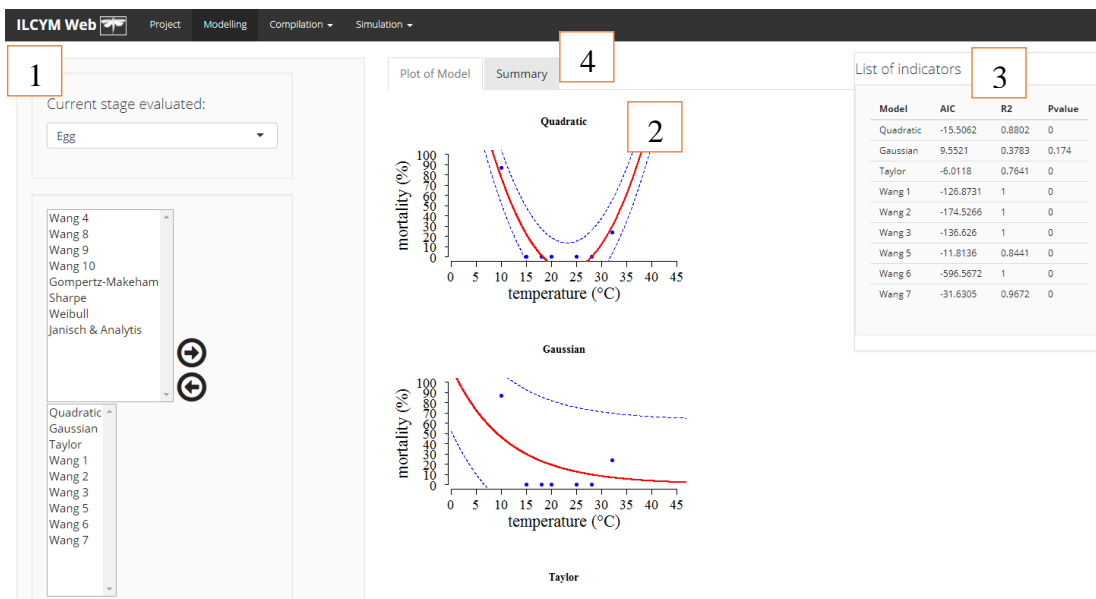


ii) If need select other group of sub-models use right arrow again.



then the analysis will start automatically when do click in **OK** and this will provide a statistical output, a list of indicators and a figure showing the data points entered in the analysis and the resulting mortality curve according the temperature.

Below is ILCYM's window for seven sub-model selections (use the scroll bar to see the other model charts selected):



Red box 1: show the options (state, model, axis and buttons)

Red box 2: indicates the adjusted nonlinear model (all models selected)

Red box 3: indicates the best-fitted model (as list)

Red box 4: indicates the summary of the fitted model (only when one model is selected)

You can choose all models and compare, such case several charts will appear with the modeling result and a unique window for indicators comparison (red box 3).

So, the statistical criteria for selecting best sub-model will appear (red box 4) and the best model should be selected using the best criteria and the best realistic chart.

List of indicators

Model	AIC	R2	Pvalue
Quadratic	-15.5062	0.8802	0
Gaussian	9.5521	0.3783	0.174
Taylor	-6.0118	0.7641	0
Wang 1	-126.8731	1	0
Wang 2	-174.5266	1	0
Wang 3	-136.626	1	0
Wang 5	-11.8136	0.8441	0
Wang 6	-596.5672	1	0
Wang 7	-31.6305	0.9672	0

ILCYM Web Project Modelling Compilation Simulation

Current stage evaluated:

Range of the x axis:

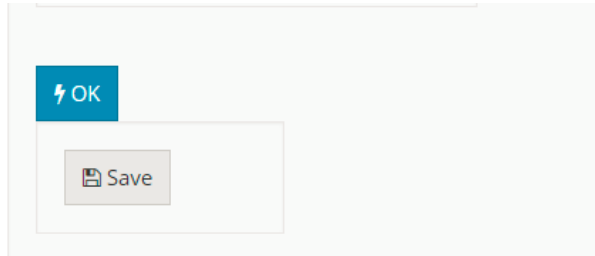
Range of the y axis in %:

Plot of Model Summary

List of indicators

Wang 3

To modify the scales, legend's coordinates of the graphs, modify on the left side menu of the module and to visualize the changes **click** on the "OK" button.



This window will show below of all options a button called **Save (only appears when there is one model selected)**, then do click on this button only if you agree to the selected function or select other model distribution based on the model selection criteria.

At optimum temperature for development, the mortality is lowest but increases at high and low temperature depending on the insect species.

The statistical analysis shows the estimation of the parameters of the best model used to quantify the effect of the temperature on the mortality.

e) Total oviposition

The oviposition or reproduction of insects can be described by three temperature dependent components: the total oviposition, the oviposition time and the oviposition rate.

In ILCYM, total oviposition represents the expected total number of eggs laid per an insect female during her whole life span as a function of temperature. This relationship is modeled with a nonlinear function as shown in the graph below. The best sub-model can be selected based on the available statistic just like in the previous life stages.

The window below displays how total oviposition is estimated in ILCYM. Under **Project** select **Total oviposition:**

Select an option

Select a Project

1. Project location

D:/LAPTOP/ILCYM/Trialeurodes Vap - Pr

Open Project

2. Select a variable

Total Oviposition

ILCYM contains different models for total oviposition; these models are represented by the name of the first authors who first developed the equation i.e. Quadratic, Whang, etc. or common name. There are series of models developed from the original equations.

Then go **Modeling** to choose one of the options for each field (as the below image) and then proceed with your analysis.

Current stage evaluated:

Female

Quadratic
Gaussian
Taylor
Wang 5
Wang 6
Wang 7
Wang 8
Wang 9
Wang 10
Sharpe
Gompertz-Makeham
Weibull

Plot of Model Summary

The first left part of the module displays the insect state that the user will evaluate (**change to evaluate other state**) as well as options to select the best model, either by comparing various sub-models or all at once or separately by choosing a sub-model (use CTRL).

In this menu, you can operate multiple selections or single selection **Multiple selections**

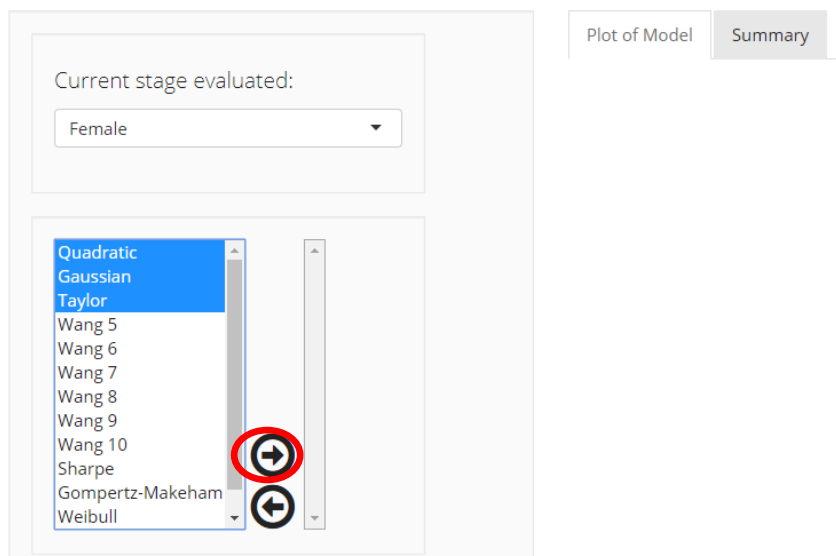
i) Select all sub-models and click in at once and choose the best fitted sub-model using inbuilt selection criteria.



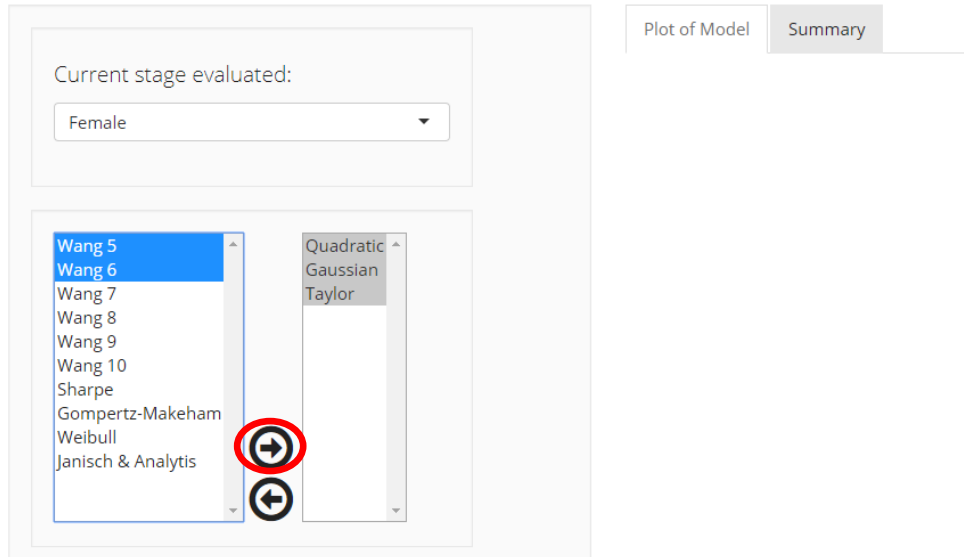
Means "right arrow" to select any model or models.



Means "left arrow" to deselect any model or models.



ii) If need select other group of sub-models use right arrow again.



then the analysis will start automatically when do click in **OK** and this will provide a statistical output, a list of indicators and a figure showing the data points entered in the analysis and the resulting total oviposition curve according the temperature.

Below is ILCYM's window for seven sub-model selections (use the scroll bar to see the other model charts selected):

1

Current stage evaluated:
Female

Wang 7
Wang 8
Wang 9
Wang 10
Sharpe
Gompertz-Makeham
Weibull
Janisch & Analytis
Quadratic

Quadratic
Gaussian
Taylor

Range of the x axis:
0 45 100

4

Plot of Model Summary

2

Gaussian

fecundity/female

temperature (°C)

Taylor

fecundity/female

temperature (°C)

Wang 5

3

List of indicators

Model	AIC	R2	Pvalue
Gaussian	36.1241	0.8645	0.458
Taylor	34.1564	0.8636	0.136
Wang 5	27.9404	0.9606	0.039
Wang 6	28.7453	0.969	0.223

Red box 1: show the options (state, model, axis and buttons)

Red box 2: indicates the adjusted nonlinear model (all models selected)

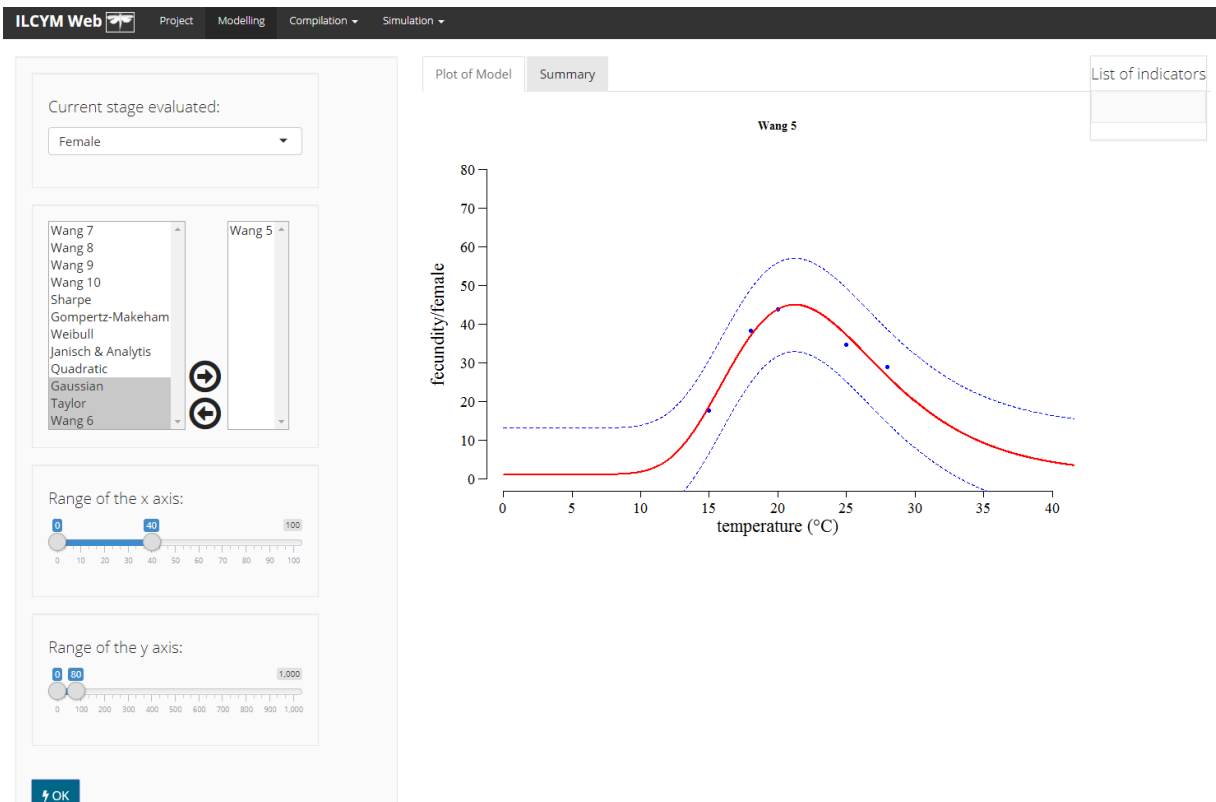
Red box 3: indicates the best-fitted model (as list)

Red box 4: indicates the summary of the fitted model (only when one model is selected)

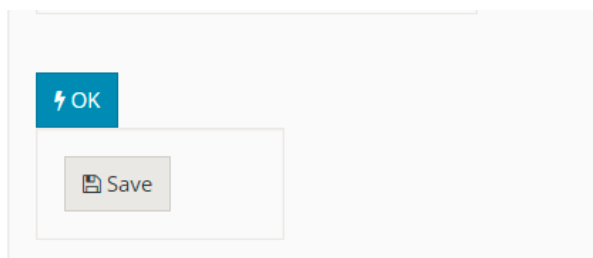
You can choose all models and compare, such case several charts will appear with the modeling result and a unique window for indicators comparison (red box 3).

So, the statistical criteria for selecting best sub-model will appear (red box 4) and the best model should be selected using the best criteria and the best realistic chart.

List of indicators			
Model	AIC	R2	Pvalue
Gaussian	36.1241	0.8645	0.458
Taylor	34.1564	0.8636	0.136
Wang 5	27.9404	0.9606	0.039
Wang 6	28.7453	0.969	0.223



To modify the scales, legend's coordinates of the graphs, modify on the left side menu of the module and to visualize the changes **click** on the "**OK**" button.



This window will show below of all options a button called **Save (only appears when there is one model selected)**, then do click on this button only if you agree to the selected function or select other model distribution based on the model selection criteria.

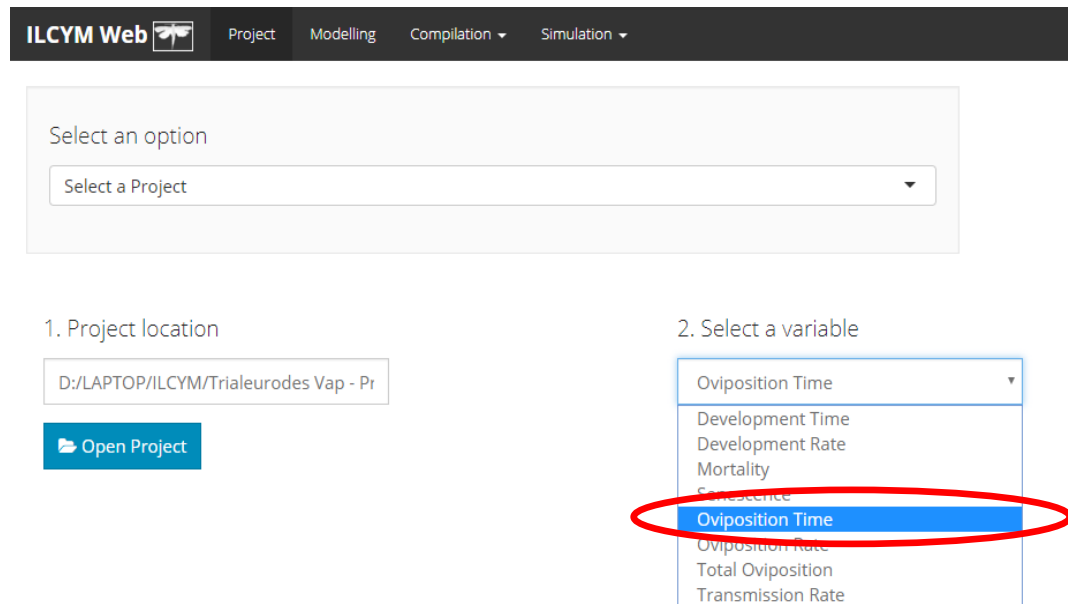
e) Oviposition time

The oviposition time is the lifetime reproductive of each female in days. This variable is evaluated at a determined temperature. The process of model

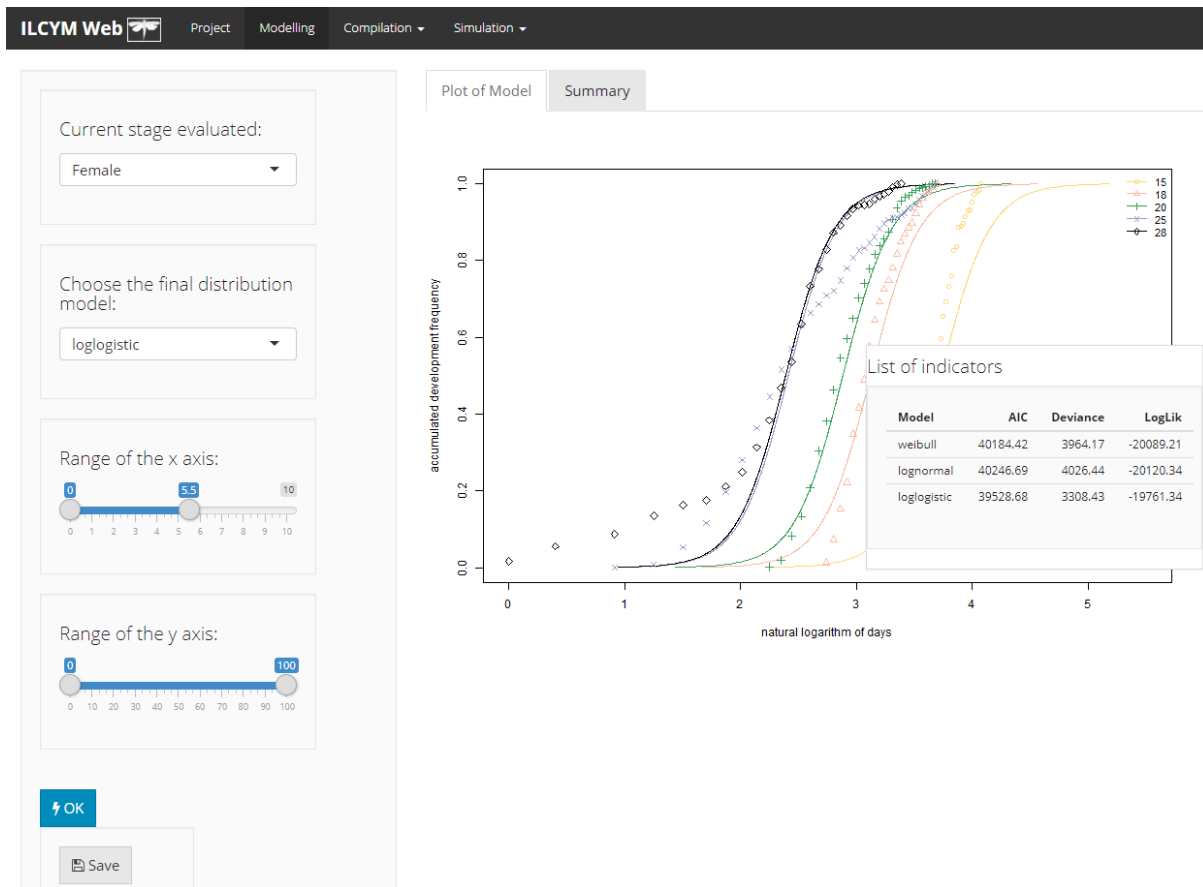
selection is identical as on **Development Time**, the data are fit to three distribution models (Weibull, Lognormal, and Loglogistic). The user selects the best model based on added selection criterion such as the Akaike selection criterion (AIC). On the base of the selected function the "median development times" with 95% confidence limits are estimated (output statistics are explained on subsequent pages).

The window below displays how development time is estimated in ILCYM.

Under **Project** select **Oviposition Time**:



So, the statistical criteria for selecting best sub-model and using the best realistic chart.

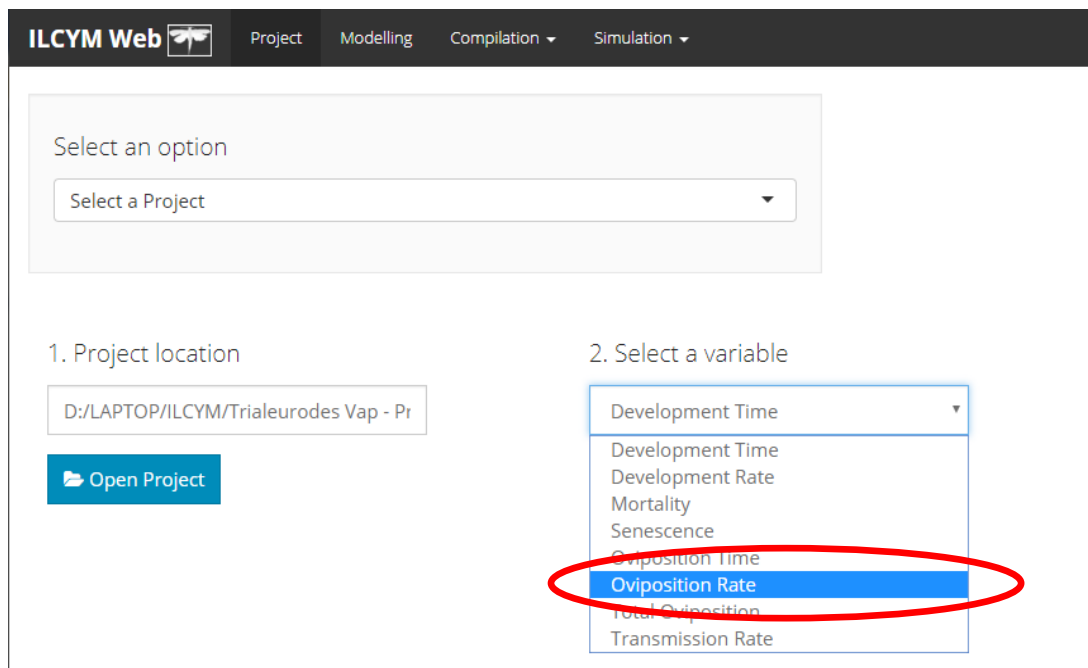


e) Oviposition rate

Considering the oviposition time estimated, the sub-model in this section describes the temperature-dependent **oviposition rate**. ILCYM software provides several sub-models just as for **development rate** that can be used for describing temperature-dependent oviposition rate. The process of model selection is identical as on **development rate**.

The window below displays how development rate is estimated in ILCYM.

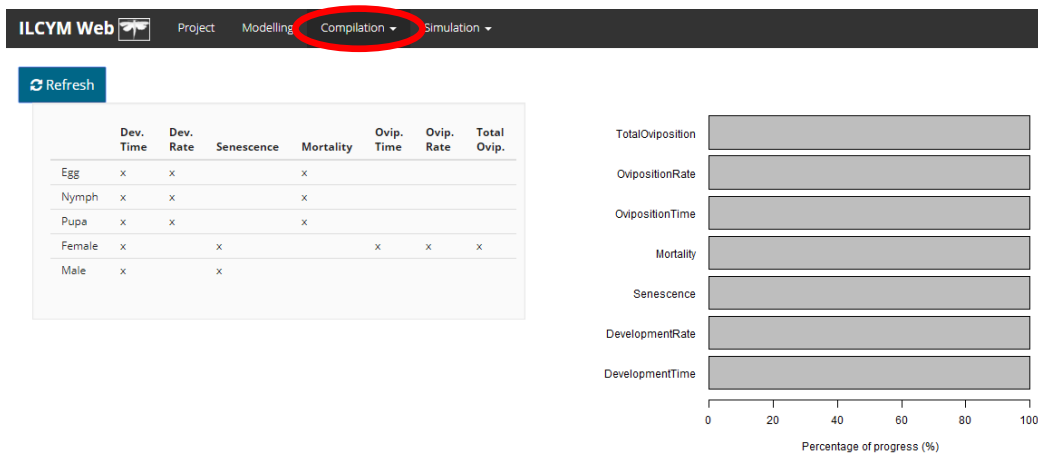
Under **Project** select **Oviposition Rate**:



3.1.7 Project progress

To know about the progress of your project, ILCYM has a tool that show at each moment the stage of the progress in developing a phenology this tool can be found in **Compilation / Phenology progress**

The screen below shows the insect developmental stages that have been evaluated; the stages evaluated are check (the ones that have not been marked) are the ones that cannot be evaluated under the conditions the experiments have been made. Do click in **Refresh**



3.1.8 Project summarize

“En proceso al 70%, falta incluir tablas de 4 variables”

3.2 Validation and Simulations

ILCYM users can conduct two (2) type of simulations: stochastic and deterministic. For each simulation the life table parameters of your species are estimated. The simulations are found in the **Simulations Menu** below.

3.2.1 Stochastic Simulation

ILCYM stochastically simulates a user-defined number of life tables, each with a user-defined number of individuals, through rate summation and random determination for each individual's survival, development to the next stage, and sex under constant or fluctuating temperature. Stochasticity in reproduction is calculated according to the variance observed in the data on total oviposition per female used for developing the model.

Developing

a) Stochastic Simulation at fluctuating temperature

Developing

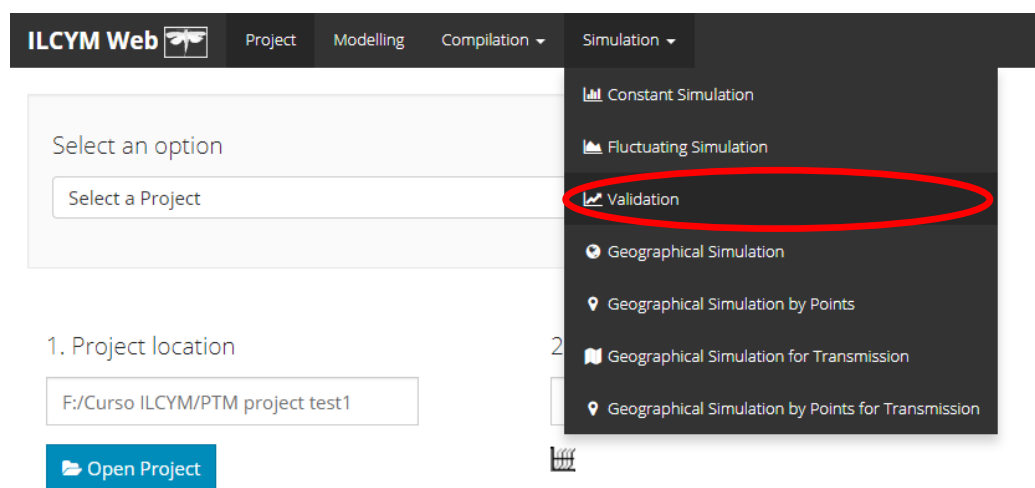
b) Stochastic simulation at constant temperatures

Developing

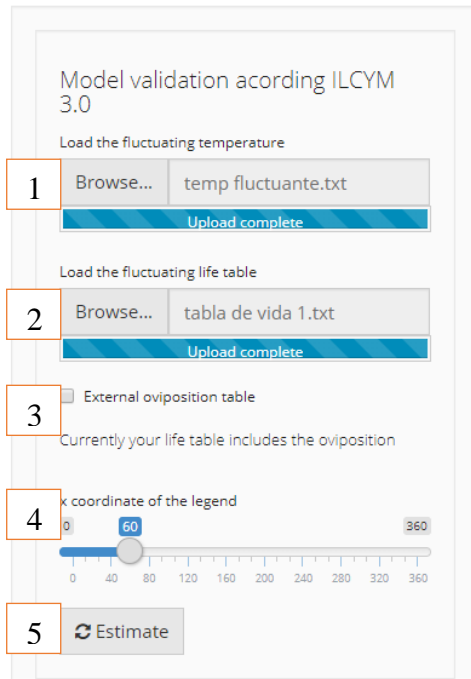
3.2.2 Model validation (validation of established model is done using stochastic simulation)

The validation tool in ILCYM allows the user to evaluate the ability of the developed phenology model to reproduce the insect species behavior under fluctuating temperature conditions.

The window below displays how **Validation** is done in ILCYM. Under **Simulation** select **Validation**:



This is achieved by comparing experimental life table data obtained from fluctuating temperature studies with model outputs produced by using the same temperature records as input data.



Red box 1: this button allows loading the temperature data; this data must be in daily format. The columns mean longitude and latitude.

File	Edit	Format	View	Help
13.4	25.0			
13.7	25.4			
14.6	29.9			
17.7	29.9			
15.4	31.1			
14.0	28.9			
15.9	25.1			
12.7	23.5			
14.5	25.8			
16.7	25.9			
14.3	25.9			
13.7	25.8			
15.9	27.0			
14.7	27.0			
12.3	19.5			
13.6	23.5			
14.4	23.5			
13.4	26.1			

Red box 2: for inputting life-table files used to validate your developed model with fluctuating temperature (according the temperature uploaded in “Red box 1” that has same number of observations).

The **dots** are experimental results and the **lines** are phenology model outputs.

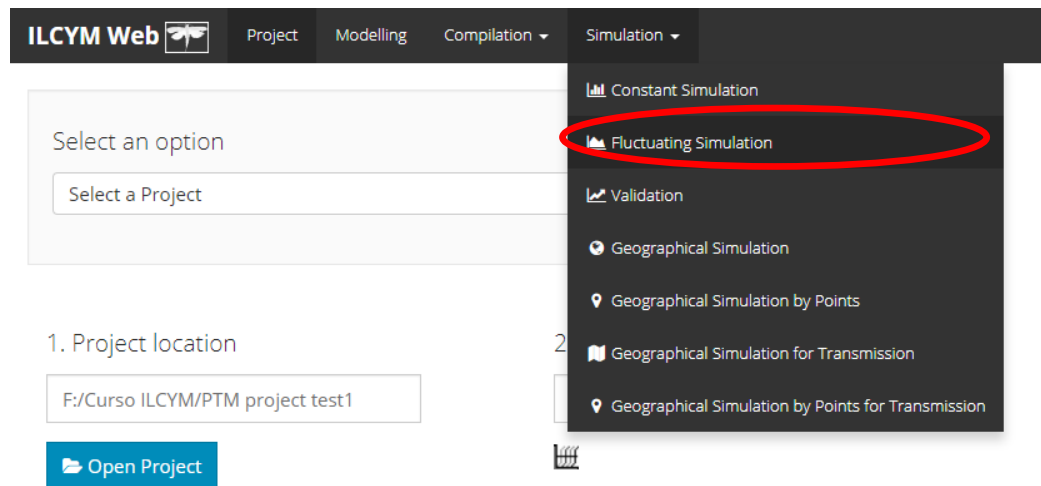
3.2.3 Deterministic simulation

The deterministic simulation simulates population using a rate summation and cohort up-dating approach throughout a long-term period (one or more years) with multiple overlapping generations for a specific location based on minimum and maximum daily temperatures and visually output the potential population increase. At the present stage of ILCYM development, this simulation considers only the growth process as an unbounded process in which the population grows without limit if uncontrolled. Such simulation can be conducted under constant or fluctuating temperature within a period of a generation, one year and several years.

a) Deterministic Simulation at fluctuating temperature

This module simulates life-tables for the subsequent years.

The window below displays how this simulation is done in ILCYM. Under **Simulation** select **Fluctuating Simulation**:



Below is ILCYM's window shows the inputs and sub-tools.

Fluctuating simulation according ILCYM 3.0

Number of insects

1

Load the fluctuating temperature

2 No file selected

x coordinate of the legend

3 0 360

4

Red box 1: indicates the number of insects used for the simulation.

Red box 2: this button allows loading the temperature data; this data must be in daily format. The columns mean minimum and maximum temperature.

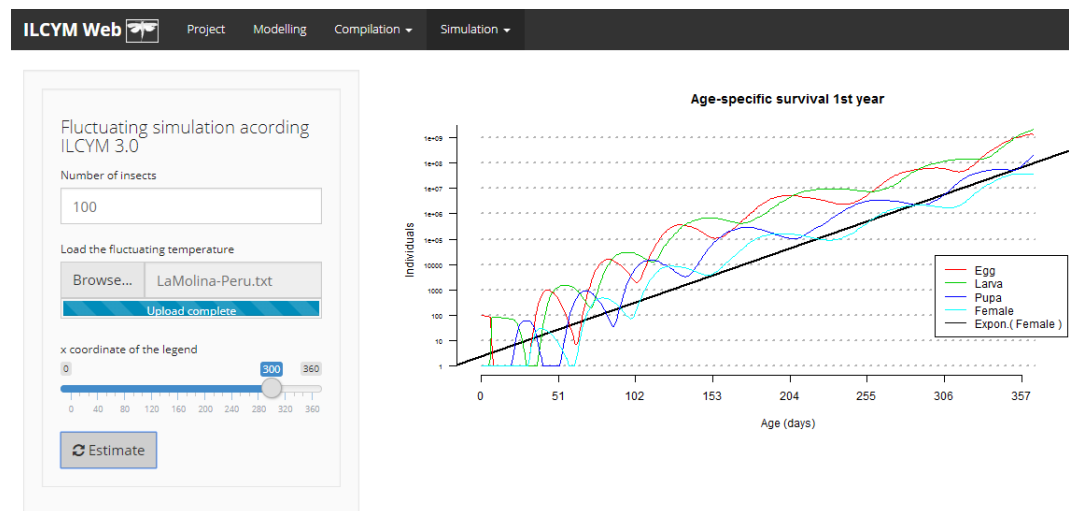
File	Edit	Format	View	Help
13.4	25.0			
13.7	25.4			
14.6	29.9			
17.7	29.9			
15.4	31.1			
14.0	28.9			
15.9	25.1			
12.7	23.5			
14.5	25.8			
16.7	25.9			
14.3	25.9			
13.7	25.8			
15.9	27.0			
14.7	27.0			
12.3	19.5			
13.6	23.5			
14.4	23.5			
13.4	26.1			

Red box 3: indicates how to fit the axis legend.

Red box 4: start the simulation process.

The figure below displays the evolution of number of individuals for each life stage over time. The simulation started with 100 eggs. Over time, these eggs

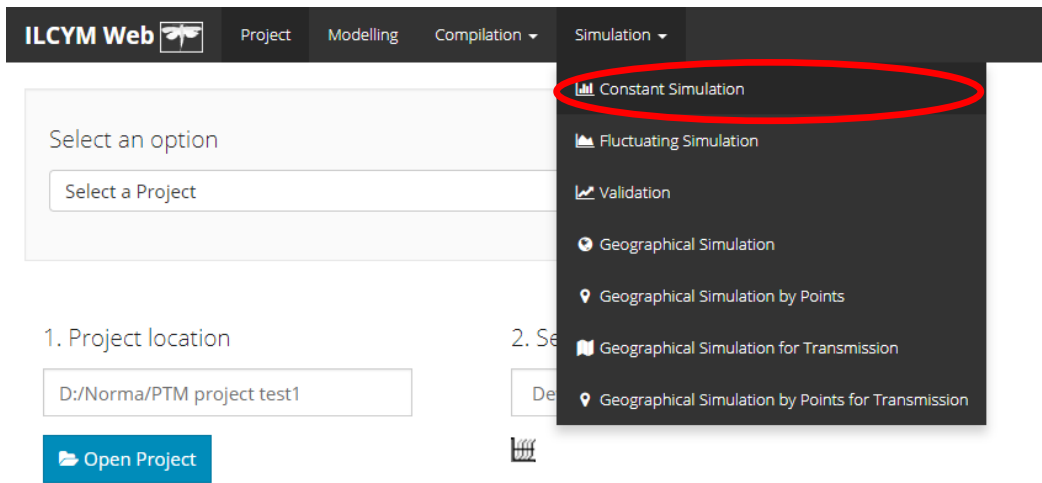
passed through different life stages or dies. When the population contains adult female (in this example first females emerges after about 80 days) new eggs are added to the population through oviposition (reproduction). First generations can be differentiated by the waves described by lines; however, with each new generation the overlap of generations increases. Once the population's structure stabilized, the figure would show straight lines for each life stages.



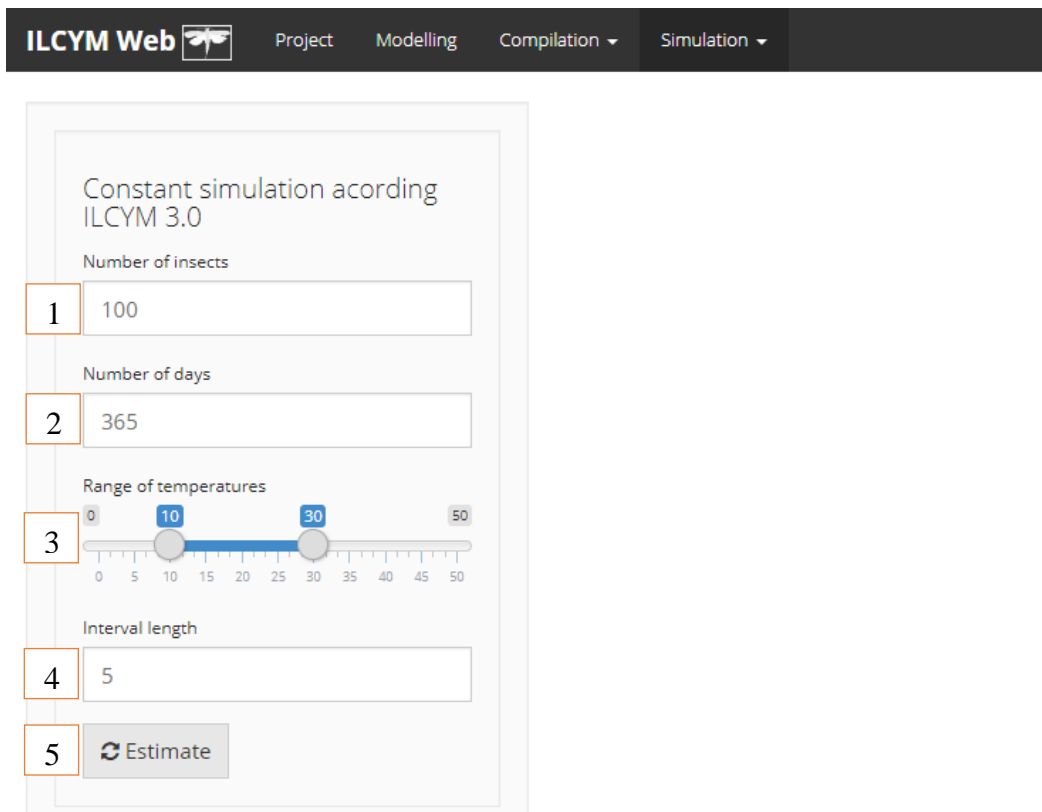
b) Deterministic simulation at constant temperatures

This simulation can also be conducted at several constant temperatures at the difference that the user simply input the number of temperatures with no repetitions because the result will always be the same.

The window below displays how this simulation is done in ILCYM. Under **Simulation** select **Constant Simulation**:



Below is ILCYM's window shows the inputs and sub-tools.



Red box 1: indicates the number of insects to simulate.

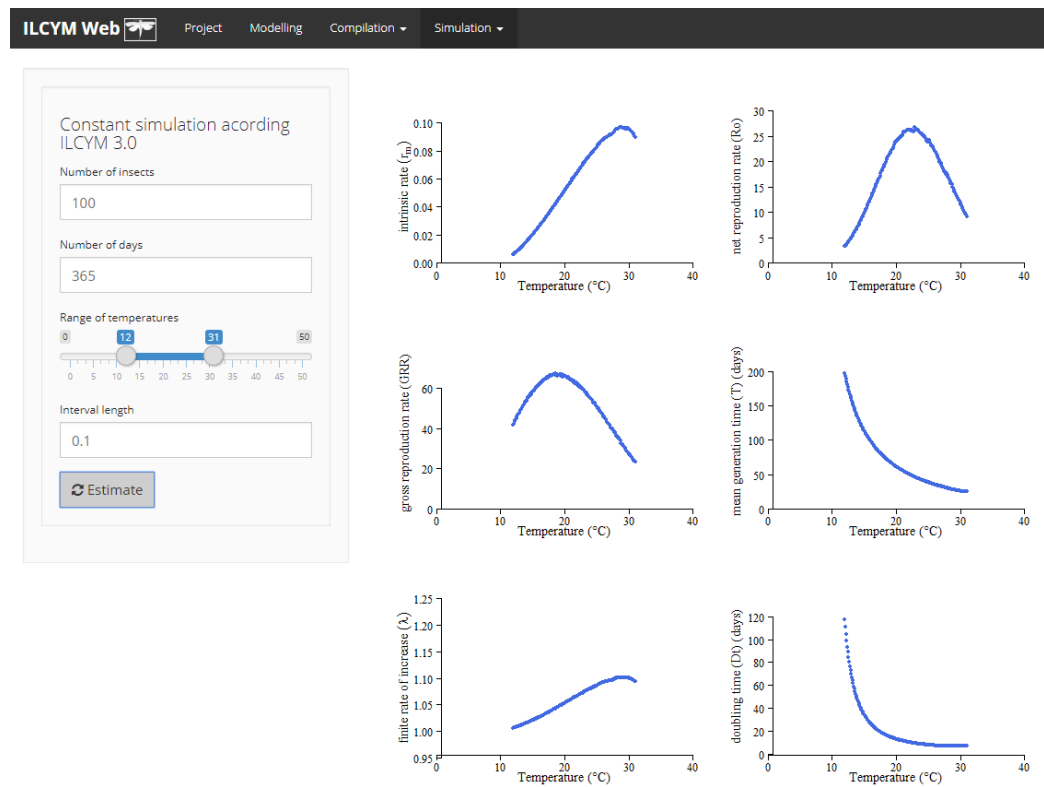
Red box 2: indicates the number of days to evaluate.

Red box 3: indicates the range of temperatures to simulate.

Red box 4: indicates the interval length, this defines number of intervals according the range selected in **Red box 3**.

Red box 5: start the simulation process.

So, the output graph for the constant simulation is shown:

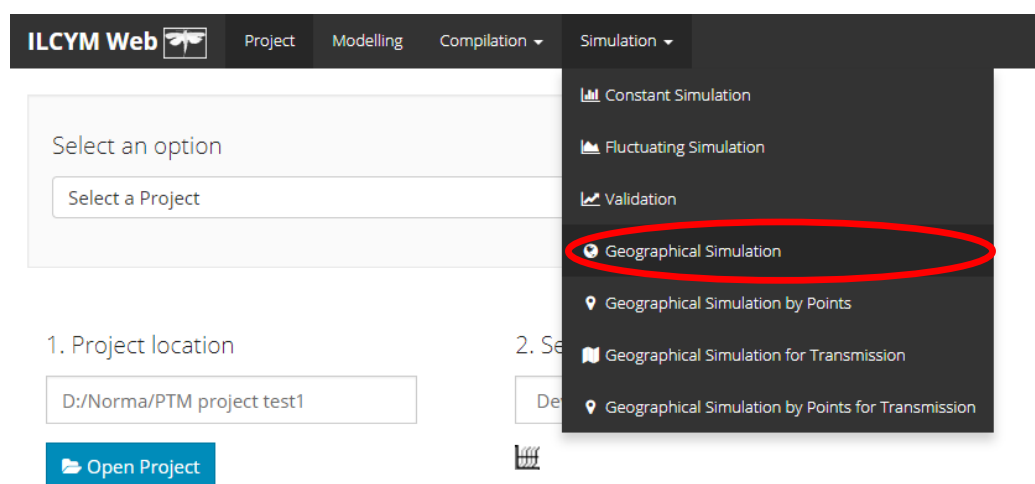


Note: In these simulations, always remember to input temperature values within the range that the insect under investigation can properly develop, if you input a temperature that is not suitable for development, ILCYM will output **NA** for life table parameter values

3.3 Potential Population Distribution and Mapping

Populations are spatially simulated through grid-based within a defined area according to grid-specific daily temperatures interpolated from available databases. If the study insect is a pest, the tool can plot indices based on simulation results for visualizing the establishment risk, the spread and damage potential of that pest species on a map.

The window below displays how Geographical Simulation is done in ILCYM. Under **Simulation** select **Geographical Simulation**:



3.3.1 Climate data

ILCYM can simulate maps at different resolution p.e. 10 minutes which is equivalent of 18 x 18 Km, 5 minutes equal to 9 x 9 km, 2.5 minutes equal to 4.5 x 4.5 Km and 30 seconds that is equal to 0.9 x 0.9km. The lower resolution, for example 10 minutes, are used to map larger areas such as the whole world, highest resolutions give detailed information in the map, ILCYM's climate input data are in **.flt** format.

a) Current temperature data

The temperature data used for spatial simulations (present scenario) were obtained from WorldClim available at <http://www.worldclim.org/>. The database is a set of global climate layers (grids) with different spatial resolutions that contains monthly average minimum, maximum and mean temperatures that were

interpolated from historical temperature records worldwide (NOAA data) between 1950 and 2000. The data are well documented in Hijmans et al. (2005). For spatial population simulations and model output validations at different locations (point by point) temperature data directly obtained from local weather stations can be used.

b) Future temperature change data

For simulating population parameters for *P. operculella* for the year 2050 (climate change scenario) ILCYM's input downscaled data to project temperature changes. The predictions based on the WorldClim database are described by Govindasamy et al. (2003). The downscaling of data which was conducted by Ramirez and Jarvis (2010) is freely accessible at <http://gisweb.ciat.cgiar.org/GCMPPage>. ILCYM's was also adapted to input temperature datasets from other sources such as CliMond data base used in CLIMEX software.

c) Temperature data format

The data from WorldClim and majority of available data sources are in **ascii**, **bil** or **ArcGIS** raster files. However ILCYM uses **.flt** data format (float type). When running the potential population mapping in ILCYM you need to convert your input data file in **.flt** using the following steps:

- i) **Converting .tif file in .flt:**
 - **Step 1:** Developing.
 - **Step 2:** Developing.
- ii) **Converting ArcGIS raster files in .flt:** go to ArcGIS package and follow the instructions for converting ArcGIS Raster files to Float.

3.3.5 Spatial simulations and mapping

Below is ILCYM's window shows the inputs and sub-tools.

a) Estimating life table population parameters

ILCYM simultaneously extracts for a selected region the daily or monthly maximum and minimum temperature data for one year (365 days or 12 months

data sets) with their respective geographical coordinates from the database. The extracted temperature data are organized in either in 365x2 (for daily data) or 12x2 (for monthly) matrices using the longitude as column and latitude as rows representing 365 or 12 matrices each for the minimum and maximum temperatures. Thereafter, a point object is created for each geographical coordinate (longitude and latitude) in the form of a table with two columns (the first column includes the minimum temperatures and the second the maximum temperatures that is directly used for spatial phenological simulation. With these temperatures and the phenology model of the species, the generation length, the net reproduction rate, the intrinsic rate of population increase, the finite rate of increase and the doubling time are estimated (Kroschel *et al.* 2013).

Temperature inclusion in the phenology model

Using cosines approximation of temperature, the indices can be mapped under present and projected SRES emission scenarios for predicting responses to present and future climates.

Calculation of Indices

From life table parameters, formulations yielding to three indices are conducted (Kroschel *et al.* 2013).

i) Establishment (survival) index (ERI)

The establishment risk maps visualize the capacity of invasive pest species to establish permanent populations based on spatial and temporal variability in temperature. They assist identifying the regions where a species has the potential to pose an invasive threat after the pest's introduction.

The map plots an index (establishment risk index, ERI), which is the ratio between periods (time intervals) in which population are expected to increase and total periods within a year. The index is defined as the number of time ILCYM 3.0 User Manual 134 intervals with a net reproduction rate, R_0 , above 1 ($I_i=1$) divided by the total number of time intervals within a year (I_i). By default, the maps (as

presented in the atlas) are generated by using a 1-month time scale; however, the calculation can be also based on other time scales (for example, 1-day intervals). The formula for using monthly intervals is as follows:

$$ERI = \frac{\sum_{i=1}^{12} I_i}{I_T}$$

in which I_i is the interval of the month i (with $i = 1, 2, 3, \dots, 12$) and its value is 1 if the population is expected to increase within this interval ($I_i = 1$ if $R_0 \geq 1$) and the value is 0 if the population is expected to decrease ($I_i = 0$ if $R_0 < 1$) according to the established temperature-driven phenology model, and the total number of intervals, I_T , is 12. If the index is calculated on a daily time scale the formula becomes:

$$ERI = \frac{\sum_{i=1}^{365} I_i}{I_T}$$

where I_i than is the interval of day i (with $i = 1, 2, 3, \dots, 365$) and the total number of intervals, I_T , becomes 365.

The ERI takes values between 0 and 1. A ERI=1 represents areas where the specie's population is expected to grow throughout the year. An ERI<1 characterizes areas in which population growth is restricted to certain periods of the year; for example, an ERI=0.25 indicates an area where populations are expected to grow only during 3 month (3/12) of the year and decrease during the other 9 month (9/12).

If the index is used for a prospective antagonist species (p.e. parasitoids) considered for release as a non-native biological control agent, the index expresses the capacity or potential to establish in an area that might be considered for inundative or inoculative release of the species. In these cases, the index represents the establishment

potential of the species, which is desired for long-term control of the target pest species.

Generally, by default, the maps are generated using a monthly time scale that is adequate for multivoltine species; these species have generally a short generation time with overlapping generations. However, such a short time interval is not appropriate for univoltine species, which produce a single generation within a year, because single life stages only develop during certain periods of the year. Hence life table parameters, like the net reproduction rate, calculated for a given period are not representative for the species population development. For estimating the establishment risk of univoltine species, the whole life cycle of the pest need to be simulated throughout the year (at best for several years with real temperature records as input data) using ILCYM's "deterministic simulation" tool. If the population increases during a year the establishment risk can be considered high.

It should be also noted that the index is based on data and information describing the temperature-dependent phenology of the species and the temperature variability observed within a restricted area (generally, the simulation is based on temperature interpolated from historical data). Therefore, the index does not indicate the risk of introduction, which depends on many other factors (potential pathways of introduction). Effects of other biotic or abiotic factors that might depress pest populations are not included in the calculation; for example, the availability of host species. The latter can be addressed by simulating the index only for areas in which pest-specific host plants are produced (i.e. by using the area of production as a filter in GIS modeling, as applied in the potato pest atlas). For pest antagonists, similarly, areas can be filtered by using only areas where the target pest prevails today.

ii) Generation index (*G*)

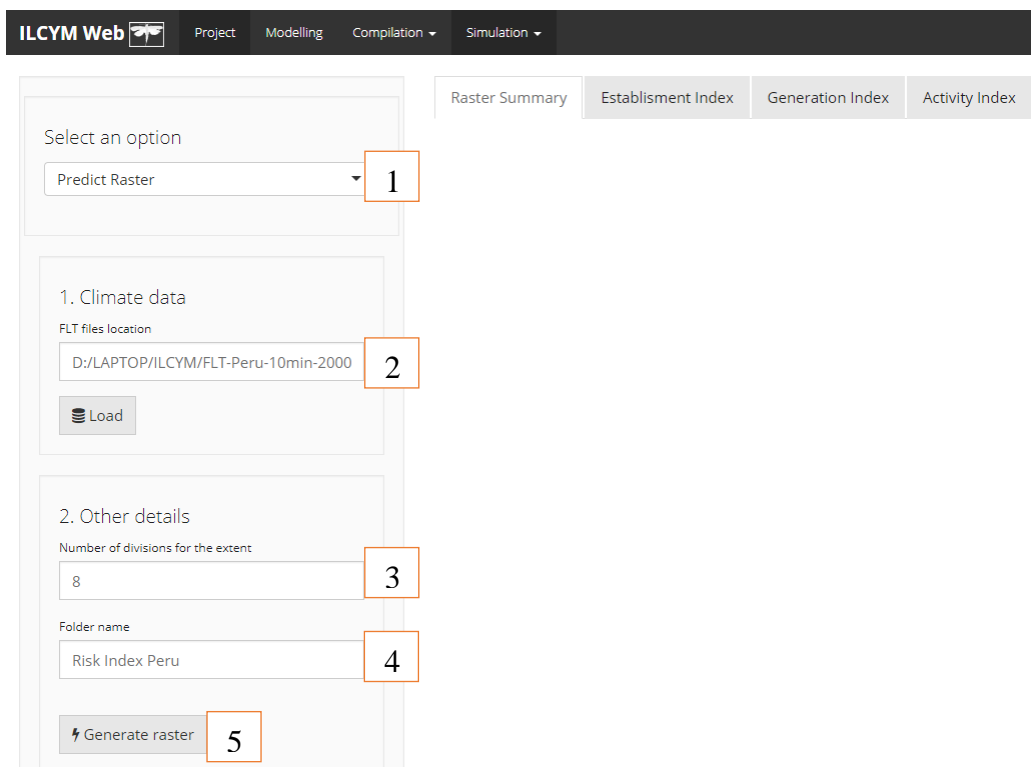
The generation index estimates the mean number of generations that may be produced within a given year. The index is computed by averaging the sum of estimated generation lengths, calculated for each Julian day.

iii) Activity index (A)

This index is explicitly related to the finite rate of population increase, which takes the whole life history of the pest into consideration; for example, an index value of 4 would illustrate a potential population increase by a factor of 10,000 within one year (all other population limiting factors, including food availability, etc., are neglected).

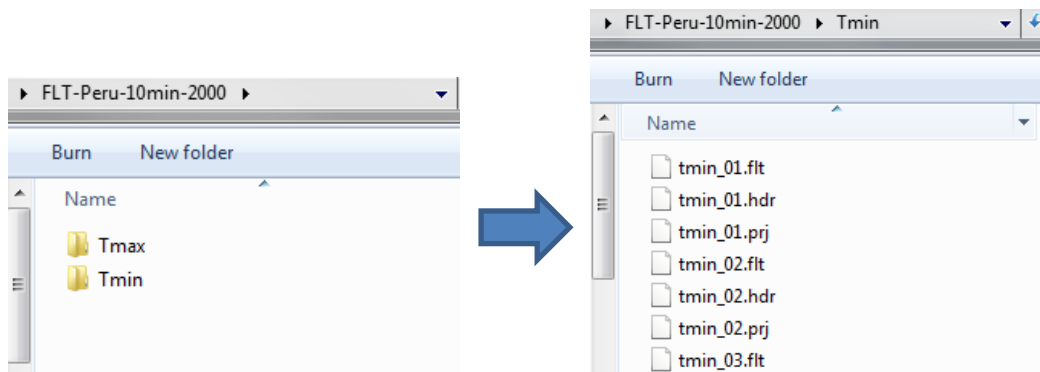
b) Simulation process

Below is ILCYM's window shows the inputs and sub-tools to simulate.



Red box 1: indicates the number of insects to simulate.

Red box 2: this button allows loading the temperature data; this data must be in .flt format. Should select a particular folder that contains 2 sub-folders with the name "Tmin" and "Tmax".



Red box 3: indicates the number of divisions, if the capacity of the computer is low, a greater number of divisions must be selected.

Red box 4: start the spatial simulation process.

c) Indexes mapping

After the simulation, check the histogram to define the intervals of each index (check the maximum value and the variability in the histogram).



Then edit:

Red box 1: indicates the intervals to ERI index (don't change it).

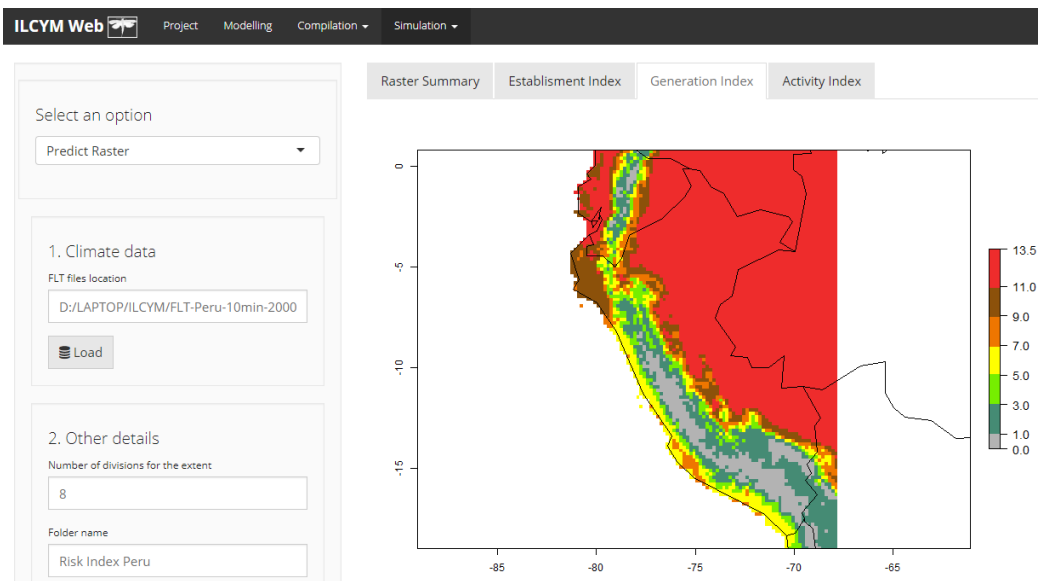
Red box 2: indicates the intervals to GI index (don't remove the commas).

Red box 3: indicates the intervals to AI index (don't remove the commas).

Red box 4: start to generate the risk maps.

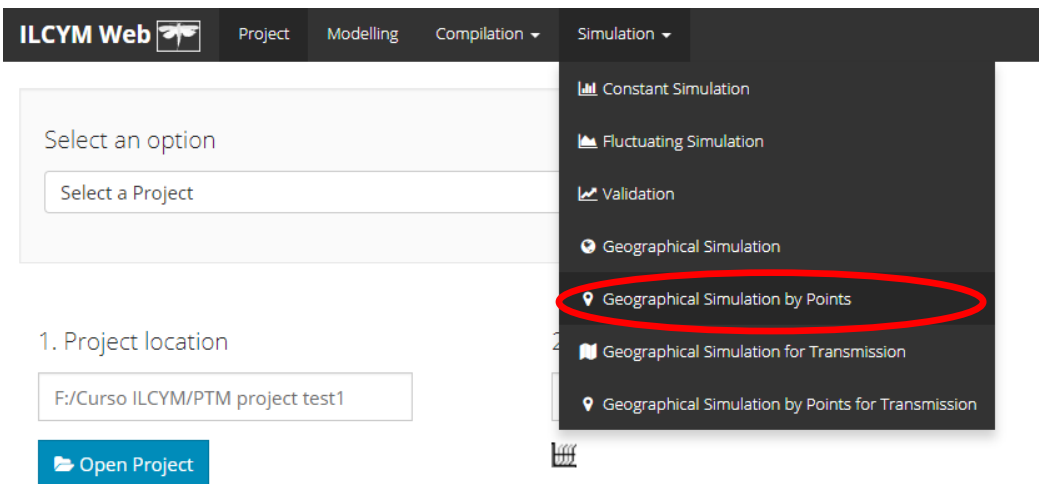
Red box 5: Click in each title to watch the map.

So, the map for each Index is shown (GI as example):

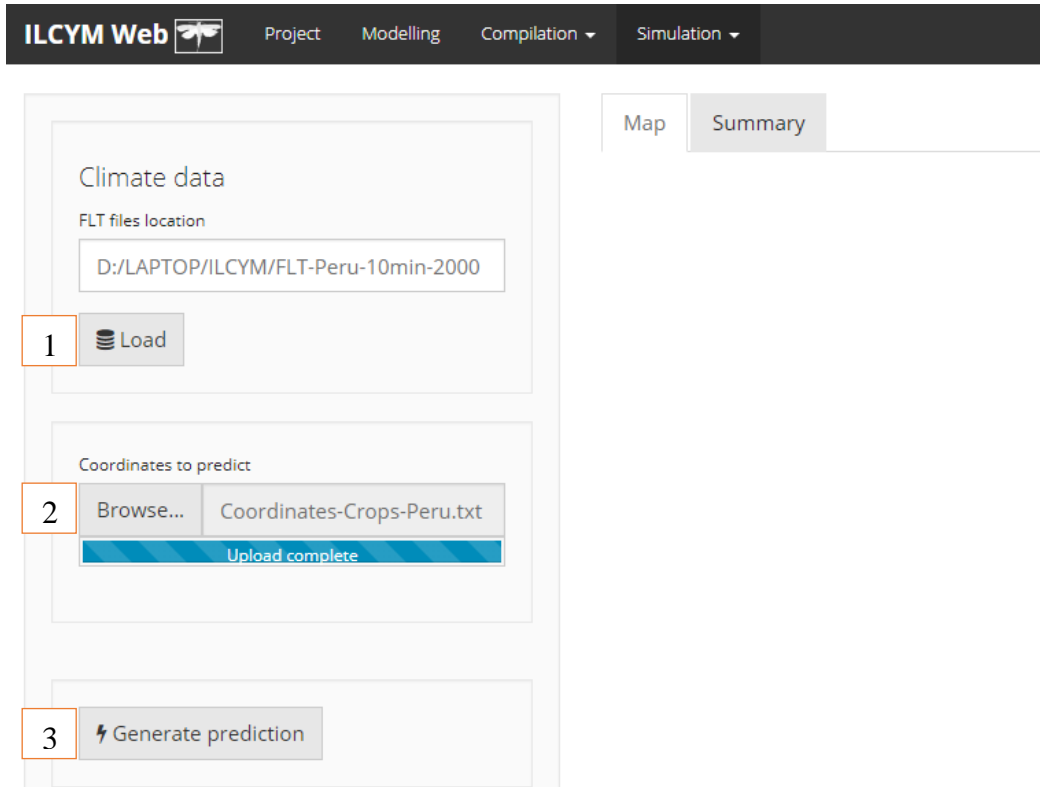


c) Simulation by Points

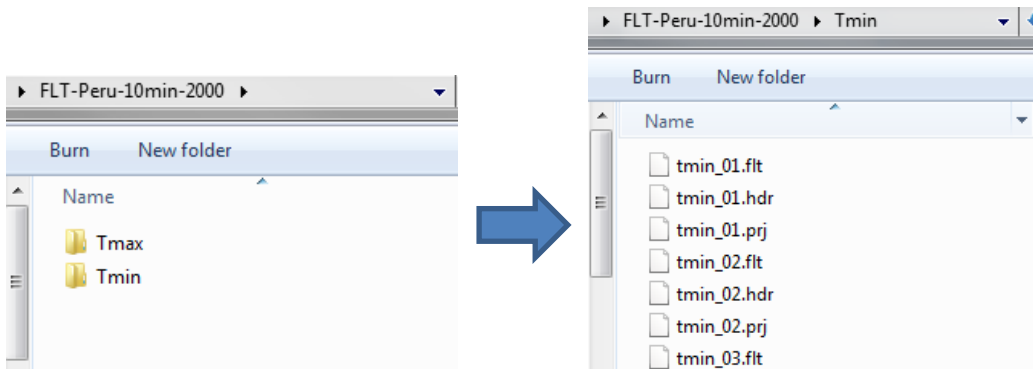
The window below displays how this simulation is done in ILCYM. Under **Simulation** select **Simulation by Points**:



Below is ILCYM's window shows the inputs and sub-tools.



Red box 1: Define the area that contains all points according to Red box 2; this button allows loading the temperature data; this data must be in .flt format. Should select a folder that contains 2 sub-folders with the name “Tmin” and “Tmax”.



Red box 2: this button allows loading the coordinates of all locations; this data must be in daily format. The columns mean longitude and latitude

```

Coordinates-Crops-Peru.txt - Notepad
File Edit Format View Help
|-79.299991      -7.797892
|-75.321897     -11.943649
|-76.317023     -9.962002
|-76.950285     -12.148246
|-75.282318     -15.005898
|-71.347046     -16.372172

```

Red box 3: start the simulation process.

Move the mouse to the points shown, then the indexes for each location or point will show:

The screenshot displays the ILCYM Web interface. At the top, there is a navigation menu with options: Project, Modelling, Compilation, and Simulation. Below this, the interface is divided into two main sections. On the left, there is a control panel with three sections: 'Climate data' with an input field for 'FLT files location' (D:/LAPTOP/ILCYM/FLT-Peru-10min-2000) and a 'Load' button; 'Coordinates to predict' with a 'Browse...' button, a text field containing 'Coordinates-Crops-Peru.txt', and a blue 'Upload complete' button; and a 'Generate prediction' button with a lightning bolt icon. On the right, there is a map of Peru with several blue location pins. A tooltip is visible over one of the pins, displaying the text 'ERI= 1 ; GI= 7.85 ; AI= 12.5'. The map also shows various regions and cities in Peru, such as Quito, Guayaquil, Iquitos, Lima, Cusco, and Arequipa.

I. ILCYM's common errors

4.1 ILCYM's crashing or hanging

Developing

4.2 Loading map

Developing

II. Glossary

Activity Index: This index is used in risk mapping and is explicitly related to the finite rate of population increase.

Actual oviposition time: This term is used to represent the female parasitoid exact length of the oviposition period.

Age Distribution: The proportion of individuals in a population of same age in each class.

Age-Specific Fertility Rate: The number of progenies per individual within a specific age interval during a specified time.

Age-Specific Mortality Rate: The fraction of individuals in a population that die during a given age interval.

Doubling Time: The time it would take a population to double, given no changes in age-specific mortality or fertility rates. Any change in the fertility or the mortality graphs changes doubling time.

Establishment Risk Index: This index is used in risk mapping and identifies those areas in which an insect pest may survive. The index is 1 when a certain proportion of all immature life stages of the pest survive throughout the year.

Finite Rate of Increase (Lambda): A measure of the rate of growth of a population. The amount that the population must be multiplied by to give the population size in the next time unit (assuming the population is in stable age distribution) .

Generation Index: This index is used in risk mapping and estimates the mean number of generations that may be produced within a year.

Generation Time: The average age at which a female gives birth to her offspring. This is equivalent to the time that it takes for a population to increase by a factor equal to the Net Reproductive Rate.

Intrinsic Rate of Increase (rm): A measure of the rate of growth of a population. This is the instantaneous rate of change (per individual per time interval), assuming the population is in stable age distribution. It is equal to the natural log (ln) of the Finite Rate of Increase.

Mean Life Expectancy: How long an individual can be expected to live, on average. This is influenced only by the age-specific mortality graph.

Net Reproductive Rate (Ro): The average number of offspring an individual in a population will produce in his/her lifetime. Unlike the Total Fertility Rate, Ro depends on age specific mortality rates.

Sex Ratio: The fraction of the population that is female. Technically, this value is not a "ratio", but this has become a common way of representing the gender distribution of a population. The primary sex ratio is the proportion of births that are female.

Stable Age Distribution: The age distribution which the population will reach if allowed to progress until there is no longer a change in the distribution.

Survivorship: The probability that an individual survives from age zero to a given age.

Total Fertility Rate (TFR): The total number of offspring a female would have, on average, if she were to live to the maximum age (Compare with Net Reproductive Rate).

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Appendix

Table 1. Functions fitted to development time in ILCYM software

ID	Function	Expression	Reference
Dichotomy functions			
1	Logit	$F_i(X_1) = P(Y = 1 / X_1, X_{2i}) = \frac{1}{1 + e^{-(B_1 X_1 + B_{2i} X_{2i})}}$	
2	Probit	$E[Y / X] = P(Y = 1 / X_1, X_{2i}) = \int_{-\infty}^z \frac{1}{\sqrt{2\pi}} e^{-\frac{t^2}{2}} dt$ $Z = B_1 X_1 + B_{2i} X_{2i}$ $F_i(X_1) = E[Y / X] = \Phi(Z) = \Phi(B_1 X_1 + B_{2i} X_{2i})$ $\Phi^{-1}(P(Y = 1 / X_1, X_{2i})) = B_1 X_1 + B_{2i} X_{2i}$	
3	Cloglog	$F_i(X_1) = P(Y = 1 / X_1, X_2) = 1 - e^{-e^{(B_1 X_1 + B_{2i} X_{2i})}}$ $\ln(-\ln(P(Y = 1))) = B_1 X_1 + B_{2i} X_{2i}$	
Exponential functions			
1	Exponential modified 1	$F(X_1) = 1 - e^{-(a * X_1 + b * X_1^2 + c * X_1^3)}$	
2	Gamma	$f(x) = \frac{1}{b^a * \Gamma(a)} T^{a-1} e^{-\left(\frac{x}{b}\right)}$ $F(X_1) = \int_0^{X_1} (f(x)) dx$	
3	Exponential modified 2	$F(X_1) = \frac{1}{1 + e^{(a+b * X_1)}}$	

4	Exponential modified 3	$F(X_1) = 1 - e^{-a^*X_1^b}$	
5	Exponential modified 4	$F(X_1) = 1 - e^{-\left(\frac{X_1-a}{n}\right)^b}$	
6	Weibull	$F(X_1) = 1 - e^{-\left(\frac{X_1}{b}\right)^a}$	

For dichotomy functions:

X_1 = natural logarithm of the days observed

X_{2i} = *ith* temperature, considered as a categorical variable, so that the value to replace in the linear part of formula is either 0 or 1.

$Y = \begin{cases} \text{success}(1): \text{The state lasted until the individual turn to next state} \\ \text{failure}(0): \text{The state does not change or the individual died before adulthood} \end{cases}$

For exponential functions:

$F_i(X_1)$ = cumulated relative frequency of the days observed for the *ith* temperature

X_1 = normalized age (days / median survival time) of each temperature

$F(X_1)$ = cumulated relative frequency of the days observed of each temperature

Table 2. Sub-models fitted to development rate in ILCYM software

ID	Name	Equation	Comment	Reference
1	Sharpe & DeMichele 1	$r(T) = \frac{p' \cdot \frac{T}{T_o'} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_o'} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T} \right) \right]} + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T} \right) \right]}}$ $p' = a + b * T_o'$ $T_o' = \frac{\Delta H_L - \Delta H_H}{R * \log \left(-\frac{\Delta H_L}{\Delta H_H} \right) + \left(\frac{\Delta H_L}{T_L} \right) - \left(\frac{\Delta H_H}{T_L} \right)}$	5P	
2	Sharpe & DeMichele 2	$r(T) = \frac{p' \cdot \frac{T}{T_o} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_o} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T} \right) \right]} + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T} \right) \right]}}$ $p' = a + b * T_o$	6P	
3	Sharpe & DeMichele 3	$r(T) = \frac{p \cdot \frac{T}{T_o} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_o} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T} \right) \right]} + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T} \right) \right]}}$	7P	Sharpe and DeMichele 1977
4	Sharpe & DeMichele 4	$r(T) = p \cdot \frac{T}{T_o} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_o} - \frac{1}{T} \right) \right]}$	3P	

5	Sharpe & DeMichele 5	$r(T) = \frac{p \cdot \frac{T}{T_0} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T} \right) \right]}}$	5P	
6	Sharpe & DeMichele 6	$r(T) = \frac{p \cdot \frac{T}{T_0} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T} \right) \right]}}$	5P	
7	Sharpe & DeMichele 7	$r(T) = p' \cdot \frac{T}{T_0} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T} \right) \right]}$ $p' = a + b \cdot T_0'$	2P	

8	Sharpe & DeMichele 8	$r(T) = \frac{p' \cdot \frac{T}{T_0} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T} \right) \right]}}$ $p' = a + b \cdot T_0'$	4P	
9	Sharpe & DeMichele 9	$r(T) = \frac{p' \cdot \frac{T}{T_0} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T} \right) \right]}}$ $p' = a + b \cdot T_0'$	4P	
10	Sharpe & DeMichele 10	$r(T) = \frac{p \cdot \frac{T}{T_0} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T} \right) \right]} + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T} \right) \right]}}$ $H_H' = 1 \quad T_H' = 1$	4P	Sporleder <i>et al.</i> (2004)
11	Sharpe & DeMichele 11	$r(T) = \frac{p^* \cdot \frac{T}{T_0} \cdot e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T} \right) \right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T} \right) \right]} + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T} \right) \right]}}$	6P	

12	Sharpe & DeMichele 12	$r(T) = \frac{P' * \frac{T}{T_0} * e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T}\right)\right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T}\right)\right]} + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T}\right)\right]}}$ $P' = a + b * T_0$	5P	
13	Sharpe & DeMichele 13	$r(T) = \frac{P * \frac{T}{T_0} * e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T}\right)\right]}}{1 + e^{\left[\frac{\Delta H_L}{R} \left(\frac{1}{T_L} - \frac{1}{T}\right)\right]}}$	4P	
14	Sharpe & DeMichele 14	$r(T) = \frac{P * \frac{T}{T_0} * e^{\left[\frac{\Delta H_A}{R} \left(\frac{1}{T_0} - \frac{1}{T}\right)\right]}}{1 + e^{\left[\frac{\Delta H_H}{R} \left(\frac{1}{T_H} - \frac{1}{T}\right)\right]}}$	4P	

15	Deva 1	$r(T) = b(T - T_{\min}) \quad T \geq T_{\max}$ $r(T) = 0 \quad T < T_{\max}$	2P	Dallwits and Higgins 1992
16	Deva 2	$r(T) = b_1 (10^{-v^2}) (1 - b_5 + b_5 v^2)$ $v = \frac{(u + e^{b_4(u)})}{c_2} \quad u = \frac{(T - b_3)}{(b_3 - b_2)} - c_1$ $c_1 = \frac{1}{1 + 0.28b_4 + 0.72 \ln(1 + b_4)} \quad c_2 = \frac{1 + b_4}{1 + 1.5b_4 + 0.39b_4^2}$	5P	Dallwits and Higgins 1992
17	Logan 1	$r(T) = Y * (e^{p*T} - e^{\left(p*T_{\max} - \frac{(T_{\max} - T)}{v}\right)})$	4P	Longan 1976
18	Logan 2	$r(T) = \alpha \left(\frac{1}{1 + k * e^{-p*T}} - e^{-\frac{(T_{\max} - T)}{v}} \right)$	5P	Longan 1976
19	Briere 1	$r(T) = a * T(T - T_o) \left(\sqrt{T_{\max} - T} \right)$	3P T ≤ Tmax	Briere et al. 1999
20	Briere 2	$r(T) = a * T(T - T_o) (T_{\max} - T)^d$	d ∈ Z → T ∈ R d ∉ Z → T ≤ Tmax	Briere et al. 1999
21	Stinner 1	$r(T) = \frac{R_{\max} \left(1 + e^{k_1 + k_2 (T_{opc})} \right)}{1 + e^{k_1 + k_2 (T)}}$	4P	Stinner et al. 1974
22	Hilber & logan 1	$r(T) = Y \left(\frac{T^2}{T^2 + d^2} - e^{-\frac{(T_{\max} - T)}{v}} \right)$	4P	Hilber and logan 1983
23	Lactin 1	$r(T) = e^{p*T} - e^{-\frac{(p*T_i - (T - T_i))}{dt}} + \lambda$	4P	Lactin et al. 1995
24	Linear	$r(T) = a + b * T$	2P	
25	Exponential simple	$r(T) = b_1 * e^{b_2 * T}$	2P	
26	Tb model	$r(T) = sy * e^{\left(b(T - T_b) - e^{\left(\frac{b(T - T_b)}{DT_b} \right)} \right)}$	4P	
27	Exponential model	$r(T) = sy * e^{b(T - T_b)}$	3P	
28	Exponential	$r(T) = e^{b(T - T_{\min})} - 1$	2P	
29	Ratkowsky 1	$r(T) = b(T - T_b)^2$	2P	Ratkowsky et al. 1982
30	Davidson	$r(T) = \frac{k}{1 + e^{a - bT}}$	2P	Davidson 1942, 1944

31	Pradham	$r(T) = R_m e^{\left[\frac{-1}{2} \left(\frac{T-T_m}{T_\sigma} \right)^2 \right]}$	3P	Pradham 1945
32	Angilletta Jr.	$r(T) = a * e^{\left[\frac{-1}{2} \left(\frac{ T-b }{c} \right)^d \right]}$	4P	Angilletta Jr. 2006
33	Stinner 2	$r(T) = \frac{MaxDevRate * e^{k_1+k_2T_{opt}}}{1 + e^{k_1+k_2T}}$	4P	Stinner 1974
34	Hilbert	$r(T) = \Psi \left[\frac{(T - T_b)^2}{((T - T_b) + D^2)} \right] - e^{-\frac{(T_m - (T - T_b))}{\Delta T}}$	5P	Hilbert and Logan 1983
35	Lactin 2	$r(T) = e^{\rho T} - e^{\left(\rho T_{Max} - \frac{T_{Max} - T}{\Delta} \right)}$	5P	Lactin et al. 1995
36	Anlytis 1	$r(T) = P\delta^n (1 - \delta)^m \quad \delta = \frac{T - T_{min}}{T_{max} - T_{min}}$	5P n ∈ Z → T ∈ R m ∈ Z → T ∈ R n ∉ Z → T ≥ Tmin m ∉ Z → T ≤ Tmx	Analysis 1977
37	Anlytis 2	$r(T) = [P\delta^n (1 - \delta)^m] \quad \delta = \frac{T - T_{min}}{T_{max} - T_{min}}$	5P n ∈ Z → T ∈ R m ∈ Z → T ∈ R n ∉ Z → T ≥ Tmin m ∉ Z → T ≤ Tmx	Analysis 1980
38	Anlytis 3	$r(T) = a(T - T_{min})^n (T_{max} - T)^m$	5P n ∈ Z → T ∈ R m ∈ Z → T ∈ R n ∉ Z → T ≥ Tmin m ∉ Z → T ≤ Tmx	Analysis 1977
39	Allahyari	$r(T) = P\delta^n (1 - \delta^m) \quad \delta = \frac{T - T_{min}}{T_{max} - T_{min}}$	5P n ∈ Z → T ∈ R m ∈ Z → T ∈ R n ∉ Z → T ≥ Tmin m ∉ Z → T ≥ Tmin	Allahyari 2005
40	Briere 3	$r(T) = a(T - T_b)(T_L - T)^{\frac{1}{2}}$	3P	Briere et al. 1999
41	Briere 4	$r(T) = a(T - T_b)(T_L - T)^{\frac{1}{n}} \quad T \leq T_L$	3P	Briere et al. 1999

42	Kontodimas 1	$r(T) = a(T - T_{\min})^2(T_{\max} - T)$	3P	Kontodimas 2004
43	Kontodimas 2	$r(T) = \frac{2}{D_{\min}(e^{K(T-T_{opt})} + e^{-\lambda(T-T_{opt})})}$	4 P	Kontodimas 2004
44	Kontodimas 3	$r(T) = \frac{T * e^{\left(\frac{a-b}{T}\right)}}{1 + e^{\left(\frac{c-d}{T}\right)} + e^{\left(\frac{f-g}{T}\right)}}$	6P	Kontodimas 2004
45	Ratkowsky 2	$r(T) = \left[a(T - T_{\min}) \left(1 - e^{b(T - T_{\max})} \right) \right]^2$	4P	Ratkowsky et al. 1982
46	Janish 1	$r(T) = \frac{2}{D_{\min}(e^{K(T-T_{opt})} + e^{-K(T-T_{opt})})}$	3P	
47	Janish 2	$r(T) = \frac{2C}{a^{(T-T_m)} + b^{(T_m-T)}}$	3P	
48	Tanigoshi	$r(T) = a_0 + a_1T + a_2T^2 + a_3T^3$	4P	Tanigoshi and Browne 2004
49	Wang-Lan-Ding	$r(T) = k \frac{\left(1 - e^{-a(T-T_{\min})} \right) \left(1 - e^{b(T-T_{\max})} \right)}{1 + e^{-r(T-c)}}$	7P	Wang et al. 1982
50	Stinner 3	$r(T) = \frac{c_1}{1 + e^{(k_1+k_2*T)}}$	3P	
51	Stinner 4	$r(T) = \frac{c_1}{1 + e^{(k_1+k_2*T)}} + \frac{c_2}{1 + e^{(k_1+k_2(2*T_0-T))}}$	5P	
52	Logan 3	$r(T) = sy * e^{\left(b(T-T_{\min}) - e^{\left(b*T_{\max} - \frac{(T_{\max} - (T - T_{\min}))}{Db} \right)} \right)}$	5P	
53	Logan 4	$r(T) = \alpha \left(\frac{1}{1 + k * e^{-b(T-T_{\min})}} - e^{-\frac{(T_{\max} - (T - T_{\min}))}{Dt}} \right)$	5P	

54	Logan-5	$r(T) = \alpha \left(\frac{1}{1 + k * e^{-b(T)}} - e^{-\frac{(T_{max}-T)}{Dt}} \right)$	6P	
55	Hilber & logan 2	$r(T) = \psi \left(\frac{T^2}{T^2 + D} - e^{-\frac{(T_{max}-T)}{Dt}} \right)$	4P	
56	Hilber & logan 3	$r(T) = \psi \left(\frac{(T - T_{min})^2}{(T - T_{min})^2 + D} - e^{-\frac{(T_{max} - (T - T_{min}))}{Dt}} \right) + \theta$	6P	
57	Taylor	$r(T) = r_m * e^{-\frac{1}{2} \left(\frac{T - T_{opt}}{T_{roh}} \right)^2}$	3P	
58	Lactin 3	$r(T) = e^{\rho * T} - e^{\left(\rho * T_{Max} - \frac{T_{Max} - T}{\Delta} \right)} + \lambda$	4P	
59	Sigmoid or Logistic	$r(T) = \frac{c_1}{1 + e^{a+b*T}}$	3P	

- T temperature in Degree Celcius

- $r(T)$ development rate at temperature T

$R = 1987 \text{ cal degree}^{-1} \text{ mol}^{-1}$

Table 3. Sub-models fitted to mortality in ILCYM software

ID	Model	Equation	Comment	Reference
1	Quadratic	$m(T) = c + b * T + a * T^2$	3P	
2	Linear root	$m(T) = c + b * T + a(\sqrt{T})$	3P	
3	Negative Linear root	$m(T) = c + b * T + a\left(\frac{1}{\sqrt{T}}\right)$	3P	
4	Quadratic negative exponent	$m(T) = c + b * T + a\left(\frac{1}{T^2}\right)$	3P	
5	Linear negative exponent	$m(T) = c + b * T + a\left(\frac{1}{T}\right)$	3P	
6	Logarithmic	$m(T) = c + b * T + a * \log(T)$	3P $T \geq 0$	
7	Gaussian denominator	$m(T) = \frac{1}{1 + a * e^{-b\left(\frac{T-c}{d}\right)^2}}$	4P	
8	Gaussian	$m(T) = a * e^{-b\left(\frac{T-T_0}{c}\right)^2}$	4P	
9	Simple gaussian	$m(T) = y_0 + a * e^{-\frac{1}{2}\left(\frac{T-T_0}{b}\right)^2}$	4P	
10	Gaussian with log	$m(T) = y_0 + a * e^{-\frac{1}{2}\left(\frac{\log\left(\frac{T}{T_0}\right)}{b}\right)^2}$	4P	
11	Polynomial model 1	$m(T) = b_1 + b_2 T + b_3 T^d$	4P $d \in \mathbb{Z} \rightarrow T \in \mathbb{R}$ $d \notin \mathbb{Z} \rightarrow T \geq 0$	
12	Polynomial model 2	$m(T) = e^{(b_1 + b_2 * T + b_3 * T^2)}$	3P	

13	Polynomial model 3	$m(T) = 1 - \left(\frac{b_4}{1 + b_5 * e^{(b_1 + b_2 * T + b_3 * T^2)}} \right)$	5P	
14	Polynomial model 4	$m(T) = e^{(b_1 + b_2 * T + b_3 * \sqrt{T})}$	$T \geq 0$	
15	Polynomial model 5	$m(T) = 1 - \left(\frac{b_4}{1 + b_5 * e^{(b_1 + b_2 * T + b_3 * \sqrt{T})}} \right)$	3P $T \geq 0$	
16	Polynomial model 6	$m(T) = e^{(b_1 + b_2 * T + b_3 * (\frac{1}{\sqrt{T}}))}$	3P $T > 0$	
17	Polynomial model 7	$m(T) = 1 - \left(\frac{b_4}{1 + b_5 * e^{(b_1 + b_2 * T + b_3 * (\frac{1}{\sqrt{T}}))}} \right)$	5P $T > 0$	
18	Polynomial model 8	$m(T) = e^{(b_1 + b_2 * T + b_3 * (\frac{1}{T}))}$	3P $T \neq 0$	
19	Polynomial model 9	$m(T) = 1 - \left(\frac{b_4}{1 + b_5 * e^{(b_1 + b_2 * T + b_3 * (\frac{1}{T}))}} \right)$	5P	
20	Polynomial model 10	$m(T) = e^{(b_1 + b_2 * T + b_3 * T^d)}$	4P $d \in \mathbb{Z} \rightarrow T \in \mathbb{R}$ $d \notin \mathbb{Z} \rightarrow T \geq 0$	
21	Polynomial model 11	$m(T) = 1 - \left(\frac{b_4}{1 + b_5 * e^{(b_1 + b_2 * T + b_3 * T^d)}} \right)$	6P $d \in \mathbb{Z} \rightarrow T \in \mathbb{R}$ $d \notin \mathbb{Z} \rightarrow T \geq 0$	
22	Polynomial model 12	$m(T) = e^{(b_1 + b_2 * T + b_3 * \log(T))}$	3P $T \geq 0$	
23	Polynomial model 13	$m(T) = 1 - \left(\frac{b_4}{1 + b_5 * e^{(b_1 + b_2 * T + b_3 * \log(T))}} \right)$	5P $T \geq 0$	

24	Taylor 1	$m(T) = 1 - rm^* e^{\left(-\frac{1}{2} \left(\frac{T - T_{opt}}{T_{roh}}\right)^2\right)}$	3P	
25	Taylor 2	$m(T) = 1 - rm^* e^{\left(-\frac{1}{2} \left(\frac{\ln(T) - \ln(T_{opt})}{T_{roh}}\right)^2\right)}$	3PT ≥ 0	
26	Wang 1	$m(T) = 1 - \frac{1}{e^{\left(\left(1 + e^{\left(\frac{T - T_{opt}}{B}\right)}\right)\left(1 + e^{\left(\frac{T_{opt} - T}{B}\right)}\right)^* H\right)}}$	3P	
27	Wang 2	$m(T) = 1 - \frac{1}{e^{\left(\left(1 + e^{\left(\frac{T - T_l}{B}\right)}\right)\left(1 + e^{\left(\frac{T_h - T}{B}\right)}\right)^* H\right)}}$	4P	
28	Wang 3	$m(T) = 1 - \frac{1}{e^{\left(\left(1 + e^{\left(\frac{T - T_{opt}}{B_l}\right)}\right)\left(1 + e^{\left(\frac{T_{opt} - T}{B_h}\right)}\right)^* H\right)}}$	4P	
29	Wang 4	$m(T) = 1 - \frac{1}{e^{\left(\left(1 + e^{\left(\frac{T - T_l}{B_l}\right)}\right)\left(1 + e^{\left(\frac{T_h - T}{B_h}\right)}\right)^* H\right)}}$	5P	
30	Wang 5	$m(T) = 1 - \frac{H}{e^{\left(\left(1 + e^{\left(\frac{T - T_{opt}}{B}\right)}\right)\left(1 + e^{\left(\frac{T_{opt} - T}{B}\right)}\right)\right)}}$	3P	
31	Wang 6	$m(T) = 1 - \frac{H}{e^{\left(\left(1 + e^{\left(\frac{T - T_l}{B}\right)}\right)\left(1 + e^{\left(\frac{T_h - T}{B}\right)}\right)^* H\right)}}$	4P	
32	Wang 7	$m(T) = 1 - \frac{H}{e^{\left(\left(1 + e^{\left(\frac{T - T_{opt}}{B_l}\right)}\right)\left(1 + e^{\left(\frac{T_{opt} - T}{B_h}\right)}\right)^* H\right)}}$	4P	

33	Wang 8	$m(T) = 1 - \frac{H}{e^{\left(\left(1 + e^{\left(\frac{T-T_l}{B_l} \right)} \right) \left(1 + e^{\left(\frac{T_h-T}{B_h} \right)} \right) \right) * H}}$	5P	
34	Shape	$m(T) = Bm + \left(\left(1 - \left(\frac{1}{1 + e^A + e^B} \right) \right) * (1 - Bm) \right)$ $A = \left(\frac{H_l}{1.987} \right) * \left(\left(\frac{1}{T_l} \right) - \left(\frac{1}{(T + 273.15)} \right) \right)$ $B = \left(\frac{H_h}{1.987} \right) * \left(\left(\frac{1}{T_h} \right) - \left(\frac{1}{(T + 273.15)} \right) \right)$	5P	
35	Marc	$m(T) = \left(1 - e^{-e^{(a_1 + b_1 * T)}} \right) + \left(1 - e^{-e^{(a_2 + b_2 * T)}} \right)$	4P	
36	DeMoivre	$m(T) = (w - T)^{-1}$	1P	
37	Gompertz	$m(T) = a_1 * e^{(b_1 * T)} + a_2 * e^{(b_2 * T)}$	4P	
38	Gompertz-Makeham	$m(T) = a_1 * e^{(b_1 * T)} + a_2 * e^{(b_2 * T)} + c_1$	5P	
39	Weibull	$m(T) = a * (T - b)^n$	3P	
40	Briere 1	$m(T) = a * T(T - T_0)(T_l - T)^{\left(\frac{1}{d} \right)}$	4P T ≤ Tl	
41	Briere 2	$m(T) = e^{\left(a * T(T - T_0)(T_l - T)^{\frac{1}{d}} \right)}$	4P T ≤ Tl	
42	Analytis	$m(T) = a(T - T_{\min})^n (T_{\max} - T)^m$	5P n ∈ Z → T ∈ R m ∈ Z → T ∈ R n ∉ Z → T ≥ Tmi n m ∉ Z → T ≤ Tmax	

43	Janisch & Analytis	$m(T) = \frac{1}{\left(\frac{D_{\min}}{2}\right) \left(e^{k(T-T_p)} + e^{-\lambda(T-T_p)}\right)}$	4P	
44	Wang 9	$m(T) = a \left(1 - \left(e^{\left(\frac{T-T_l}{B}\right)} \right) \left(1 - \left(e^{\left(\frac{T_h-T}{B}\right)} \right) \right) \right)$	4P	
45	Wang 10	$m(T) = e^{\left(a \left(1 - \left(e^{\left(\frac{T-T_l}{B}\right)} \right) \left(1 - \left(e^{\left(\frac{T_h-T}{B}\right)} \right) \right) \right) \right)}$	5P	

- T

temperature in Celcius

- $m(T)$ mortality function at temperature

Table 4. Sub-models fitted to adult senescence in ILCYM software

The sub-models fitted to adult senescence in ILCYM software are the same (they also maintain their respective ID) as shown in Table 2 excluding the sub-models listed below:

ID	Name
1	Sharpe & DeMichele 1
2	Sharpe & DeMichele 2
3	Sharpe & DeMichele 3
4	Sharpe & DeMichele 4
5	Sharpe & DeMichele 5
6	Sharpe & DeMichele 6
7	Sharpe & DeMichele 7
8	Sharpe & DeMichele 8
9	Sharpe & DeMichele 9
10	Sharpe & DeMichele 10
15	Deva 1
16	Deva 2
17	Logan 1
18	Logan 2
19	Briere 1
20	Briere 2
21	Stinner
22	Hilber & logan
23	Lactin 1
36	Anlytis 1
37	Anlytis 2

38	Anlytis 3
39	Allahyari
40	Briere 3
41	Briere 4
42	Kontodimas 1
43	Kontodimas 2
45	Ratkowsky 2

Table 5. Sub-models fitted to total oviposition in ILCYM software

The sub-models fitted to adult total oviposition in ILCYM software are the same (they also maintain their respective ID) as shown in Table 3 without the sub-models listed below:

ID	Name
26	Wang 1
27	Wang 2
28	Wang 3
29	Wang 4
35	Marc
36	DeMoivre

Table 6. Functions fitted to relative oviposition in ILCYM software

ID	Function	Expression	Reference
1	Exponential modified 1	$l(T) = 1 - e^{-(a*T + b*T^2 + c*T^3)}$	
2	Gamma	$f(x) = \frac{1}{b^a * \Gamma(a)} T^{a-1} e^{-\left(\frac{x}{b}\right)}$ $l(T) = \int_0^T (f(x)) dx$	
3	Exponential modified 2	$l(T) = \frac{1}{1 + e^{(a+b*T)}}$	
4	Exponential modified 3	$l(T) = 1 - e^{-a*T^b}$	
5	Exponential modified 4	$l(T) = 1 - e^{-\left(\frac{T-a}{n}\right)^b}$	
6	Weibull	$l(T) = 1 - e^{-\left(\frac{T}{b}\right)^a}$	

- T temperature in Celcius

- $l(T)$ relative oviposition function at temperature

Table 7. Functions fitted to oviposition time in ILCYM software

The functions fitted to parasitoid oviposition time in ILCYM software are the same (they also maintain their respective ID) as in shown Table 6.

Table 8. Sub-models fitted to temperature parasitoid rate in ILCYM software

The sub-models fitted to temperature dependent parasitoid rate in ILCYM software are the same (they also maintain their respective ID) as shown in Table 3.