An algorithm for data reconstruction from published articles – Application on insect life tables

D.N. Kareithi¹,²*, D. Salifu¹, N. Owuor², S. Subramanian¹ and E.Z.H. Tonnang³

Abstract: Data collection in life table experiments is generally time-consuming and costly such that data reconstruction of published information provides an avenue to access the original data for purposes of further investigation. In this paper, we present an algorithm that reconstructs life table raw data using a summary of results from published articles. We present the steps of the development and implementation (in the R computer language) of the algorithm, its scope of application, assumptions, and limitations. Statistical background of the algorithm is also presented. The developed algorithm was then applied to reconstruction of life table data of two insect species, Chilo partellus and Busseola fusca, from published information. Welch’s two-sample t-test was applied to test the difference between the original and reconstructed data of the insect life stages. C. Partellus results were not significantly different, but, for B. fusca, pupa development time, and larva and pupa development rate were significantly different at the 95% confidence level. It is concluded that the algorithm could be used to reconstruct original data sets from cohort life table data sets of insects, given published information and sample sizes.

Subjects: Science; Mathematics & Statistics; Applied Mathematics; Mathematics for Biology & Medicine; Mathematical Biology

Keywords: data reconstruction; cohort studies; life tables; algorithm

1. Introduction

Insect life tables are a convenient method for summarizing the amount of mortality in each generation of an insect population. Generally, life table data provide a detailed description of the...
survivorship, development, and expectation of life and gives the researcher an opportunity to assess and evaluate the impact of various factors on the population (Carey, 2001). In the study of populations, life tables are usually used to highlight the various growth parameters in the life history of the species. The construction of a life table is an important component in understanding the population dynamics (demography and biology) of a species as explained by Deevey (1947).

Life table data, unlike other data collected for research, is collected in stages, starting from birth, then continuing with frequent observations on the demographical processes of the population of the species under study. These demographic processes include births, life stages, deaths, emigration, evolving, and any other process that affects the sample size and composition of the population. The timing and frequency of these processes are the interests in a life table, adopting the time of these events as indicators of interest. Life table data collected over a specific time period is called a time-specific life table (Carey, 2001). A longitudinal perspective and follow-up of a generation of a population from birth through the consecutive ages till death of all individuals in the generation is known as a cohort life table (Carey, 2001). Both categories can either be complete or be abridged, where complete means the functions are computed for each day of life while an abridged life table deals with age intervals greater than 1 day, such as over a complete stage (Bellows, Von Driesche, & Elkinton, 1992; Deevey, 1947). The distinction between complete and abridged has solely to do with the length of the time period considered.

Once a population of interest is chosen and an observation time period is defined, the construction of a life table generally involves the following five phases (Deevey, 1947; Dublin, Lotka, & Spiegelman, 1950): select a sample size and depending on a factor the species is exposed to, observe and record the current stage of the population, observe and record the number of individuals alive at each stage, calculate the number dead at each stage, and observe and record the duration of each stage.

Preparation of life tables, therefore, requires considerable resources and time as several subjects are followed over time. The availability of data obtained from research activities is a challenge that continues to persist. Data reconstruction techniques provide an opportunity to obtain information from published studies. Existing studies on data reconstruction have focused largely on geographical information system, such as reconstruction of maps, image reconstruction (Ediev & Gisser, 2007), genotype data (Stephens et al., 2001; Stephens & Donnelly, 2003), and dose response for patients (Kahneman, Krueger, Schkade, Schwarz, & Stone, 2004). Methodological difficulties have been pointed out as one of the challenges in reconstructing data from multiple published articles (Kita, 1993). Sometimes source articles from which the data is to be reconstructed may not have complete information. Another challenge to data reconstruction is that published articles report data in intervals, for example, 6-month intervals or an age range, a mean age, and breaking it down or re-estimating the values to fit in time step of a day interval require much time and skill (Kita, 1993). Another difficulty in using published or reported data is the problem of dealing with gross errors, misreporting, and coverage errors (Ediev & Gisser, 2007). Further, the inability to confirm the findings by comparing results from the reconstruction to real collected information poses a challenge.

In pest management, life tables provide an important tool in understanding the changes in the population of insect pests during different developmental stages throughout their life stages. Life tables may reveal when a pest population suffers high mortality. Such knowledge can be used to make time-based application of intervention for the management of the insect pest. Data collection in life table studies is generally time-consuming and costly such that if such data are available in publications and one would wish to carry out further research on them, reconstruction of the original data would be an advantage and economical as compared to repeating the data collection. This paper, therefore, presents an algorithm that has been developed for reconstruction of published lifetable data that can be used by researchers in pest management science.

We describe how the algorithm can be applied in reconstructing life tables on published mortality rates, development rate, and total oviposition per female of an insect species. We assess
the effectiveness and accuracy of the algorithm by replicating the original analyses using the reconstructed data. The results are discussed in light of opportunities, limitations, and implications of the use of the algorithm in life table data.

1.1. Life stages of invertebrates
Life tables of vertebrates such as fishes, amphibians, reptiles, birds, and mammals have no well-structured or defined life stages, while invertebrates such as arthropods and worms have specific and defined life stages from inception till death. Some of the most common stages are discussed in the following section.

1.2. Egg
The egg stage begins with the females of the population under study laying eggs after fertilization. For insects and other animals, the eggs can be laid either internally or externally (eggs laid on leaves, in water, or on the ground, for example). Usually, the development and survival of eggs depend highly on local temperature, oxygen, and water (Potter, Davidowitz, & Woods, 2009; Woods, 2010). During this stage, the life table characteristics that can be observed include mortality, development rate, development time, stage duration, and the number of individuals that transit to the next stage, usually the larva stage (Diamond & Kingsolver, 2009).

1.3. Larva
The eggs hatch into larvae, which start feeding, and some either become locomotive or remain in a dormant state (Gordh & Headrick, 2001). This is the stage where an insect grows most in size. Some insects have other substages within the larval stage called instars, whereas other species go straight to pupa. Just as with eggs, the life table characteristics observed for larva include mortality, development rate, development time, stage duration, and the number of individuals that transit to the next stage, the pupa stage.

1.4. Pupa
When the larvae develop, they move to the pupa stage. In this stage, the insects are known to rest, form their wings or other internal organs, and develop to form adults (Gordh & Headrick, 2001). Life table characteristics observed for pupa include mortality, development rate, development time, stage duration, and the number of individuals that transition to adult.

1.5. Adult
Adults constitute the last stage of development. All living organisms have this stage, and it is the end of a generation and also the beginning of another generation through the eggs laid by the female of the species. The life table characteristics observed for adults include mortality, senescence rate, and the life span.

The following assumptions are made on the data collected at each insect stage: (1) a constant daily survival rate within stages, (2) the duration of a life stage is considered to be identical for all individuals that move to the subsequent stages, (3) the unit of observation or time step is a day, and (4) all model parameters are presented in the published article for adequate application data reconstruction.

2. Algorithm for life table data reconstruction
The life table algorithm for insect population reconstruction presented here adopts an improvised approach to estimate the number of individuals entering a stage during development. The number of eggs at the beginning of the study and the results presented in the published information are key elements for successful reconstruction, as these variables are used as starting values of the algorithm. The approach also requires knowledge of the duration of all stages of the life cycle of the insect. Using the model parameters, the sample size, and the approximation of the life stage duration, we computed the total number of insects expected at the end of each stage of the experiment, which are then distributed using a uniform distribution according to the number of
days. The uniform distribution approach was adopted, as it contains values that are between two limits \( \alpha \) and \( \beta \), which, in the developed methodology, refer to the beginning of the stage and the last day of the stage. To assess the performance and accuracy of the algorithm, values analyzed from the reconstructed data were compared to the originally published information (Table 2).

To reconstruct data based on published scientific articles, books, or papers, the procedure is as follows:

1. Identify the information published, ensure that the pre-requisites of reconstruction are obtained.
2. Identify the initial day of the egg hatch. This can be obtained from books on the species of interest.
3. Enter the identified information in the algorithm, i.e. temperature ranges, the median number of days, \( T_{50} \), and the model parameters based on model reported.
4. Write the inverse of the model identified.
5. Compute life table dynamics as needed (the reconstruction).
6. Export results as desired.

The reconstruction algorithm was implemented in R programming language version 3.2.1 (Team, R.C., 2014) with detailed steps, to make it easier for the end user to follow and apply.

3. Application of the developed algorithm on insect life table reconstruction

To illustrate the steps, the algorithm presented was applied to two populations of insects to reconstruct the life tables and the results obtained from the reconstructed life tables were compared with those published. The following sections describe in detail the application of the algorithm.

3.1. Data description

Species used for reconstruction are the noctuid lepidopteran stem borer Busseola fusca (Khadioli et al., 2014b) and the Swinhole Chilo partellus Lepidoptera, Crambidae (Khadioli et al., 2014a) (Table 1). These data were selected because they represent the varied scenarios for the application of the developed algorithm and further satisfy the data assumptions of information published. Reports of studies of the parameters produced when fitting the various models were input directly to the algorithm. For those whose parameters were not provided but models used were given, we estimated the parameters using the method of solving simultaneous equations as recommended by (Broyden, 1965; Haavelmo, 1943; Zellner & Theil, 1962). This is possible given the number of parameters to be estimated and values along the line of best fit.

3.2. Reconstruction

For both species, the models used in analysis and consequently reconstruction are development time: Logit, development rate: Sharpe DeMichelle, mortality: second-order exponential polynomial, total oviposition: polynomial regression.
| Species          | n   | Stage | Temperature levels | Parameters                  | Provided | Model used                        | Source                                      |
|------------------|-----|-------|--------------------|-----------------------------|---------|-----------------------------------|---------------------------------------------|
| Chilo partellus  | 200 | Egg   | 18,20,25,30,32,35  | Mortality                   | Yes     | 2nd-Order exponential polynomial | Khadioli et al. (2014a)                     |
|                  |     |       |                    | Development time            | Yes     | Logit                             |
|                  |     |       |                    | Development rate            | Yes     | Sharpe DeMichelle                 |
|                  | 200 | Larva | 18,20,25,30,32,35  | Mortality                   | Yes     | 2nd-Order exponential polynomial |                                             |
|                  |     |       |                    | Development time            | Yes     | Logit                             |
|                  |     |       |                    | Development rate            | Yes     | Sharpe DeMichelle                 |
|                  | 177 | Pupa  | 18,20,25,30,32,35  | Mortality                   | Yes     | 2nd-Order exponential polynomial |                                             |
|                  |     |       |                    | Development time            | Yes     | Logit                             |
|                  |     |       |                    | Development rate            | Yes     | Sharpe DeMichelle                 |
|                  |     |       |                    | Total oviposition           | No      | Polynomial regression             |                                             |
| Busseola fusca   | 200 | Egg   | 15,18,20,25,30,32  | Mortality                   | No      | 2nd Order Exponential Polynomial  | Khadioli et al. (2014b)                     |
|                  |     |       |                    | Development time            | Yes     | Logit                             |
|                  |     |       |                    | Development rate            | Yes     | Logan 4                           |
|                  | 200 | Larva | 15,18,20,25,30,32  | Mortality                   | No      | 2nd-Order exponential polynomial |                                             |
|                  |     |       |                    | Development time            | Yes     | Logit                             |
|                  |     |       |                    | Development rate            | Yes     | Logan 1                           |
|                  | 200 | Pupa  | 15,18,20,25,30,32  | Mortality                   | No      | 2nd-Order exponential polynomial |                                             |
|                  |     |       |                    | Development time            | Yes     | Logit                             |
|                  |     |       |                    | Development rate            | Yes     | Logan 1                           |
|                  |     |       |                    | Total oviposition           | Yes     | Polynomial regression             |                                             |
3.2.1. Development rate and median development time

3.2.1.1. Development time. For development time, the probability that an insect whose stage lasted until the next stage change given the \( i \)-th temperature at a fixed day is used to estimate the median development time. On the development rate, the Sharpe de Michele model (Sharpe, Curry, DeMichele, & Cole, 1977) was used:

\[
r(T) = \frac{\rho T_0 e^{H_A R}}{1 + e^{\frac{\Delta H_L}{R} + e^{\frac{\Delta H_H}{R}}}}
\]

In Equation (1) the dependent variable \( r \) = Development rate (1/day). The independent variable, \( T \) = temperature in °C, is considered as a continuous variable in this case. \( T_0 \) is a constant temperature, usually taken to be 25; \( T_i \) is the temperature at which the rate-controlling enzyme is half active and half low-temperature inactive, \( H_A \) is the enthalpy of activation of the reaction catalyzed by a rate-controlling enzyme, \( \Delta H_L \) is the change in enthalpy associated with low-temperature inactivation of the enzyme, \( T_H \) is the temperature at which the rate-controlling enzyme is half active and half high temperature inactive, \( \Delta H_H \) is the change in the enthalpy associated with high-temperature inactivation of the enzyme, \( R \) is the universal gas constant, and \( \rho \) is the developmental rate assuming no enzyme activation (Schoolfield, Sharpe, & Magnuson, 1981; Sharpe et al., 1977; Wagner, Wu, Sharpe, Schoolfield, & Coulson, 1984).

The algorithm as applied to re-estimate development rate and development time was as follows:

(i) Identify the information published
(ii) Identify models used and their estimated parameters. If parameters are not published, re-estimate the parameters using a system of solving linear equations
(iii) Identify assumptions used and temperature ranges
(iv) Identify the set of starting values, the sample size, \( n \)
(v) Enter temperature ranges
(vi) Enter the median number of days, \( T_{50} \)
(vii) Enter model parameters based on model reported
(viii) Write the inverse of the model identified
(ix) Compute development time/development rate
(x) Export results as desired

The methodology involves simplifying Equation (1) to
where \( RT_i \) is the development rate at the \( i \)-th temperature; \( Y, \rho, \) and \( V \) are parameters to be estimated; and \( T_{\text{max}} \) is the maximum temperature for development.

Let \( DT_i \) be the median development time at \( i \)-th temperature, then

\[
DT_i = \frac{1}{RT_i} = \frac{1}{\{Y\left(e^{\rho T_i} - e^{\rho T_{\text{max}}}ight)\}^{\frac{1}{V}}}
\]

For example, \( C.\ partellus \) (Larva): \( Y = 0.03, \rho = 0.17, T_{\text{max}} = 37.58, \) and \( V = 5.51. \)

\[\therefore DT_i = 333.33 \left(e^{0.17 T_i} - e^{-0.43 \cdot 0.18 T_i}\right)^{-1} \]

Substituting \( T_i \) for \( i = 18, 20, 25, 30, 32, 35 \) in Equation (3) yields reconstructed \( DT_i \) values for the Swinhole Chilo partellus Lepidoptera, Crambidae that are compared with published median development time values as shown in Table 2. The respective development time results for each temperature and species are as shown on Table A1.

3.2.1.2. Development rate. Making \( RT_i \) the subject in Equation (3) of Section 3.2.1 yields

\[
RT_i = \frac{1}{\text{Reconstructed } DT_i}
\]

Substituting values of Table 1 in Equation (4) yields reconstructed \( RT_i \) values as shown in Table 3. The respective development rate results for each temperature and species are as shown on Table B1.

3.2.2. Cohort life table

To reconstruct the cohort life table, the mortality rate was used. If \( p \) is the observed mortality rate and \( q \) the survival rate, the species mortality rate therefore becomes

\[
p = 1 - q
\]

and survival becomes

\[
q = 1 - p
\]

Mortality for Busseola fusca (Khadioli et al., 2014b) and the Swinhole Chilo partellus (Lepidoptera, Crambidae) (Khadioli et al., 2014a) was estimated from a second-order exponential polynomial, which is the simplified Gompertz–Makeham model (Gompertz, 1825).

### Table 3. Published vs. reconstructed development rate for the Swinhole Chilo partellus Lepidoptera, Crambidae

| \( T_i \) | Published (Khadioli et al., 2014a) | Reconstructed \( RT_i \) |
|---|---|---|
| 18 | 0.01 | 0.02 |
| 20 | 0.02 | 0.03 |
| 25 | 0.03 | 0.04 |
| 30 | 0.05 | 0.06 |
| 32 | 0.04 | 0.06 |
| 35 | 0.04 | 0.05 |
The algorithm as applied to reconstruct the cohort life table was as follows:

(i) Identify the information published (mortality rate)
(ii) Identify models used and their estimated parameters. If parameters are not published, re-estimate the parameters using a system of solving linear equations
(iii) Identify assumptions used and levels of factor used in the study (e.g. temperature)
(iv) Identify the set of starting values, the sample size, \( n \)
(v) Enter temperature ranges
(vi) Enter the median number of days, \( T_{50} \)
(vii) Enter initial days when first egg hatches (obtained from secondary literature). In subsequent stages, the final day in the previous stage is used as initial days (Richards, Waloff, & Spradbery, 1960)
(viii) Compute mortality rate and consequently survival rate
(ix) Compute total number that developed at the end of each experiment at each temperature
(x) Distribute the total number in ix) using uniform distribution using \( \alpha = 0 \) and \( \beta = \) sample size in iv
(xi) Compute daily number developed
(xii) Export results arranged as desired

The methodology applies Gompertz’s (1825) mortality equation:

\[
MT_i = e^{(b_1 + b_2 T_i + b_3 T_i^2)} \text{ where } b_1 + b_2 T_i + b_3 T_i^2 \leq 0 \quad (7)
\]

where \( MT_i \) is the mortality rate and \( b_1, b_2, \) and \( b_3 \) are parameters to be estimated (Gompertz, 1825). The restriction \( b_1 + b_2 T_i + b_3 T_i^2 \leq 0 \) means that \( b_1, b_2, \) and \( b_3 \) are constrained.

From Equation (6) in Section 3.2.2, Equation (7) can be used to estimate the survival rate, \( ST_i \), as

\[
ST_i = (1 - MT_i) \quad (8)
\]

Let \( n_i \) be the sample size for each temperature \( T_i \), \( DT_i \) be the median development days for each temperature \( T_i \), \( IN_i^1 \) be the day the first egg hatches, for each temperature \( T_i \), \( DS_i \) be the number that survived daily, and \( Total\ D_i \) be the total number of insects that developed for any specific stage. According to Richards et al. (1960) method, estimation of the total number that survived daily is essential for any life table construction or reconstruction. They state that this number is bound between two values \([a,b]\), where \( a \) is the total number surviving in the last stage and \( b \) the number that will have survived by the end of the stage Richards et al. (1960). This is a uniform distribution with limits \([a,b]\).

\[
Total\ D_i = (\text{survival rate} \times \text{sample size}) = (1 - MT_i) \times n_i \quad (9)
\]

Using the uniform distribution with limits \([a,b]\), where \( a \) and \( b \) are the number of days the stage lasts, the total number of insects that survived the entire stage is

\[
\sum_{a}^{b} Total\ D_i = \sum_{a}^{b} (1 - MT_i) \times n_i \quad (10)
\]

where \( a \) is the initial number of days from the last stage and \( b \) is the last day of each stage.

Given the daily number that survive over the period, \( DS_i \), the number that survived per day is

\[
DS_i = \frac{Total\ D_i}{\sum_{a}^{b} PS_i} \quad \text{ where } \ L_i \leq \text{day}_i \leq (IN_i + DT_i)
\]
\[ DS_i = \frac{(1-MT_i) \cdot n_i \cdot PS_i}{\sum DS_i} \quad IN_i \leq \text{day}_i \leq (IN_i + DT_i) \] (11)

Example: for \( i = 25 \), parameters obtained in the previous example are \( b_1 = 6.27 \), \( b_2 = -0.59 \), and \( b_3 = 0.01 \), \( T_i = 25 \), \( n_i = 165 \), \( DT_i = 33 \), \( IN_i = 10 \).

\[ MT_{25} = e^{6.27 + (-0.59 \cdot 25) + (0.01 \cdot 625)} = 0.1075 \]

\[ TD_{25} = (1 - 0.1075) \cdot 165 = 147 \] (12)

| \( T_i \) | \( y_i \) | \( n_i \) | \( DS_i \) |
|-------|-------|-------|-------|
| 25    | 10    | 165   | 7     |
| 25    | 11    | 165   | 7     |
| 25    | 12    | 165   | 8     |
| 25    | 13    | 165   | 3     |
| 25    | 14    | 165   | 6     |
| 25    | 15    | 165   | 4     |
| 25    | 16    | 165   | 2     |
| 25    | 17    | 165   | 2     |
| 25    | 18    | 165   | 3     |
| 25    | 19    | 165   | 3     |
| 25    | 20    | 165   | 5     |
| 25    | 21    | 165   | 3     |
| 25    | 22    | 165   | 5     |
| 25    | 23    | 165   | 7     |
| 25    | 24    | 165   | 7     |
| 25    | 25    | 165   | 0     |
| 25    | 26    | 165   | 7     |
| 25    | 27    | 165   | 7     |
| 25    | 28    | 165   | 4     |
| 25    | 29    | 165   | 4     |
| 25    | 30    | 165   | 3     |
| 25    | 31    | 165   | 5     |
| 25    | 32    | 165   | 4     |
| 25    | 33    | 165   | 2     |
| 25    | 34    | 165   | 3     |
| 25    | 35    | 165   | 1     |
| 25    | 36    | 165   | 5     |
| 25    | 37    | 165   | 1     |
| 25    | 38    | 165   | 5     |
| 25    | 39    | 165   | 7     |
| 25    | 40    | 165   | 5     |
| 25    | 41    | 165   | 6     |
| 25    | 42    | 165   | 6     |

Table 4. Daily number that survived for \( T = 250 \)

\[ = 147 \]
Simulating 33 random numbers from the uniform distribution that lie between 0 and 165, with seed set to $879^2$

the number that survives each of the 33 days $= \frac{147}{\sum DS_i} * DS_i$, $10 \leq day_i \leq 43$ \hspace{1cm} (13)

Equation (13) yields estimates of the number that survived each day as shown in Table 4. The respective mortality table results for each temperature and species are as shown on Table C1.

In cases where $b_1$, $b_2$, and $b_3$ are not provided, but specific $MT_i$ have been reported, $b_1$, $b_2$, and $b_3$ can be estimated using the system of solving simultaneous equations for three unknowns based on

$$b_1 + b_2 T_1 + b_3 T_1^2 = \ln( MT_1 )$$
$$b_1 + b_2 T_2 + b_3 T_2^2 = \ln( MT_2 )$$
$$b_1 + b_2 T_3 + b_3 T_3^2 = \ln( MT_3 )$$ \hspace{1cm} (14)

3.2.3. Reproduction

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. The total oviposition represents the expected total number of eggs laid per an insect female during her whole life span and it is expressed as a function of temperature. This relationship is modeled with a nonlinear function just as in mortality.

The algorithm as applied to reconstruct the female oviposition file was

(i) Identify models used and their estimated parameters. If parameters are not published, re-estimate the parameters using a system of solving linear equations
(ii) Identify assumptions used and levels of factor used in study (e.g. temperature)
(iii) Identify the set of starting values, the female numbers, $F_n$
(iv) Enter temperature ranges
(v) Enter the median number of days, $T_{50}$
(vi) Enter initial days (obtained from, final day in previous stage)
(vii) Compute total number of females that developed at the end of each experiment at each temperature
(viii) Compute total number of eggs at the end of each experiment at each temperature
(ix) Export results arranged as desired

Mathematically, the methodology applied total oviposition using the Quadratic model:

$$FT_i = b_1 + b_2 T_i + b_3 T_i^2$$ \hspace{1cm} (15)

where $b_1$, $b_2$, and $b_3$ are parameters to be estimated, $FT_i$ is the average number of eggs laid at temperature $T_i$. Demographically, this is the gross reproduction rate (Deevey, 1947).

Let $FD_i$ be the total number of eggs laid by all females, $F_n$ is the number of females in the experiment for each temperature $T_i$.

The total female development days $FD_i$ then becomes

$$FD_i = (Total \ Oviposition \times \ number \ of \ females)$$
$$= (FT_i) \times F_n$$ \hspace{1cm} (16)
Using Microsoft Excel to distribute the total number of eggs laid \(FD_i\) to the female numbers \(Fn_i\) in the median female development days \(FDT_i\).

In cases where \(b_1, b_2,\) and \(b_3\) are not provided, but specific \(MT_i\) have been reported, \(b_1, b_2,\) and \(b_3\) can be estimated using the system of solving simultaneous equations for three unknowns based on

\[
\begin{align*}
\frac{b_1 + b_2 T_1 + b_3 T_1^2}{FT_1} &= \\
\frac{b_1 + b_2 T_2 + b_3 T_2^2}{FT_2} &= \\
\frac{b_1 + b_2 T_3 + b_3 T_3^2}{FT_3} &= \\
\end{align*}
\]

\(17\)

For \(C.\) partellus, \(b_1, b_2,\) and \(b_3\) were not provided, but some \(FT_{18}, FT_{25}\) and \(FT_{35}\) were provided. Using the set of Equations \(17\)

\[
\begin{align*}
\frac{b_1 + 18b_2 + 324b_3}{205.7} &= \\
\frac{b_1 + 25b_2 + 625b_3}{375.3} &= \\
\frac{b_1 + 35b_2 + 1225b_3}{46} &= \\
\end{align*}
\]

Yielded \(b_1 = -1743.44, b_2 = 168.81\) and \(b_3 = -3.36\)

Therefore, for \(T_i = 25, Fn_i = 43, FDT_i = 10\)

\(FT_{25} = 375.3\)

\(FD_{25} = 375.3 \times 43 \approx 16138\)

Distributing the 16138 eggs over 43 females in 10 days yields the oviposition Table 5. The respective oviposition results for each temperature and species are as shown on Table D1.

### 3.3. Accuracy tests

The reconstructed data were analyzed using ILCYM software (Tonnang et al., 2013), which was the same software used by original authors to model original insect behavior. The output from the reconstructed data was then compared with the published data. The Shapiro–Wilk normality test was conducted and the results showed that the \(p\)-value was greater than the alpha level of 0.05 and thus the null hypothesis that the data came from a normally distributed population could not be rejected. The two-sided Aspin–Welch–Satterthwaite two-sample \(t\)-test (Welch, 1937) was used to test whether there are any statistically significant differences between results obtained from the reconstructed data and the results published for development time, development rate, mortality, and total oviposition for all immature life stages (Table 2). The test assumes normal distribution of the two populations being tested and unequal variances, testing the hypothesis that true difference in means between published and reconstructed estimates is equal to zero.

### 4. Results

Results from the two-sided two-sample \(t\)-test show that all of \(C.\) partellus results were not significantly different, but for \(B.\) fusca, pupa development time and larva and pupa development rate were significantly different at 95% confidence level (Table 6).

### 5. Discussion

The algorithm as described in Section 2 yielded accurate estimates as shown in Table 6. However, the algorithm assumed that (1) data sets analyzed in the published paper are from laboratory-reared cohorts and as such the data used for publication had little or no errors from external factors and are only affected by variables under study and (2) interval of measurement in the original data is 1 day. Information regarding this assumption is indicated in the 'Materials and methods' part of the published paper. (3) If there is any censoring, it is interval-censored data and retrieves the interval
Table 5. Eggs laid distributions

| $T_i$ | Day1 | Day2 | Day3 | Day4 | Day5 | Day6 | Day7 | Day8 | Day9 | Day10 |
|-------|------|------|------|------|------|------|------|------|------|-------|
| 25    | 47   | 24   | 53   | 2    | 63   | 66   | 31   | 60   | 44   | 68    |
| 25    | 32   | 48   | 47   | 42   | 68   | 4    | 68   | 56   | 36   | 21    |
| 25    | 8    | 36   | 36   | 17   | 57   | 65   | 26   | 23   | 37   | 21    |
| 25    | 58   | 2    | 2    | 73   | 60   | 47   | 63   | 1    | 31   | 9     |
| 25    | 36   | 31   | 30   | 20   | 51   | 46   | 11   | 40   | 6    | 20    |
| 25    | 53   | 28   | 66   | 18   | 44   | 29   | 21   | 25   | 59   | 70    |
| 25    | 72   | 9    | 54   | 44   | 73   | 52   | 14   | 41   | 16   | 4     |
| 25    | 17   | 14   | 41   | 67   | 35   | 37   | 69   | 7    | 49   | 11    |
| 25    | 50   | 69   | 71   | 6    | 62   | 7    | 55   | 30   | 55   | 40    |
| 25    | 12   | 40   | 58   | 9    | 32   | 3    | 68   | 29   | 35   | 12    |
| 25    | 54   | 62   | 23   | 24   | 31   | 15   | 59   | 52   | 15   | 36    |
| 25    | 7    | 25   | 31   | 54   | 41   | 17   | 59   | 9    | 31   | 73    |
| 25    | 62   | 36   | 35   | 41   | 29   | 64   | 48   | 34   | 47   | 23    |
| 25    | 72   | 15   | 7    | 44   | 39   | 10   | 61   | 67   | 54   | 28    |
| 25    | 59   | 48   | 36   | 48   | 70   | 2    | 62   | 31   | 22   | 29    |
| 25    | 68   | 40   | 45   | 44   | 67   | 43   | 16   | 52   | 21   | 38    |
| 25    | 56   | 72   | 1    | 60   | 21   | 23   | 33   | 70   | 34   | 65    |
| 25    | 8    | 71   | 73   | 51   | 2    | 18   | 48   | 2    | 31   | 61    |
| 25    | 57   | 1    | 36   | 72   | 49   | 49   | 47   | 20   | 7    | 20    |
| 25    | 2    | 70   | 59   | 44   | 25   | 62   | 59   | 49   | 21   | 67    |
| 25    | 24   | 50   | 42   | 71   | 10   | 73   | 32   | 30   | 52   | 41    |
| 25    | 4    | 51   | 17   | 11   | 23   | 61   | 57   | 70   | 14   | 46    |
| 25    | 2    | 32   | 35   | 62   | 15   | 9    | 57   | 21   | 67   | 24    |
| 25    | 45   | 23   | 28   | 49   | 52   | 29   | 47   | 63   | 22   | 38    |
| 25    | 72   | 1    | 8    | 55   | 8    | 40   | 61   | 26   | 23   | 12    |
| 25    | 48   | 53   | 5    | 68   | 61   | 42   | 12   | 23   | 29   | 31    |
| 25    | 41   | 52   | 29   | 12   | 40   | 32   | 9    | 51   | 67   | 64    |
| 25    | 68   | 15   | 5    | 32   | 66   | 21   | 45   | 10   | 1    | 49    |
| 25    | 62   | 52   | 46   | 63   | 18   | 63   | 27   | 5    | 70   | 5      |
| 25    | 18   | 2    | 54   | 18   | 10   | 69   | 54   | 37   | 34   | 3      |
| 25    | 55   | 37   | 62   | 71   | 29   | 25   | 15   | 61   | 68   | 29    |
| 25    | 20   | 1    | 55   | 57   | 69   | 66   | 69   | 44   | 47   | 53    |
| 25    | 54   | 18   | 43   | 23   | 53   | 45   | 67   | 14   | 24   | 52    |
| 25    | 37   | 57   | 45   | 25   | 21   | 65   | 8    | 54   | 18   | 51    |
| 25    | 31   | 69   | 45   | 38   | 29   | 29   | 49   | 23   | 10   | 9      |
| 25    | 2    | 40   | 63   | 31   | 21   | 24   | 23   | 49   | 24   | 3      |
| 25    | 41   | 9    | 7    | 56   | 56   | 64   | 36   | 35   | 55   | 40    |
| 25    | 36   | 9    | 24   | 51   | 15   | 10   | 43   | 17   | 50   | 68    |
| 25    | 67   | 68   | 61   | 12   | 31   | 55   | 40   | 22   | 35   | 73    |
| 25    | 24   | 32   | 28   | 34   | 50   | 13   | 70   | 29   | 49   | 71    |
| 25    | 33   | 57   | 45   | 26   | 25   | 41   | 54   | 70   | 2    | 29    |
| 25    | 27   | 60   | 10   | 20   | 58   | 7    | 36   | 40   | 24   | 25    |

= 16,138

1Rows represent the number of each female, columns represent each day.
limits from the previous row, (4) all eggs laid were fertile and that failure to hatch was due to natural
mortality and not accident damage during handling, (5) mortality rates in all stages were equally
applicable to males and females, and (6) individuals of a species are reared at a series of constant
temperatures.

From our two examples, it is apparent that it is possible to re-estimate development rate and
development time, to reconstruct a species’ life table, and to reconstruct the female file based on
any published information, without having to set up the whole experiment. The differences in
B. fusca’s data and corresponding reconstructed data could be attributed to either chance or
inaccurate results reported. The algorithm that has been proposed in this paper is simple and
flexible yet realistic. It has a few technical requirements. However, the use of the algorithm is
limited to laboratory-reared species. This is because species in the natural environment are
dynamic and factors that affect their development, survivorship, and ability to lay eggs are varied,
whereas in the laboratory, the researcher can limit and control for these factors.

The data in many reports and published papers, although obtained and presented properly for their
original purposes, need to meet the assumptions stated for the reconstruction to be successful. Many
articles presented part or all data graphically. This becomes a challenge in the reconstruction process,
unless the models are listed in the ‘Materials and methods’ section of the legacy information. This also
makes it challenging to the algorithm when it is unable to re-estimate some of the parameters and
results in computational difficulties (NAs), rendering the reconstruction of some values improbable.

### Table 6. t-Test results comparing original estimates and reconstructed estimates at $\alpha = 0.05$

| Species       | Parameter          | Stage     | $t_{df}$ | $p$  |
|---------------|--------------------|-----------|----------|------|
| *Busseola fusca* | Development time   | Egg       | $t_{8.2} = 1.37$ | 0.20 |
|                |                    | Larva     | $t_{7.6} = 2.08$ | 0.07 |
|                |                    | Pupa      | $t_{8.8} = 2.52$ | 0.03**|
|                |                    | Adult male| $t_{8.7} = 0.81$ | 0.44 |
|                |                    | Adult female| $t_{10} = 0.63$ | 0.54 |
|                | Development rate   | Egg       | $t_{7.1} = -1.94$ | 0.09 |
|                |                    | Larva     | $t_{7.2} = -2.65$ | 0.03**|
|                |                    | Pupa      | $t_{6.2} = -2.95$ | 0.02**|
|                | Mortality          | Egg       | $t_{8.8} = 1.93$ | 0.08 |
|                |                    | Larva     | $t_{6.8} = 1.42$ | 0.20 |
|                |                    | Pupa      | $t_{8.1} = -0.02$ | 0.98 |
|                | Total oviposition  |           | $t_{5.9} = -0.50$ | 0.63 |
| *Chilo partellus* | Development time   | Egg       | $t_{9.6} = 0.85$ | 0.42 |
|                |                    | Larva     | $t_{8.1} = 1.19$ | 0.27 |
|                |                    | Pupa      | $t_{9.7} = 0.71$ | 0.50 |
|                |                    | Adult male| $t_{7.6} = 1.32$ | 0.22 |
|                |                    | Adult female| $t_{3.5} = 1.47$ | 0.17 |
|                | Development rate   | Egg       | $t_{8.9} = -0.52$ | 0.61 |
|                |                    | Larva     | $t_{9.5} = -1.43$ | 0.19 |
|                |                    | Pupa      | $t_{8.9} = -1.01$ | 0.34 |
|                | Mortality          | Egg       | $t_{1} = 0.04$ | 0.97 |
|                |                    | Larva     | $t_{10} = -0.09$ | 0.93 |
|                |                    | Pupa      | $t_{10} = -0.16$ | 0.87 |
|                | Total oviposition  |           | $t_{10} = -1.30$ | 0.96 |

*Denote significant difference at $\alpha = 0.05$
During initial versions of the algorithm, we attempted distributing the total number at the end of the experiment using the Fibonacci sequence (Falcon & Plaza, 2007; Falcón & Plaza, 2007; Horadam, 1961; Zhang, 1997), using the theory as in Er (1984) on sums of Fibonacci numbers by matrix methods. This methodology, however, yielded an output with values that were skewed to the left, implying a significant percentage of zero’s in the first few days of the larva and pupa stages of both insects. This became problematic when the tool used for verification of the data produced, ILCYM, showed that there was a failure of convergence. This could be attributed to the fact that the tool used to test the results employs maximum likelihood method of estimation to estimate the parameters. As a result, we had to take another approach to the reconstruction of the life table data and in the end used the uniform distribution. The algorithm is therefore limited when key data such as sample sizes and total number of the species are not reported. This limitation made it impossible to reconstruct the life tables of the mealybug, Phenacoccus solenopsis Tinsley (Hemiptera: Pseudococcidae) (Fand, Tonnang, Kumar, Kamble, & Bal, 2014), noctuid lepidopteran stem borers, Sesamia calamistis, and the Potato Tuberworm, Phthorimaea operculella Zelia (Sporeider, Kroschel, Quispe, & Lagnaoui, 2004). The algorithms we developed here are therefore recommended for use for any user who is limited in resources or time and needs to develop a comprehensive life table based on published data for purposes of study where temperature variations are concerned.

The algorithms discussed in this paper were specifically generated for the complete life table and made use of these parameters. This opens up further areas to be explored, to find out if the same algorithms can be used for other types of life tables. This research also opened up a gap where future researchers can establish if the same and other algorithms developed can be used for natural populations and also if the same algorithms hold for other factors other than temperature. In the circumstance where there are missing parameters, constructing and solving the system of simultaneous equations guide the estimation.

A computer code written in R programming language is available as an R package (pending publication of the package) and from the author’s GitHub account (https://github.com/DeeKareithi/Insect-LifeTable-Reconstruction–ILTR) to carry out the calculations described in this paper.

Acknowledgements
The first author of this paper is a MSc Biometry student who worked on the development and implementation of the algorithm while on Dissertation Research Internship Programme (DRIP) at icipe. The authors gratefully acknowledge the financial support given by the Federal Ministry of Co-operation and Development (BMZ), Germany. The data used to test the algorithm were collected at icipe.

Funding
The authors received no direct funding for this research.

Author details
D.N. Kareithi1,2
E-mail: njerikareithi@gmail.com
D. Salifu3
E-mail: salifudaisy@gmail.com
N. Owuor3
E-mail: onyango@uonbi.ac.ke
S. Subramanian1
E-mail: ssusubramanian@icipe.org
E.Z.H. Tonnang1
E-mail: htonnang@gmail.com

1 International Centre for Insect Physiology and Ecology (ICIPE), University of Nairobi School of Biological Sciences, P.O.Box 30772-00100, Nairobi, Kenya.
2 School of Mathematics, University of Nairobi, P.O.Box 30197-00100, Nairobi, Kenya.
3 Ecological Modeling, International Maize and Wheat Improvement Center ( CIMMYT ), Nairobi, Kenya.

References
Bellows, T. S., Jr, Van Driesche, R. G., & Ekington, J. S. (1992). Life-table construction and analysis in the evaluation of natural enemies. Annual Review of Entomology, 37, 587–612. doi:10.1146/annurev.en.37.010192.003103
Broyden, C. G. (1965). A class of methods for solving nonlinear simultaneous equations. Mathematics of Computation, 19, 577–593. doi:10.1090/S0025-5718-1965-0198670-6
Carey, J. R. (2001). Insect biodiversity. Annual Review of Entomology, 46, 79–110. doi:10.1146/annurev.ento.46.1.79
Deevey, E. S. (1947). Life tables for natural populations of animals. The Quarterly Review of Biology, 22, 283–314. doi:10.1086/395888

Notes
1. IN, Can be obtained from secondary literature.
2. The seed set may vary from user to user. The change in seed does not affect the general distribution of the population as the central limit theory will hold.
Diamond, S. E., & Kingsolver, J. G. (2009). Environmental dependence of thermal reaction norms: Host plant quality can reverse the temperature-size rule. The American Naturalist, 175, 1–10. doi:10.1086/648602

Dublin, L. I., Latka, A. J., & Spiegelman, M. (1950). Length of life (Revised ed.). JSTOR.

Ediev, D., & Gisser, R. (2007). Reconstruction of historical series of life tables and of age-sex structures for the Austrian population in the 19th and the first half of the 20th century. Vienna Yearbook of Population Research, 2007, 327–355. doi:10.1553/populationyearbook

Er, M. C. (1984). Sums of Fibonacci numbers by matrix methods. Fibonacci Quarterly, 22, 204–207.

Falcón, S., & Plaza, Á. (2007). The k-Fibonacci sequence and the Pascal 2-triangle. Chaos, Solitons, and Fractals, 33, 38–49. doi:10.1016/j.chaos.2006.10.022

Falcón, S., & Plaza, Á. (2007). On the Fibonacci k-numbers. Chaos, Solitons, and Fractals, 32, 1615–1624. doi:10.1016/j.chaos.2006.09.022

Fand, B. B., Tonnang, H. E., Kumar, M., Kambie, A. L., & Bol, S. K. (2014). A temperature-based phenology model for predicting development, survival and population growth potential of the mealybug, Phenacoccus solenopsis Tinsley (Hemiptera: Pseudococcidae). Crop Protection, 55, 98–108. doi:10.1016/j.cropro.2013.10.020

Gompertz, B. (1825). On the nature of the function expressive of the law of human mortality, and on a new mode of determining the value of life contingencies. Philosophical Transactions of the Royal Society of London, 115, 513–583. doi:10.1098/rstl.1825.0026

Gordh, G., & Headrick, D. (2001). A dictionary of entomology. New York, NY: Oxon (CABI Publishing). ISBN 0-85199-291-9 (hardcover). doi:10.1002/mnnz.20020780210

Haavelmo, T. (1943). The statistical implications of a system of simultaneous equations. Journal of Economic Entomology, 37(1), 1–12.

Horadam, A. F. (1961). A generalized Fibonacci sequence. The American Mathematical Monthly, 68, 455–459. doi:10.1080/0022250X.1961.1198969

Kahneman, D., Krueger, A. B., Schkade, D. A., Schwarz, N., & Stone, A. A. (2004). A survey method for characterizing daily life experience: The day reconstruction method. Science, 306, 1776–1780. doi:10.1126/science.1103572

Khadioli, N., Tonnang, Z. E. H., Muchugu, E., Ong’amo, G., Achia, T., Kipchirichir, I., & Le Ru, B. (2014a). Effect of temperature on the phenology of Chilo partellus (Swinhoe)(Lepidoptera, Crambidae); simulation and visualization of the potential future distribution of C. partellus in Africa under warmer temperatures through the development of life-table parameters. Bulletin of Entomological Research, 104, 809–822.

Khadioli, N., Tonnang, Z. E. H., Ong’amo, G., Achia, T., Kipchirichir, I., Kroschel, J., & Le Ru, B. (2014b). Effect of temperature on the life history parameters of noctuid lepidopteran stem borers, Busseola fusca and Sesamia calamistis. The Annals of Applied Biology, 165, 373–386. doi:10.1111/aab.12157

Kita, M. W. (1993). Getting the most from incomplete data: Some things are solved, others are not. Journal of Insurance Medicine, 25(2). Retrieved from https://oaimedicine.com/journal-of-insurance-medicine/jim/1993/025-02-0149.pdf

Potter, K., Davidowitz, G., & Woods, H. A. (2009). Insect eggs protected from high temperatures by limited homeothermy of plant leaves. Journal of Experimental Biology, 212, 3448–3454. doi:10.1242/jeb.033365

Richards, O. W., Woloff, N., & Spradbery, J. P. (1960). The measurement of mortality in an insect population in which recruitment and mortality widely overlap. Oikos, 11, 306–310. doi:10.2307/3564689

Schoolfield, R. M., Sharpe, P. J. H., & Magnuson, C. E. (1981). Non-linear regression of biological temperature-dependent rate models based on absolute reaction-rate theory. Journal of Theoretical Biology, 88, 719–731. doi:10.1016/0022-5193(81)90246-0

Sharpe, J. P., Curry, G. L., DeMichele, D. W., & Cole, C. L. (1977). Distribution model of organism development times. Journal of Theoretical Biology, 66, 21–38. doi:10.1016/0022-5193(77)90309-5

Sporleder, M., Kroschel, J., Quispe, M. R. G., & Lagoinha, A. (2004). A temperature-based simulation model for the potato tubeworm, Phtorhamoia operculiella Zeller (Lepidoptera: Gelechiidae). Environmental Entomology, 33, 477–486. doi:10.1603/0046-225X-33.3.147

Stephens, M., & Donnelly, P. (2003). A comparison of bayesian methods for haplotype reconstruction from population genotype data. American Journal of Human Genetics, 73(5), 1162–1169. doi:10.1086/379378

Stephens, M., Smith, N. J., & Donnelly, P. (2001). A new statistical method for haplotype reconstruction from population data. American Journal of Human Genetics, 68(4), 978–989. doi:10.1086/319501

Team, R.C. (2016). R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing. 2013. ISBN 3-900051-07-0.

Tonhong, H. E. Z., Caruapomma, P., Gonzales, J. C., Juarez, H., Kroschel, J., & Sporleder, M. (2013). Insect life cycle modelling (ILCYM) software - a new tool for regional and global insect pest risk assessments under current and future climate change scenarios. Potential Invasive Pests of Agricultural Crops, 23, 412. doi:10.1079/781845938291.0412

Warrier, T. L., Wu, H.-I., Sharpe, P. J., Schoolfield, R. M., & Coulson, R. N. (1984). Modeling insect development rates: A literature review and application of a biophysical model. Annals of the Entomological Society of America, 77, 208–220. doi:10.1093/aes/77.2.208

Welch, B. L. (1937). On the z-test in randomized blocks and Latin squares. Biometrika, 29, 21–52. doi:10.1093/biomet/29.1.21

Woods, H. A. (2010). Water loss and gas exchange by eggs of Manduca sexta: Trading off costs and benefits. Journal of Insect Physiology, 56, 480–487. doi:10.1016/j.jinsphys.2009.05.020

Zellner, A., & Theil, H. (1962). Three-stage least squares: Simultaneous estimation of simultaneous equations. Journal of Economic Entomology, 30, 54–78.

Zhang, W. (1997). Some identities involving the Fibonacci numbers. Fibonacci Quarterly, 35, 225–228.
## Table A1. Development time results

|       | Egg | Larva | Pupa | Male | Female |
|-------|-----|-------|------|------|--------|
| $T_i$ | Pub. | Recon. | Pub. | Recon. | Pub. | Recon. | Pub. | Recon. | Pub. | Recon. | Pub. | Recon. | Pub. | Recon. |
| 18    | 13.8 | 8.946 | 18   | 82   | 18    | 21.4 | 17   | 18   | 11    | 18    | 12    | 18    | 12    | 12    |
| 20    | 11.4 | 7.078 | 20   | 59.4 | 20    | 16.6 | 14   | 20   | 8.4   | 20    | 11.4  | 9     |       |
| 25    | 6.4  | 5.225 | 25   | 32.8 | 25    | 9.3  | 8    | 25   | 9.8   | 25    | 10.3  | 5     |       |
| 30    | 4.9  | 4.25  | 30   | 21.9 | 30    | 7    | 5    | 30   | 7.8   | 4     | 30    | 7.4   | 3     |
| 32    | 4.4  | 4.794 | 32   | 24.2 | 32    | 6.8  | 5    | 32   | 7.6   | 4     | 32    | 7.1   | 4     |
| 35    | 4.8  | -     | 35   | 28.3 | 35    | 7.7  | 6    | 35   | 5.9   | 4     | 35    | 5     | 4     |
|       |      |       |      |      | Model: Binomial (cloglog) | Binomial (cloglog) | binomial (cloglog) | Binomial (logit) | Binomial (logit) |
|       |      |       |      |      | AIC: 284.155 | 1628.836 | 403.849 | 293.783 | 190.803 |
|       | $R^2$ |       |      |      | 0.985 | 0.975 | 0.929 | 0.915 |

### C. partellus Published vs. Reconstructed Development Time

|       | 15   |     | 15   |     | 15   |     | 15   |     | 15   |     | 15   |     | 15   |     |
|-------|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|------|-----|
| $T_i$ | 19.12| 13.164 | 15   | 167.78 | 15   | 79.211 | 15   | 36.95 | 20.504 | 15   | 11.65 | 10.022 | 15   | 12.38 | 11.414 |
| 18    | 12.86| 10.862 | 18   | 96.68 | 18   | 57.359 | 18   | 27.72 | 16.053 | 18   | 10.87 | 8.832 | 18   | 11.07 | 11.018 |
| 20    | 9.67 | 5.857 | 20   | 90.12 | 20   | 31.757 | 20   | 21.31 | 8.675 | 20   | 9.92 | 8.779 | 20   | 10.47 | 9.536 |
| 25    | 7.2  | 4.145 | 25   | 50.69 | 25   | 20.946 | 25   | 14.67 | 6.085 | 25   | 8.67 | 6.919 | 25   | 9.998 | 6.375 |
| 28    | 7.52 | 3.776 | 28   | 41.28 | 28   | 23.071 | 28   | 13.94 | 5.92 | 28   | 7.09 | 6.407 | 28   | 7     | 6.563 |
| 30    | 6.54 | 4.07 | 30   | 58.12 | 30   | 26.756 | 30   | 16.6  | 6.761 | 30   | 4.43 | 5.318 | 30   | 4.71  | 4.593 |
|       |      |      |      |      | Model: Binomial (logit) | Binomial (logit) | Binomial (logit) | Binomial (cloglog) | Binomial (cloglog) |
|       |      |      |      |      | AIC: 1729.965 | 1045.681 | 505.95 | 546.707 | 383.184 |
|       | $R^2$ |      |      |      | 0.976 | 0.991 | 0.986 | 0.925 |

### B. fusca Published vs. Reconstructed Development Time
### Table B1. Development rate results

| *C. partellus* | *B. fusca* |
|---------------|-----------|
| **Egg** | **Larva** | **Pupa** | **Egg** | **Larva** | **Pupa** |
| $T_i$ | Pub. | Recon | $T_i$ | Pub. | Recon | $T_i$ | Pub. | Recon | $T_i$ | Pub. | Recon |
| 18 | 0.0725 | 0.1118 | 18 | 0.0467 | 0.0588 | 15 | 0.0253 | 0.0760 | 15 | 0.0060 | 0.0126 |
| 20 | 0.0877 | 0.1413 | 20 | 0.0602 | 0.0714 | 18 | 0.0921 | 0.0103 | 18 | 0.0174 | 0.0361 |
| 25 | 0.1563 | 0.1914 | 25 | 0.1075 | 0.1250 | 20 | 0.1034 | 0.1707 | 20 | 0.0315 | 0.1153 |
| 30 | 0.2041 | 0.2353 | 30 | 0.1429 | 0.2000 | 25 | 0.1389 | 0.2413 | 25 | 0.0477 | 0.0682 |
| 32 | 0.2273 | 0.2086 | 32 | 0.1471 | 0.2000 | 28 | 0.1330 | 0.2648 | 28 | 0.0433 | 0.0717 |
| 35 | 0.2083 | – | 35 | 0.1299 | 0.1667 | 30 | 0.1529 | 0.2457 | 30 | 0.0374 | 0.1479 |

Model: Sharpe DeMichele

| AIC | R² |
|-----|----|
| 46.96 | 0.968 |

$C. partellus$ and $B. fusca$ Published vs. Reconstructed Development Rate
### Table C1. Mortality results

|                | C. partellus | B. fusca |
|----------------|--------------|----------|
|                | Egg          | Larva    | Pupa     | Egg          | Larva    | Pupa     |
| $T_i$          |              |          |          |              |          |          |
| 18             | 0.8240       | 0.3290   | 0.1540   | 15           | 0.8184   | 0.6740   |
|                | 0.8250       | 0.3350   | 0.1810   |              | 0.7250   | 0.9000   |
| 20             | 0.5840       | 0.2165   | 0.0693   | 18           | 0.6718   | 0.6370   |
|                | 0.5800       | 0.2280   | 0.0780   |              | 0.5840   | 0.3300   |
| 25             | 0.3890       | 0.1075   | 0.0268   | 20           | 0.4550   | 0.3180   |
|                | 0.3850       | 0.1210   | 0.0240   |              | 0.4480   | 0.4350   |
| 30             | 0.4970       | 0.0880   | 0.0046   | 25           | 0.7070   | 0.2460   |
|                | 0.5000       | 0.0820   | 0.0450   |              | 0.5780   | 0.4970   |
| 32             | 0.6580       | 0.0935   | 0.0880   | 28           | 0.9610   | 0.5020   |
|                | 0.6510       | 0.1060   | 0.0860   |              | 0.7190   | 0.1070   |
| 35             | 1.0000       | 0.1188   | 0.3600   | 30           | 0.9900   | 0.8200   |
|                | 0.9800       | 0.1130   | 0.3610   |              | 0.8100   | 0.3850   |

**Model**
- 2nd-degree nonlinear regression model
- Second-degree nonlinear regression model

|                |              |          |          |              |          |          |
|----------------|--------------|----------|----------|--------------|----------|----------|
| $T_i$          | Pub. Recon.  | Pub. Recon. | Pub. Recon. | Pub. Recon. | Pub. Recon. | Pub. Recon. |
| 18             | 30.498       | 34.564   | 55.012   | -5.5967     | -1.0937   | -11.1439 |
| 20             | 0.996        | 0.991    | 0.98     | 0.7497      | 0.7309    | 0.9457   |

*Kareithi et al., Cogent Mathematics & Statistics (2019), 6: 1701377*
## Appendix D

|                | C. partellus | B. fusca |
|----------------|--------------|----------|
| $T_1$          | Pub.         | Recon.   | $T_1$          | Pub.         | Recon.   |
| 18             | 205.7000     | 205.7320 | 15             | 102.75       | 205.6786 |
| 20             | 287.7798     | 287.6960 | 18             | 243.3800     | 219.9500 |
| 25             | 375.3000     | 375.4420 | 20             | 298.7500     | 375.2857 |
| 30             | 294.7067     | 294.8080 | 25             | 252.2100     | 230.6154 |
| 32             | 215.3976     | 215.3150 | 28             | 166.5000     | 181.3462 |
| 35             | 46.0000      | 46.0740  | 30             | 155.5000     | 139.0000 |

Model: Second-degree nonlinear regression model

|                | C. partellus | B. fusca |
|----------------|--------------|----------|
| AIC            | 26.706       | 70.4226  |
| $R^2$          | 0.998        | 0.7431   |

Kareithi et al., Cogent Mathematics & Statistics (2019), 6: 1701377

https://doi.org/10.1080/25742558.2019.1701377