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Statistical Inference on Associated Fertility Life Table Parameters Using Jackknife Technique: Computational Aspects

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ABSTRACT Knowledge of population growth potential is crucial for studying population dynamics and for establishing management tactics for pest control. Estimation of population growth can be achieved with fertility life tables because they synthesize data on reproduction and mortality of a population. The five main parameters associated with a fertility life table are as follows: (1) the net reproductive rate (R_0), (2) the intrinsic rate of increase (r_m), (3) the mean generation time (T), (4) the doubling time (Dt), and (5) the finite rate of increase (λ). Jackknife and bootstrap techniques are used to calculate the variance of the r_m estimate, which can be extended to the other parameters of life tables. Those methods are computer-intensive, their application requires the development of efficient algorithms, and their implementation is based on a programming language that encompasses quickness and reliability. The objectives of this article are to discuss statistical and computational aspects related to estimation of life table parameters and to present a SAS program that uses jackknife to estimate parameters for fertility life tables. The SAS program presented here allows the calculation of confidence intervals for all estimated parameters, as well as provides one-sided and two-sided t -tests to perform pairwise or multiple comparison between groups, with their respective P values.

KEY WORDS fertility life tables, intrinsic rate of increase, jackknife technique, computer program, SAS program

FERTILITY LIFE TABLES are appropriate to study the dynamics of animal populations, especially arthropods, as an intermediate process for estimating parameters related to the population growth potential, also called demographic parameters. Methods for construction, description, and analysis of life tables for animal populations can be found in Deevey (1947), Birch (1948), and Southwood (1978). Examples of practical use of life tables are abundant in the literature (Elliot et al. 1988, Kieckhefer and Elliott 1989, Michels and Behle 1989, Vargas and Carey 1990, Fernandez-Casalderrey 1992, Zeng et al. 1993, Brodsgaard 1994, Hance et al. 1994, Chakraborty et al. 1996, Sharma et al. 1997). In addition, the population growth potential of insects and mites can be used as an indicator in studies that aim to assess environmental effects of agricultural technologies and practices (Stark and Wennergren 1995, Nascimento et al. 1998). For instance, in the risk assessment of biocontrol agents, it is important to know their possible negative effects on beneficial arthropods population dynamics.

The parameters usually estimated from fertility life tables are the net reproductive rate (R_0); the intrinsic rate of increase (r_m); the mean generation time (T); the doubling time (Dt), and the finite rate of increase (λ). To compare life table parameters of different groups using statistical tests, it is necessary to have information on the uncertainty degree associated with its estimates, expressed as their variances. Information on variances for estimates coming from individual observations like longevity, immature development

time, or number of eggs per female are easily obtained by calculating the variability among observed values from individuals of the same group, the so-called internal or within group variance. However, the same procedure cannot be applied to synthetic parameters like R_0 , r_m , T , Dt , and λ , which summarize information on immature development, reproduction, and survival into a single statistic. In that case, variances can be calculated by the Monte Carlo methods, such as bootstrap, jackknife, and randomization tests. Detailed information on those methods applied to biological sciences can be found in Manly (1991). Generally, estimates of associated life table parameters are reported in the literature without any measure of uncertainty. In some cases, inappropriate methods like analysis of variance and multiple range tests are employed (Vargas and Nishida 1985, Zeng et al. 1993). Only a few authors (Elliot et al. 1988, Kieckhefer and Elliott 1989, Smith 1992, Smith 1993) reported standard error for the r_m estimate, using the jackknife method applied to life table analysis proposed by Meyer et al. (1986).

The r_m estimation using the iterative method is a computer-intensive technique itself. In addition, another computer intensive technique, the jackknife, is required to assess r_m estimate uncertainty. In this way, to jointly use both techniques it is necessary to develop effective algorithms and to implement them using a computer language which provides speed and reliability for the estimation process.

Hulting et al. (1990) developed a computer program in Pascal to estimate r_m and R_0 with standard error and approximate confidence intervals. However, this program shows two main limitations: while running the program for all the groups concurrently it is necessary to assume the same immature stage survivorship for all groups; and it does not include statistical tests for comparing groups. Hulting et al. (1990) only suggest using the r_m estimates and their respective standard error from the program output to perform either specific pairwise t -tests or multiple comparisons using Student–Newman–Keuls test (Snedecor and Cochran 1980). In our current article, we discuss statistical and computational aspects related to estimation of life table parameters; present a computer program without the limitations mentioned above; and expand the use of jackknife to generate estimates for the other associated fertility life table parameters, with their respective confidence intervals. These were achieved with the development of algorithms for estimating R_0 , R_m , T , Dt , and λ , with their respective jackknife variances and confidence intervals, and for performing specific pairwise comparisons between populations, using one- or two-tailed t -tests based on jackknife variance estimates. We also present a multiple comparison approach that should be used when there are more than two test populations.

Materials and Methods

Data Collection and Organization. The information to construct fertility life tables should be collected from completely randomized experiments. According to this experimental design, n adult mated females are randomly assigned to G groups. The requirement for completely randomized design is not related to the life table construction itself, but to theoretical requisite for using the jackknife method. Females are observed at constant time periods, for example, days or weeks, until their death, with records of survivors and numbers of eggs laid. For ease of calculations, the span between two consecutive time periods is represented by its midpoint, that is, the female age plus 0.5, the so-called pivotal age (x).

The information needed for constructing a fertility life table is as follows.

Number of Females per Group (NF_g). The number of mated females in each group g ($g = 1, 2, \dots, G$).

Initiation of Adult Stage ($t0_{gi}$). Time span between the day of oviposition that originated a female i ($i = 1, 2, \dots, n_g$) of a group g and the day when that female becomes an adult.

Longevity (tf_{gi}). Time span between the day of oviposition when a female i of a group g is born and the day of its death.

Number of Eggs ($NEGG_{gix}$). Number of eggs laid by female i of group g , in each pivotal age x .

Total of Eggs ($NEGG_{gx}$). Total number of eggs laid by all females of group g , at the pivotal age x .

$$NEGG_{gx} = \sum_{i=1}^{n_g} NEGG_{gix}$$

Ratio of Females (SR_g). Because it is not possible to identify sex at the egg stage, the ratio of female eggs is estimated by taking a sample of N_g eggs from each group and observing them up to the adulthood; thereafter, the number of adult females (NAF_g) is divided by the total number of adults (NA_g). That sample must be collected from eggs laid by all the females during the entire oviposition period. So, the ratio of females for each group, called sex ratio, is expressed by

$$SR_g = \frac{NAF_g}{NA_g}$$

Immature Stages Survivorship ($SURV_g$). Percent of offspring females alive until adulthood, also called preimaginal survivorship, is calculated by dividing the number of females alive until adulthood by N_g , where N_g is the number of eggs taken from each group to determine the sex ratio. Thus, the same sample of eggs is used to calculate both sex ratio and preimaginal survivorship. It is calculated as follows:

$$SURV_g = \frac{NA_g}{N_g}$$

An example of a data sheet (podisus.prn) with information required to estimate parameters of fertility life tables is available (www.cnpma.embrapa.br/servicos.html). The data are originated from a study to evaluate the effects of a formulation of *Bacillus thuringiensis* Berliner variety *kurstaki* (Btk) on *Podisus nigrispinus* Dallas, in two consecutive generations, described in Nascimento et al. (1998). In that experiment, two groups were compared: predators fed nonintoxicated larva (control) and larva intoxicated with Btk (treated). The data used as a case study were from first generation only. Any data set organized for this purpose should be formatted with space delimited columns. Information listed in each column should be:

Column 1 (group): identification of the group or treatment, as a numeric or alphanumeric variable. Column 2 (female label): female identification, as a numeric or alphanumeric variable. Column 3 (x): pivotal age, the female age plus 0.5, as a numeric variable expressed in time units (days, weeks). Column 4 ($NEGG$): number of eggs laid per female at each age. Column 5 (SR): proportion of females in the population, as a numeric variable assuming values between 0 and one (extremes included). Column 6 ($SURV$): immature stage survivorship, as a numeric variable varying between 0 and one (extremes included).

Records of age at oviposition in the same group should begin at same pivotal age, that is, the minimum age at onset of adulthood. Otherwise, the number of living females at early dates would be miscalculated. Furthermore, the females that had no oviposition should be included to avoid overestimation of population growth rates.

Calculation of Parameters Associated with a Fertility Life Table. The information listed above is used to estimate parameters related to the population growth potential in each group. It is assumed that the population has an exponential growth described in the model:

$$N(t) = N_0 \times e^{r_m \times t}$$

where, $N(t)$ is the size of the population at time t ; N_0 is the initial size of the population, and r_m is a parameter related with the rate of population growth, called intrinsic rate of increase.

Algorithms were developed to calculate r_m in two ways, either by using an approximate estimate for T , or by using an iterative method based on the functional link between the Ro at each time interval and the r_m (Southwood 1978). The first method, the approximate method, is based on an approximate estimate of T . It is very easy to perform, and with it r_m can be computed using either electronic data sheets or simple calculators. The second method, the iterative method, estimates r_m based on an equality that relates female ages and net egg contributions with population growth potential. Differently from the first method, it requires more intensive utilization of computational resources.

We present below the algorithms used to calculate associated fertility life table parameters using both approximate and iterative methods. The approximate method the algorithms follow.

Net Reproductive Rate (Ro). It is the mean net contribution per female to the next generation, expressed in total of offspring females per female, during the entire oviposition period. At first, it is necessary to calculate the number of female offsprings coming from all females of the group g at each pivotal age x (m_{gx}), multiplying the total number of eggs laid at each pivotal age ($NEGG_{gx}$) by the sex ratio (SR_g):

$$m_{gx} = NEGG_{gx} \times SR_g$$

Second, it is necessary to obtain an estimate of the cumulative female survivorship at each pivotal age (l_{gx}). Cumulative survival estimation comprises the survival in the immature stages multiplied by the survival during the adult stage, which is the number of females of a group g that have survived up to time x (NSF_{gx}), expressed as a fraction of the initial number of females per group (NF_g):

$$l_{gx} = SURV_g \times \frac{NSF_{gx}}{NF_g}$$

The net contribution at pivotal age x , in group g (Ro_{gx}), represents an estimate of female eggs laid at that age that will reach the adult stage. It is calculated by summation over all females in group g of the number of female offsprings produced in the pivotal age x multiplied by cumulative female survivorship:

$$Ro_{gx} = l_{gx} \times m_{gx}$$

Therefore, the net reproductive rate of each group g is obtained by summing up the net contributions Ro_{gx} for the entire period of observation, that is, since the day of the first onset of adulthood ($min_i [x0_{gi}] = x0_g$)

until the day of the last death for the females in group g ($max_i tf_{gi} = \Omega_g$):

$$Ro_g = \sum_{x=x0_g}^{\Omega_g} Ro_{gx}$$

Mean Generation Time (T). It is the mean time span between the birth of individuals of a generation and that of the next generation. It is estimated by calculating the mean female ages for each pivotal age x , weighted by the net number of offspring from eggs laid at that age. In this way, the mean interval between generations for each group is given by the following:

$$T_g = \frac{\sum_{x=x0_g}^{\Omega_g} x \times l_{gx} \times m_{gx}}{\sum_{x=x0_g}^{\Omega_g} l_{gx} \times m_{gx}}$$

Intrinsic Rate of Increase (r_m). The expression for estimating r_m is derived from the exponential growth model, considering $t = T_g$ and $Ro_g = N_{Tg}/N_0$:

$$r_{mg} = \frac{Ln(Ro_g)}{T_g}$$

Doubling Time (Dt). It is the time span necessary for doubling the initial population. It is calculated from the exponential growth model, considering $t = T_g$ and $N_{Tg}/N_0 = 2$:

$$Dt_g = \frac{Ln(2)}{r_{mg}}$$

Finite Rate of Increase (λ). It is a multiplication factor of the original population at each time period. The decimal part of the finite rate of increase corresponds to the daily (or weekly) rate of increase expressed as a percentage. The rate of increase for each group g is as follows:

$$\lambda_g = e^{r_{mg}}$$

Accordingly, for the iterative method the algorithms are as follows.

Net Reproductive Rate (Ro). It is calculated as in the approximate method.

Intrinsic Rate of Increase (r_m). It is obtained by iteration of the equation below, searching for an r value to which the difference between the two sides of the equation is minimal (equation below). The first value of r is calculated by taking the r_m estimated by using the approximate method; then the search in the interval between $0.8 r$ and $1.2 r$ is continued until an optimum value for r is achieved:

$$\sum_{x=x0}^{\Omega_g} e^{-r \cdot x} \cdot l_x \cdot m_x = 1$$

Mean Generation Time (T). It is calculated from the exponential growth model, considering $t = T_g$ and $Ro_g = N_{Tg}/N_0$:

$$T_g = \frac{Ln(Ro_g)}{r_{mg}}$$

Table 1. Associated life table estimates for Nascimento's data (Nascimento et al. 1998): jackknife estimates (means) and associated 95% CL

Parameter	Control			Treated		
	True calculation	Jackknife estimate	95% CL	True calculation	Jackknife estimate	95% CL
Net reproductive rate – R_o (female/female)	243.927	243.927	197.258–290.597	94.650	94.650	65.746–123.553
Intrinsic rate of increase – r_m (female/female/day)	0.164	0.164	0.157–0.171	0.127	0.128	0.116–0.139
Finite rate of increase – λ (female/female/day)	1.179	1.178	1.170–1.187	1.136	1.136	1.123–1.149
Mean generation time – T (day)	33.428	33.496	4.041–4.401	35.685	35.685	33.626–37.744
Doubling time – Dt (day)	4.215	4.221		5.436	5.420	4.936–5.904

Doubling Time (Dt). It is calculated as in the approximation method.

Uncertainty Associated with Parameter Estimates. We used the jackknife method proposed by Meyer et al. (1986) to estimate the variance for r_m . This method, first proposed by Quenouille (1956) and modified later by Tukey (1958), is used mostly to estimate variance and bias of estimators. It is based on repeated recalculation of the required estimator, missing out each sample in turn. It is used to quantify uncertainty associated with parameter estimates, as an alternative to analytical procedures, in cases for which the last ones require very complicated mathematical derivation. The theoretical basis for the jackknife method is presented in Efron (1983).

Algorithms for jackknife estimation of the means and variances, and the construction of confidence intervals are described only for R_o . Similar procedures were used for the other parameters. The steps for the application of the method are the following:

Estimation of R_o , r_m , T , Dt , and λ considering the survival and oviposition data for all the n_g females of each group, referred to as true calculation. At this point, called step zero, estimates obtained are denoted as $R_{o_g}^{(0)}$, $r_{mg}^{(0)}$, $T_g^{(0)}$, $Dt_g^{(0)}$, and $\lambda_g^{(0)}$.

Repeat the procedure described in item *a* for n_g times for each group, each time excluding a different female. In so doing, in each step *i*, data of $n_g - 1$ females are taken to estimate parameters for each step, now named $R_{o_g}^{(i)}$, $r_{mg}^{(i)}$, $T_g^{(i)}$, $Dt_g^{(i)}$, and $\lambda_g^{(i)}$.

In each step *i*, pseudo-values are calculated for each parameter, subtracting the estimate in step zero from the estimate in step *i*, and weighting them with the respective number of females included. For instance, a pseudo-value of R_o for group *g*, in step *i*, is given by

$$PSVR_{o_g}^{(i)} = n_g \times R_{o_g}^{(i)} - (n_g - 1) \times R_{o_g}^{(0)}$$

After calculating all the n_g pseudo-values for R_o , for a group *g*, jackknife estimates of the mean (Ro'_g), variance [$VAR(Ro'_g)$] and standard error [$SEM(Ro'_g)$] obtained, respectively, by the following equations:

$$Ro'_g = \frac{\sum_{i=1}^{n_g} PSVR_{o_g}^{(i)}}{n_g}$$

$$VAR(Ro'_g) = \frac{\sum_{i=1}^{n_g} (PSVR_{o_g}^{(i)} - Ro'_g)^2}{(n_g - 1)}$$

$$SEM(Ro'_g) = \sqrt{\frac{VAR(Ro'_g)}{n_g}}$$

Assuming a Student *t* distribution for Ro'_g , an $100(1-\alpha)\%$ asymptotic confidence interval for R_o is given by

$$Ro'_g \pm t_{\nu, \alpha/2} \times SEM(Ro'_g)$$

where $\nu = n_g - 1$ and $t_{\nu, \alpha/2}$ is the percentile $100(\alpha/2)$ of the Student *t* distribution at ν degrees of freedom.

Comparisons of Parameters Between Groups. To perform pairwise comparisons between groups, the Student *t*-test for independent samples with different variances can be used. The Welch correction for degrees of freedom was incorporated, according to what is described in Zar (1984). The test statistics to compare, for example, R_o of two groups *a* and *b*, is as follows:

$$t_{ab} = \frac{Ro'_a - Ro'_b}{\sqrt{\frac{Var(Ro'_a)}{n_a} + \frac{Var(Ro'_b)}{n_b}}}$$

The *P* values corresponding to the two-tailed (p_T), uppertailed (p_U) and lowertailed *t*-test (p_L), are calculated using the function of cumulative Student *t* distribution (Probt) at ν_{ab}' degrees of freedom:

$$p_T = 2 \times (1 - \text{Probt}(|t_{ab}|, \nu_{ab}))$$

$$p_U = 1 - \text{Probt}(t_{ab}, \nu_{ab})$$

$$p_L = 1 - \text{Probt}(-t_{ab}, \nu_{ab})$$

When there are more than two groups, a multiple comparison approach is recommended. In that case, critical *P* values for two-tailed (γ_T) and one-tailed (uppertailed or lowertailed) *t*-test (γ_O) can be easily calculated and compared with the observed *P* values. A general procedure to do that, based on Sidák's inequality (Sidák 1967), is to find out the critical values γ that satisfy the equation presented below, where $K = G(G-1)/2$ is the number of all possible pairs formed with the *G* groups tested. The equalities for

Table 2. Estimate parameters for Nascimento's data (Nascimento et al. 1998): jackknife estimates (mean A, mean B) for each pair of groups compared (A, control; B, treated), respective standard errors [SEM(A), SEM(B)] and *p*-values for two-tailed (*P_T*), lowertailed (*P_L*), and uppertailed (*P_U*) *t*-tests for pairwise group comparison

Parameter	A	B	Mean A	SEM (A)	Mean B	SEM (B)	<i>P_T</i>	<i>P_L</i>	<i>P_U</i>
Net reproductive rate – <i>R₀</i> (female/female) ^a	1	2	243.927	21.760	94.650	12.780	<0.0001	<0.0001	1.0000
Intrinsic rate of increase – <i>r_m</i> (female/female/day) ^a	1	2	0.164	0.003	0.128	0.005	<0.0001	<0.0001	1.0000
Finite rate of increase – <i>λ</i> (female/female/day) ^a	1	2	1.178	0.004	1.136	0.005	<0.0001	<0.0001	1.0000
Mean generation time – <i>T</i> (day) ^b	1	2	33.496	0.982	35.685	0.910	0.1160	0.9420	0.0580
Doubling time – <i>Dt</i> (day) ^b	1	2	4.221	0.083	5.420	0.214	<0.0002	<0.9998	0.0001

^a Compared by uppertailed *t*-tests.
^b Compared by lowertailed *t*-tests.

two-tailed and one-tailed cases are, respectively, as follows:

$$(1 - \gamma_T)^K = (1 - \alpha / 2)$$

$$(1 - \gamma_O)^K = (1 - \alpha)$$

For example, two groups A and B differ regarding some parameter, at the 0.05 significance level, when the *P* value (*p_T*, *p_U*, *p_L*) for that comparison is smaller than its respective critical value *γ*.

Software. The program was developed using the SAS System for Windows, version 6.12. The following products were used: SAS Language (SAS Institute 1990a), SAS/GRAPH Software (SAS Institute 1990b, 1990c, 1991), SAS Macro Language (SAS Institute 1990d) and BASE SAS Procedures (SAS Institute 1990e). The computer program (LIFETABLE.SAS) and the input data set (PODISUS.PRN) can be accessed (www.cnpma.embrapa.br/servicos.html).

Results and Discussion

Jackknife estimates for *R₀*, *r_m*, *T*, *Dt*, and *λ* for the Nascimento's data (1998) with their respective 95% CL are shown in Table 1. Table 2 presents jackknife estimates, respective standard errors and *P* values correspondent to one- and two-tailed tests. When there are only two test groups and variances of a particular parameter estimate are assumed to be homogeneous, *t*-tests can be performed based on overlapping of confidence intervals. No overlapping 95% CI corresponds to the rejection of no treatment effect hypothesis at 0.05 significance level. This equivalence does not occur for other situations than the one cited above.

Estimates of *r_m* obtained with the approximate method are always lower than those calculated with the iterative one (Southwood 1978). As pointed out by the same author, the disparity between those estimates depends on the *R₀* value and on the variation in the distribution of female age at oviposition within the group. For the Nascimento's data it was observed high *R₀* values (Table 1) and high variability in oviposition ages (Fig. 1). Consequently, *r_m* values obtained with the approximate or iterative methods were noticeable discrepant: respectively, 0.137 and 0.164 for the control group and 0.106 and 0.127 for the treated group. Coats (1976), for example, estimated *r_m* for *Muscidi-*

furax uniraptor Kogan & Legner using both methods and observed that the value obtained with the approximate method was 12% less than with the iterative one. Some authors (Byale and Bilapate 1987, Sharma et al. 1994, Sharma et al. 1997) used a linear interpolation method proposed by Howe (1953) to estimate *r_m* based on the value obtained with the approximate method. This method is a very simplified version of the iterative method, in which only two arbitrary values

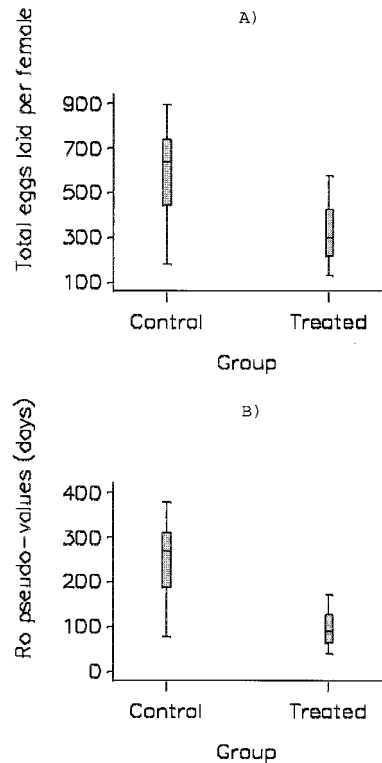


Fig. 1. Box and whisker plots for (A) Total number of eggs laid per female, (B) *R₀* pseudo-values for each group. The bottom and top edges of the box are located at the 25th and 75th percentiles. The center horizontal line is drawn at the median. The vertical lines, or whiskers, extends from the box as far as the data extend, to a distance at most 1.5 interquartile ranges. (SAS Institute 1990).

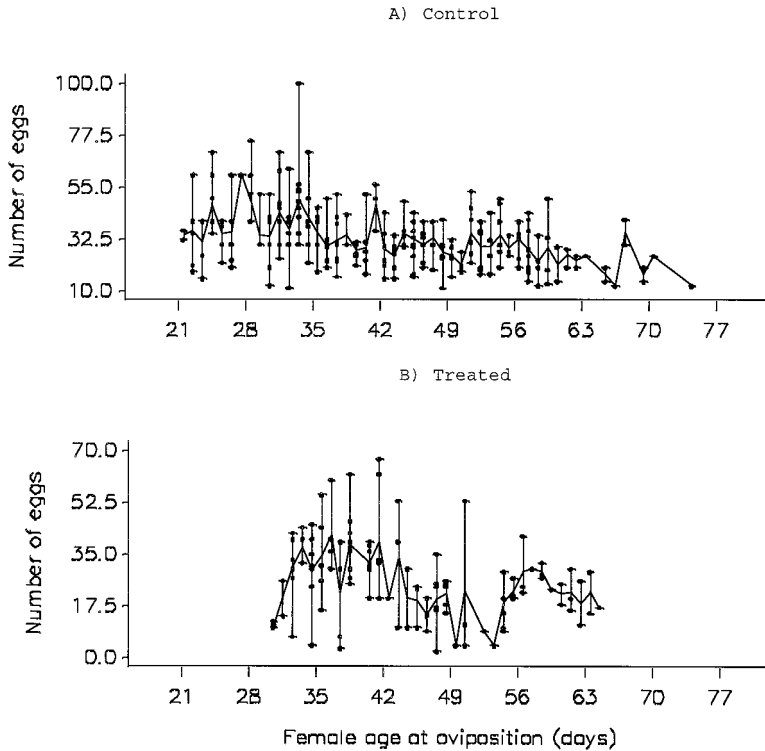


Fig. 2. Daily oviposition patterns of female *P. nigripinus* subjected to different feeding treatments. (A) Healthy larva (control). (B) Intoxicated larvae (treated). Vertical bars join minimum and maximum oviposition values at each day.

are used. The SAS program presented in this work allows estimation of r_m by using a rapid and reliable iterative procedure. The search for the best r_m is made at each step of the jackknife procedure corresponding to each time in which a female is missed out. For our case study, the maximum differences observed between the two sides of the equality based on the exponential growth model were 0.0015 and 0.0018 for control and treated groups, respectively. A possible inadequacy arises in consequence of the joint use of iterative method and jackknife procedure: the jackknife procedure requires that the minimization process be made at each jackknife step; in so doing, the resulting r_m jackknife estimate does not guarantee that the minimal distance between both sides of the equality will be achieved. This problem is more serious in the cases where the distribution of the number of eggs laid per female is asymmetric.

It is important to point out that the jackknife method, as an asymptotic procedure, is not appropriate for small samples, especially when the number of eggs laid per female has a highly skewed distribution. This problem occurs, for example, when some group has females that have little or no oviposition or a few with very high oviposition. Skewed distributions of number of eggs per female can lead to skewed distributions of jackknife Ro estimates and, consequently, to a very poor Student t approximation. In extreme cases, negative jackknife estimates can be produced

for Ro , indicating the unsuitability of the method in such situations. Jackknife estimators of means have asymptotic normal distributions, even for skewed distributions of the respective pseudo-values (Efron 1983). However, for small samples, the goodness of the Student t approximation assumed for comparing groups and for constructing confidence limits is highly dependent on the skewness of the pseudo-values probability distribution.

Box and whiskers plots of the number of eggs laid per female and Ro pseudo-values for the current case study indicated slightly asymmetrical distributions for such variables in both control and treated groups (Fig. 2). However, as intermediate sample sizes were employed, no serious problems were detected regarding asymmetrical behavior of Ro jackknife estimates distributions.

The estimates obtained without missing any female, referred to as true calculations ($Ro_g^{(0)}$, $r_{mg}^{(0)}$, $T_g^{(0)}$, $Dt_g^{(0)}$, and $\lambda_g^{(0)}$), were very similar to those calculated with the jackknife method (Table 1). Large discrepancies between estimates obtained with true calculations and with the jackknife method indicate that the last one is not adequate. In such cases, the estimates coming from the first method would be preferable. However, jackknife estimates of variance cannot be associated with true calculation estimates, and consequently no statistical tests could be performed; alternative methods like nonparametrical

bootstrap, which is less dependent on statistical assumptions, could then be employed.

An important feature of this program is the ability to perform either one- or two-tailed tests and to calculate corresponding P values. In the current case study, the effect of intoxicated diet on *P. nigrispinus* is supposed to be negative. Therefore, Ro , r_m , and λ for the control group are expected to be greater than the respective ones for the treated group; the opposite is expected to occur for T and Dt . Consequently, upper-tailed tests were used to compare the first ones, whereas lower-tailed tests were used for the last ones. When the underlying scientific hypothesis requires, using suitable one-tailed tests improves efficiency largely. As can be observed in Table 2, the P values are reduced to one-half when the adequate one-tailed tests are employed rather than the two-tailed. In this experiment it was observed that there are remarkable treatment effects for Ro , r_m , Dt , and λ . In cases like that, the differences between groups would be significant at 5% level, even if unsuitable, low-efficient two-tailed tests had been employed. However, in cases where the treatment effects are not so evident (P values ranging from 0.10 to 0.06), the decision about the significance changes when one-tailed rather than two-tailed tests are used. If a more recent approach is adopted, that is, just looking at observed P values without being concerned about choosing an arbitrary significance level, the magnitudes of the evidences against the null hypothesis are considerably different when one or two-tailed tests are carried out.

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