

Improved SAS[®] codes for life table analysis of arthropod populations

Aline de Holanda Nunes Maia¹

Alfredo José Barreto Luiz¹

Ahmad Pervez²

1 Introdução

Fertility life table (FLT) analysis of arthropod populations can capture chronic sublethal effects not detected by acute survival assays (MARINHO-PRADO, 2011; NASCIMENTO et al., 1998; NARDO et al (2001) LIU et al, 2005; LUMBIERRES et al, 2004). Inference on FLT parameters requires the use of computational methods to estimate the variance of demographic summary measures derived from information of survival and fertility of the arthropod populations under study. Jackknife-based software available for life table analysis (HULTING et al, 1990 ; MAIA et al, 2000) were developed for analyzing qualitative treatments, but such approach is frequently misused for contrasting levels of quantitative factors (GANJISAFFAR et al., 2011; PAKYARI et al., 2011; RAZMJOU et al. 2011). We present herein an extension of SAS codes already available for analysis of qualitative treatments (*lifetable.sas*, MAIA et al, 2000) now including methods for analysis of quantitative factors via jackknife-based regression analysis.

2 Material e métodos

We developed an extension of the SAS[®] program *lifetable.sas* (MAIA et al, 2000) developed for investigation on effects of qualitative treatments in arthropod demographic parameters arising from FLT analysis. The improved codes incorporated regression analysis tools for linear model fitting, influence diagnostics and residual analysis useful for studies involving quantitative treatments such as pesticide doses or temperature.

¹ Embrapa Meio Ambiente, Jaguariúna, São Paulo, email para correspondência: aline.maia@embrapa.br

² Biocontrol Laboratory, Department of Zoology, Govt. Degree College, Talwari – Tharali, Chamoli (Uttaranchal) India

As illustration, we analysed data from a study on the effect of temperature (20, 23, 25, 27 and 30 °C) on the demographic parameters the ladybird *Hippodamia variegata* (Goeze) (Coleoptera: Coccinellidae). *H. variegata* is an important predaceous ladybird that could potentially be used as a biocontrol agent of variety of aphids (NEDVED, 1999; OKMAR & PERVEZ, 2004; PERVEZ & OKMAR, 2004). Optimal augmentative rearing of the ladybird, it is necessary to optimize the temperature.

Regression models were fit the pseudovalues obtained via jackknife method applied to the life table data (MEYER et al, 1986) as described in MAIA et al (2000) by using The REG Procedure of the statistical software SAS/STAT®. The following polynomial model was used for describing the non-symmetrical patterns of temperature influence on FLT parameters :

$$Y_{ij} = \beta_0 + \beta_1 T + \beta_2 T^2 + \beta_3 T^3 + e_{ij}$$

in which Y_{ij} is the j-th FLT parameter pseudovalue for temperature level i ; the model parameters β_0 ; β_1 ; β_2 and β_3 correspond to the intercept, linear, quadratic and cubic effects respectively and e_{ij} is the random error associated to each Y_{ij} pseudovalue, $e_{ij} \sim N(0, \sigma^2)$. The pseudovalues were obtained via jackknife method applied to the life table data as described in MAIA et al (2000). Influence diagnostics and residual analysis and residual analysis were performed by using the options INFLUENCE and PREDICTD of the MODEL statement.

3 Resultados e discussões

Using the improved SAS codes we can obtain estimates of polynomial model coefficients, respective standard errors and results of associated t-tests. Results obtained for the study the influence of temperature on *H. variegata* FLT parameters are presented in Table 1.

We are using polynomial models as an approximation to more adequate non linear models for describing temperature effect. They are valid only for the range of observed data. We are currently developing SAS codes for non linear regression fitting by combining jackknife method with non linear procedures available in The NLMIXED procedure.

The computational method jackknife is used worldwide for life table analysis, despite its inherent limitations, especially in cases for which survival patterns or fertility distributions are highly asymmetrical. Whenever influence analysis points out regression outliers, the use of jackknife is arguable thus requiring the use of methods such as parametric or nonparametric bootstrap, still under development for life table analysis.

Table 1. Estimates of polynomial model coefficients used to represent the influence of temperature on *Hippodamia variegata* fertility life table parameters, obtained via The REG Procedure of the statistical software SAS/STAT®.

FLT Parameter	Effect	Estimate	Standard Error	t-statistic	p-value*
Net reproductive rate (Ro)	β_0	27332.73	3626.12	7.538	<0.01
	β_1	-3503.00	444.71	-7.877	<0.01
	β_2	148.33	17.98	8.251	<0.01
	β_3	-2.05	0.2396	-8.575	<0.01
Intrinsic rate of increase (Rm)	β_0	5.59	0.8390	6.589	<0.01
	β_1	-0.6941	0.1029	-6.746	<0.01
	β_2	0.0290	0.0042	6.968	<0.01
	β_3	-0.00039	0.00006	-7.096	<0.01
Finite rate of increase (λ)	β_0	7.48	0.9790	7.638	<0.01
	β_1	-0.8136	0.1201	-6.776	<0.01
	β_2	0.0339	0.0048	6.99	<0.01
	β_3	-0.00046	0.00006	-7.11	<0.01
Generation time (GT)	β_0	-719.39	208.28	-3.454	<0.01
	β_1	101.73	25.54	3.982	<0.01
	β_2	-4.33	1.0325	-4.198	<0.01
	β_3	0.059	0.0138	4.311	<0.01
Doubling time (DT)	β_0	-119.10	30.40	-3.916	<0.01
	β_1	16.98	3.73	4.555	<0.01
	β_2	-0.7430	0.1507	-4.906	<0.01
	β_3	0.0103	0.0020	5.145	<0.01

*Nominal significance value.

4 Conclusões

The improved codes allow the assessment of patterns of influence of quantitative factor such as temperature or agrochemical doses on demographic parameters of arthropods. The jackknife-based regression methods incorporated are adequate for data sets without critical asymmetrical behaviour for key variable such as survival and fertility. The availability of SAScodes for life regression analysis of life table parameters will be helpful for a better interpretation of life table assays.

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