

Computational resources for analysis of demographic parameters of arthropod populations

Aline de Holanda N. Maia¹; Ricardo Antônio Almeida Pazianotto¹; Alfredo José B. Luiz¹; Ahmad Pervez²

¹Embrapa Meio Ambiente, Caixa Postal 69, 13.830-000, Jaguariúna, SP, Brazil. Email: aline.maia@embrapa.br. ² Department of Zoology, Govt. Degree College, Talwari - Tharali, Chamoli (Uttaranchal), India

Demographic parameters of arthropod populations arising from fertility life table (FLT) analysis are important indicators of interactions between arthropods and the environment. As summary measures, they can capture chronic sub-lethal effects not detected by acute survival assays. Inference on FLT parameters requires the use of computational methods to estimate the variance of the referred summary measures derived from information of survival and fertility of the arthropod populations under study. Here we present and discuss two computational programs for FLT analysis: R codes including tools for analysis of quantitative or qualitative treatments (*lifetable.r*; J. Econ. Entom., 107(1), 2014) and an extension of the SAS[®] program *lifetable.sas* (J. Econ. Entom., 93(2), 2000) initially developed for analysis of qualitative treatments only. The improved codes incorporate tools for linear and nonlinear regression analysis thus allowing model fitting and residual analysis for studies involving quantitative treatments such as pesticide doses or temperature. As illustration, we present case studies on the effect of temperature and different diets on the demographic parameters of *Hippodamia variegata* (Goeze) (Coleoptera: Coccinellidae), an important aphidophagous ladybird with potential use in integrated pest management.

Key words: fertility life table, SAS codes, R codes, jackknife, regression analysis.