

Age-specific parameter estimation from individuals of unknown age in capture-recapture data

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Capture-recapture data provide a major source of information for the study of wildlife populations. Several biological and demographical questions can be addressed through capture-recapture modelling. The factors that affect survival or successful breeding probability, abundance and average residence time in stopover sites are only some of these issues to be considered. Research on the effect of age on survival though, which is a main focus in demographic analyses, is still limited. The reason for this is the unidentifiable age-at-first-capture of adult individuals for a number of species. This lack of information has forced the analysts to assume constant adult survival and therefore not to allow the study of senescence.

Pledger et al [3] developed a model for estimating stopover duration of migratory birds as well as total number of birds stopping over in a specific site. The multinomial type likelihood takes into account both the seen and the unseen birds as in the usual Jolly [1]-Seber [5] framework. The model allows for the uncertain knowledge of arrival and departure times of the individuals and provides estimates of the departure probability dependent on the unknown time since arrival. The super-population scheme, introduced by Schwarz and Arnason [4], is adopted and therefore the additions in the population between sampling occasions are also estimated. The idea is extended in order to estimate age-specific survival and capture probabilities of individuals with unknown times of birth and death in a constant study area [2].

A model which is a modification of that of Pledger is proposed in this talk. The model conditions on the probability of any individual being caught and therefore does not estimate abundance. Although approximately equivalent, the two models behave differently for relatively small sample sizes. The performances of the models under various scenarios for the parameters i.e. constant, time-varying etc. and under various assumptions are examined using simulation studies. The bias and precision of the parameter estimates provided by the two models are compared for a range of super-population sizes and model complexities. Finally, the models are applied to a long-term dataset of brushtail possums (*Trichosurus vulpecula*) and the results are compared and discussed.

References

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