Comparing survival estimates from unmarked population- and individual-level data

M. Brooks[a,c], **M. Mugabo**[b,d], **G. Rogers**[b,e], **T. Benton**[b,f], and **A. Ozgul**[a,g]

[a]Institute of Evolutionary Biology and Environmental Studies
University of Zurich
Zurich, Switzerland

[b]School of Biology
University of Leeds
Leeds, England

[c] Mollie.Brooks@ieu.uzh.ch
[d] M.Mugabo@leeds.ac.uk
[e] RogersGwen@gmail.com
[f] T.G.Benton@leeds.ac.uk
[g] Arpat.Ozgul@ieu.uzh.ch

Abstract: Models of population dynamics allow us to estimate population growth or decline and to predict responses to environmental change. Parameterizing these models typically requires demographic data at the individual level, collected by marking or - in some experimental settings - isolating individuals from the population. However, these methods can unintentionally alter demographic rates by reducing the fitness of marked individuals in the wild or changing their environment in isolation. Thus, there is a need for methods that enable the estimation of demographic rates without individual data.

Stage-structured N-mixture models were recently developed to enable the estimation of state-specific vital rates using repeated state-specific counts of populations of unmarked individuals (Zipkin et al. 2013). We extend the stage-structured N-mixture model to apply to a time series with uneven sampling intervals. Such uneven or irregular sampling periods often occur in long term monitoring programs.

We apply this method to an extensive laboratory experiment of soil mite populations. Individual vital rates were observed by isolating and monitoring individuals for 24 hour periods. Stage-specific population counts were done twice per week, creating uneven sampling times. Mites were observed eating other mites, but it is unclear if this behaviour was simply scavenging or killing. To test if mortality was higher in the population than for isolated individuals, possibly due to cannibalism, we compare estimates of daily mortality from the stage-structured N-mixture model to the individual data.

If time permits, we will present further extensions including covariates and comparison of multiple fitting algorithms.

References

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