My, how you've grown: a practical guide to modeling size transitions for Integral Projection Model (IPM) applications

Tom E.X. Miller*a and Stephen P. Ellner^b

^aDepartment of BioSciences, Rice University, Houston, TX ^bDepartment of Ecology and Evolutionary Biology, Cornell University, Ithaca, New York

April 29, 2020

Authorship statement: All authors discussed all aspects of the research and contributed to developing methods, analyzing data, and writing and revising the paper.

Data accessibility statement: No original data appear in this paper. Should the paper be accepted, all computer scripts supporting the results will be archived in an appropriate public repository such as Dryad or Figshare, with the DOI included at the end of the article.

^{*}Corresponding author. Department of BioSciences, Rice University, Houston, TX 77005-1827. Email: tom.miller@rice.edu Phone: 713-348-4218

Abstract

1 Introduction

A few stray bits:

Modeling growth in IPMs is *modeling*, not statistics. Statistical tools and tests inform the process, but do not dictate it. We are not claiming that we know how to find the "right" model for any particular data set or application through some model selection procedure. Our goal is to demonstrate how a simple workflow, using tools that were nonexistent or not readily available when IPMs came into use, makes it straightforward and relatively easy to identify when the default choice (Gaussian with possibly nonconstant variance) is a poor fit to the data, and to then choose and fit a substantially better growth model that is no harder to use in practice.

The default growth model traces back to Easterling et al. (2000). The analyses described there pre-date version 1.0 of R by several years, and they were quickly replaced by better methods such as the linear and generalized linear mixed models regression functions in R, notably the option to fit linear mixed models with nonconstant growth variance. But as Peterson et al. recently noted, despite the growing list of other options and repeated calls in the literature for greater attention to growth modeling, the general state-of-the-art in the literature remains stuck where it was 15 or so years ago, using the default model without pausing to examine critically whether or not it actually provides a good description of the data. Our goal here is to break that logjam, by building on Peterson et al. to provide a practical "new default" that researchers can follow to choose, fit, and implement better descriptions of individual growth for IPMs and any other size-structured population model.

Acknowledgements

This research was supported by US NSF grants DEB-1933497 (SPE) and