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

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Abstract

1 Introduction

Structured demographic models – matrix and integral projection models (MPMs and IPMs) – are powerful tools for data-driven modeling of population dynamics and viability that are widely used in basic and applied settings. In contrast to MPMs for populations with discrete structure (life stage, age class, etc.), IPMs are a relatively recent development (Easterling et al., 2000) best known for their ability to represent populations structured by continuous variables, most commonly size. A second, related innovation[1] of the IPM framework is its emphasis on modeling size-dependent vital rates as sub-models of the full projection model. This means that ecologists could assemble an IPM from familiar regression tools and leverage their capacity for covariates and hierarchical variance structures (i.e., random effects) to statistically describe growth, survival, reprduction, and other demographic transitions as functions of size. The relative ease and flexibility of the regression-based approach has facilitated a growing body of IPM literature that examines how covariates of individual demographic fate scale up to affect population dynamics (cite examples) and that partitions demographic heterogeneity associated with space, time, or individual identity (cite examples).

Compared to all other vital rates, growth is special.

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,

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[1] *This 'innovation' is not unique to IPMs but it was rare in MPMs before IPMs.*

and implement better descriptions of individual growth for IPMs and any other size-structured population model.

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Literature Cited

Easterling, M. R., Ellner, S. P., and Dixon, P. M. (2000). Size-specific sensitivity: applying a new structured population model. *Ecology*, 81(3):694–708.