Estimation of individual growth trajectories when repeated measures are missing - DTU Orbit (12/12/2018)

Estimation of individual growth trajectories when repeated measures are missing

Individuals in a population vary in their growth due to hidden and observed factors such as age, genetics, environment, disease, and carryover effects from past environments. Because size affects fitness, growth trajectories scale up to affect population dynamics. However, it can be difficult to estimate growth in data from wild populations with missing observations and observation error. Previous work has shown that linear mixed models (LMMs) underestimate hidden individual heterogeneity when more than 25% of repeated measures are missing. Here we demonstrate a flexible and robust way to model growth trajectories. We show that state-space models (SSMs), fit using R package growmod, are far less biased than LMMs when fit to simulated data sets with missing repeated measures and observation error. This method is much faster than Markov chain Monte Carlo methods, allowing more models to be tested in a shorter time. For the scenarios we simulated, SSMs gave estimates with little bias when up to 87.5% of repeated measures were missing. We use this method to quantify growth of Soay sheep, using data from a long-term mark-recapture study, and demonstrate that growth decreased with age, population density, weather conditions, and when individuals are reproductive. The method improves our ability to quantify how growth varies among individuals in response to their attributes and the environments they experience, with particular relevance for wild populations.

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