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ESTIMATING BUTTERFLY ABUNDANCES FROM TRANSECT COUNT DATA

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Most methods of estimating wildlife abundance are based on mark-recapture methods. With fragile or threatened species, however, capture is not feasible and abundance estimates must rely on observational count data alone. When such species have discrete generations (as insects often do), a simple estimation question arises: how can time series of count data be used to estimate the total number of individuals in a single generation? Current methods for estimating single-generation abundances with count data treat the unobserved population dynamics as deterministic, only allowing for stochasticity in the counting process. By ignoring stochasticity in population dynamics, the precision of the abundance estimate is overestimated, and confidence intervals are too small. Here, we develop a novel estimation method that accommodates stochasticity in the population dynamics and also allows more flexible specifications of birth times and sampling protocols. This work is motivated by the study of an endangered butterfly in the North Carolina sandhills.

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