

Beyond bespoke: standardizing integrated population models for comparative and range-wide studies

Integrated population models (IPMs) have become very popular in recent years due to key advantages such as making efficient use of limited data and taking full account of various sources of uncertainty. Another often-highlighted strength is the fact that flexible Bayesian implementations allow tailoring each IPM specifically to the population under study, as well as the types and structure of available data sources. While having a “bespoke” model can undoubtedly provide unique insights into the dynamics of a single population of a single species in a single location, heavily tailored models are not very well suited for larger-scale comparative and/or range-wide studies. Yet such studies, encompassing multiple populations, are what is needed to address threats to biodiversity at national and global scales.

During the same time as IPMs have gained popularity, standards for formatting, documenting, and publishing ecological data have come a long way. More and more data are being made available in standardized formats adhering to the FAIR principles, and this opens new possibilities for data integration with the aim of studying changes in biodiversity at much larger spatial scales. Importantly, this no longer applies only to species distribution models for occurrence data, but for a broader range of models for a large variety of data types, including data on population abundance and demographic rates.

Standardization of population- and demographic data allows for standardization of IPMs and IPM workflows. We illustrate this with a generalized IPM designed to be fit to commonly collected data on hole-nesting birds which has been standardized as part of the SPI-Birds Network and Database initiative. Through standardized analysis of data from multiple populations we obtain insights into the overarching drivers of the widespread population declines of migratory passerines and identify both similarities and differences the responses of different breeding populations across a latitudinal gradient.

We thus showcase how IPMs can be generalized to provide a multi-population perspective of demographic drivers across large spatial scales and highlight the importance of facilitating their use by linking them to relevant databases and by providing high-quality documentation not only for model code, but entire analysis workflows.