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Methods in Ecology and Evolution

Dear Editor

Please accept our manuscript “Improved status and trend estimates from the North American Breeding Bird Survey using a hierarchical Bayesian generalized additive model”, for publication in Methods in Ecology and Evolution as a Research Article.

In this paper, we describe a new hierarchical Bayesian statistical model for estimating population status and trend using data from the North American Breeding Bird Survey (BBS), which is demonstrably better than the models currently in use. The status and trend estimates produced by agencies in the United States and Canada are the cornerstone of avian conservation in North America, and yet many of the common conservation uses of these estimates (e.g., assessing recovery of species at risk, changes in population trends, and intermediate-term rates of change) are not well supported by the parametric structure of current model. The models that we describe are well designed to provide status and trend estimates for a wide range of conservation applications, without any of the conflicts between the purpose/use of the estimates and the assumptions and structures of the model.

We have described the models, demonstrated their application to a selection of species, provided examples of situations where these new models out-perform alternative models, conducted a full cross-validation comparison to the standard BBS model, and provided archived data and code to run the models (GitHub repository and a separate R-package “bbsBayes”).

The new models, in particular a version we refer to as GAMYE (GAM with added year-effects), provide more stable estimates of population trend, are more sensitive to changes in a species’ population trend, share information among sub-regions of a species’ range on the pattern and rate of population change, outperform the standard model in out-of-sample predictive accuracy for all species here, and allow for a useful decomposition of the population trajectory into the smooth component and the annual fluctuations. This model is useful for almost any long-term biological monitoring dataset, and the code and R-package we’ve provided here will allow other researchers to easily apply or customize this model.

An earlier version of this manuscript is available as a preprint on BioRxiv: <https://doi.org/10.1101/2020.03.26.010215>.

Thank you for your time and consideration

Adam C. Smith