



THE UNIVERSITY OF BRITISH COLUMBIA

Faculty of Forestry

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Dear Dr. Stephens:

We would like to propose an *Opinion* for *Trends in Ecology & Evolution* entitled ‘A four-step Bayesian workflow for improving ecological science.’ Given the increasing aims of forecasting and prediction today, ecologists are using more complex models to leverage larger datasets (Anderson *et al.*, 2021; Muff *et al.*, 2022). Many researchers—ourselves included—were not trained in best statistical practice for these approaches, which can lead to poor models and incorrect predictions and decisions.

- To address this pressing gap, we outline a generalizable workflow (see Fig. 1 below), which is built on fundamental scientific principles and new insights from statistics and data science (Grinsztajn *et al.*, 2021; van de Schoot *et al.*, 2021). This approach moves away from a focus on null hypothesis testing, towards estimating effect sizes, with models calibrated and better understood through simulating data at multiple steps—using a number of skills more often associated with theoretical than empirical ecology. We conclude by highlighting how adopting this workflow may improve statistical and mathematical training in ecology, including how we implement machine learning models and other new approaches.
- While there have been numerous extensive and specific articles on various aspects of model fitting and validation in recent years (e.g. Conn *et al.*, 2018; Gabry *et al.*, 2019; Tredennick *et al.*, 2021; DiRenzo *et al.*, 2023), there have been no attempts—to our knowledge—to outline a modern statistical workflow for today’s more computational evolutionary biologists and ecologists. This makes our article especially timely and novel. While it builds on advances in scientific and statistical workflows in other disciplines (Gelman *et al.*, 2020; Grinsztajn *et al.*, 2021; Schad *et al.*, 2021), it provides a unique perspective by explaining the workflow and why it is both tractable and critical now for ecology especially.
- Further, we believe this article would be ideal for *TREE* given our aims for it to be concise, direct and extremely approachable. The workflow is designed to be broadly generalizable and practical. To make sure the steps are clear and accessible we would present full example of the workflow and accompanying code (in R Markdown) to estimate trends over time in plant and animal phenology.

The manuscript is authored by an international and interdisciplinary group of ecologists, evolutionary biologists and statisticians. The workflow follows the basics of how authors EM Wolkovich, TJ Davies and WD Pearse approach model building and leverages the insights and skills of computational statistician M Betancourt who has developed fundamental statistical workflows for diverse

scientific disciplines. We realize our author list is one person beyond the desired size, but we found multiple perspectives on how to implement this workflow has been especially useful.

We hope that you will find this potential opinion submission, which provides a road-map for the many ecologists now building more complex models, suitable for publication in *Trends in Ecology & Evolution*. By integrating simulation more fully in model building and testing this workflow can fit models that are more robust and well-suited to provide new ecological insights—allowing us to refine where to put resources for better estimates, better models, and better forecasts.

Sincerely,

A handwritten signature in black ink, appearing to read 'Elizabeth M Wolkovich', with a stylized flourish at the end.

Elizabeth M Wolkovich
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University of British Columbia

Relevant recent articles As mentioned above, our article leverages advances in statistical workflows, which were developed especially by more Bayesian-focused statisticians, but designed to be applicable widely (Betancourt, 2020; Gelman *et al.*, 2020). These new approaches have been adapted to epidemiology and cognitive science (Grinsztajn *et al.*, 2021; Schad *et al.*, 2021) but our article would be the first to outline how it works in evolution and, especially, ecology. We believe an approachable, concise treatment of this workflow may be especially powerful in ecology where many researchers now have the computational toolkit to fit larger more complicated models, but lack an organizational framework to develop, test and improve bespoke models. With this new workflow, we believe many more ecologists could fit their data to bespoke mathematical models of biological systems, which in turn would yield better inference, predictions and forecasts.

Example figure

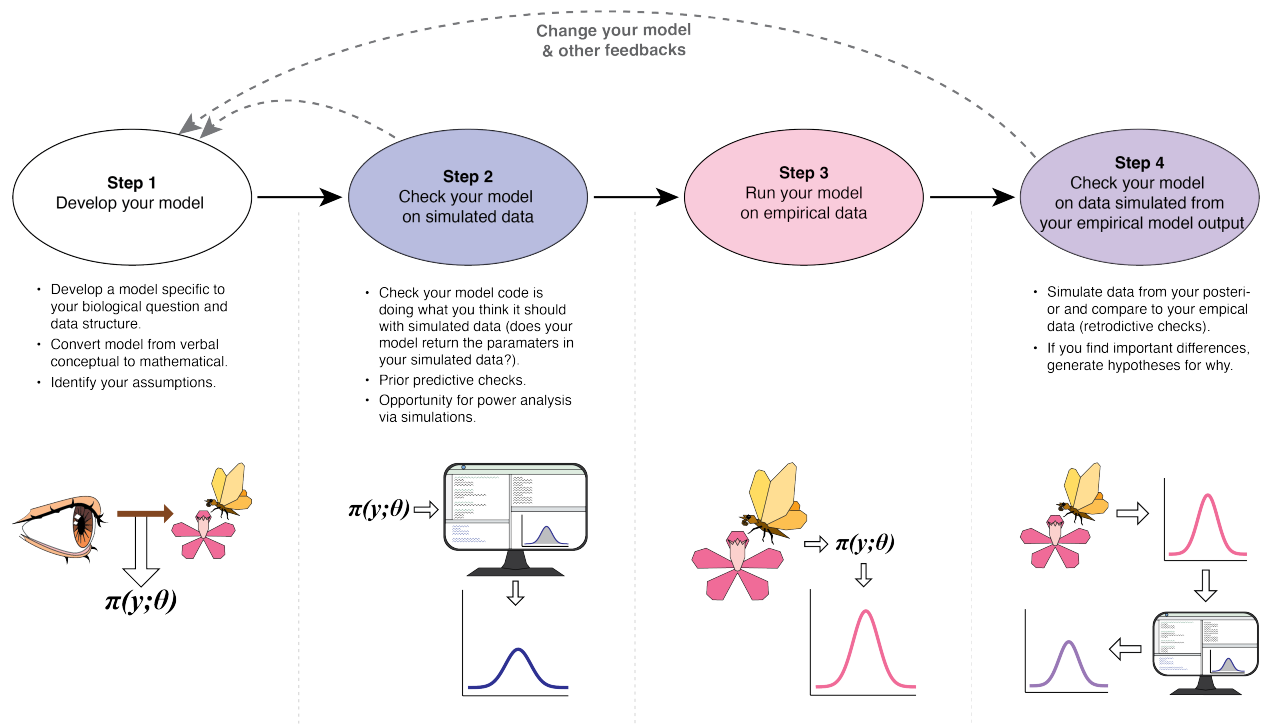


Figure 1: The four-step iterative workflow we outline can help design models for specific ecological questions, data and aims—which makes this a statistical workflow that can naturally become a scientific workflow. It makes the step that many of us focus on—running your model on your empirical data (Step 3)—far more straightforward and insightful by using simulations both before (Step 2) and after (Step 4) it to better understand the model and data together.

References

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