Methods in Ecology and Evolution

July 14, 2025

MEE Editorial Team,

We are pleased to submit our manuscript “A generalizable tool for predicting developmental phenology for wild poikilotherms” for consideration as an Application in *Methods in Ecology and Evolution.*

hatchR is a software ecosystem designed to help scientists accurately predict developmental phenology for wild poikilotherms. While originally designed specific to fishes, we present numerous application and model sources for application in a wide array of poikilotherms. The software reworks accumulated thermal unit approaches developed from *ex situ* studies, offering highly accurate predictions in wild environments. The primary functionality of the package focuses on allowing users to build custom developmental models specific to their species or populations of interest and then forecast or hindcast developmental phenology. For instance, users could predict hatching phenology using know mating dates (*e.g.*, oviposition) or, alternatively, predict mating timing from observing developmental events in the field (e.g., hatching).The tool takes user-provided temperature regimes (*e.g.*, field temperature logger data) and phenological timing (mating), applying an effective value model to estimate phenology.

To showcase the utility of hatchR, our manuscript presents three case studies. We especially highlight the utility of this software for predicting and managing populations’ responses to climate change. Our fist example demonstrates a site-specific response of Coastal Tailed Frogs (*Ascaphus truei*) to a changing climate over 30-years of daily temperature data using resources (model parameterization and temperature data) all available from published examples. In the two additional examples, we show how hatchR can be used to interrogate intra- and interspecies differences in developmental traits, specifically genetic x environment interactions, using four species of North American frogs in the genus *Lithobates* and five populations of cabbage beetles from a 3500 km latitudinal gradient. Additionally, we include a table highlighting the diversity of putative model sources across four taxonomic classes (Amphibians, Reptiles, Insects, and Crustaceans).

The software is available in two forms: 1) An R package, already on CRAN, providing the greatest flexibility for advanced applications. 2) A Shiny-based graphical user interface, designed for fisheries managers seeking an intuitive, applied tool. Both versions allow users to perform data checks, visualize trends, use existing models, or create custom parameterizations.

Beyond the manuscript, we have developed online resources guiding users from basic to advanced application of hatchR. As such, the manuscript presents only the core functionality with a total length of 3,475 words and includes two tables and four figures.

We believe our manuscript will be of broad interest to *MEE* readers, given hatchR’s applicability across diverse research contexts from localized, management-driven decisions to large-scale ecological or evolutionary research across a wide taxonomic breadth. A primarily goal of publishing in *MEE* is to reach an audience with taxonomically diverse research interests, far beyond the original application of the software.

If our manuscript is selected for review, we would like to suggest the following subject matter editors and referees, all of which possess the necessary expertise to evaluate our work objectively. To the best of our knowledge, none of the suggested individuals have any conflict of interest.

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Sincerely,

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