

Dear PLOS Computational Biology Editorial Board,

Please find attached the manuscript, "resevol: an R package for spatially explicit models of pesticide resistance given evolving pest genomes", which we hope that you will consider for publication as a software article.

The evolution of pest resistance to chemical pesticides is a widespread problem of global concern. To meet the challenges of agricultural production given pests and evolved resistance, models are needed to develop new strategies of pest management and targeted models for specific systems. We introduce the resevol R package as a highly flexible tool for developing and running individual-based models of evolving populations on a dynamic landscape, with special focus on (bio)pesticide resistance evolution. The resevol package allows users to model individuals with full digital genomes that map to traits with (potentially evolving) covariances. It accommodates a flexible range of individual life histories and mating systems. It also simulates spatially explicit landscapes with dynamic properties that rotate over time (e.g., crops produced, pesticide applied), and includes options for highly detailed landscape properties. We explain the methodological and conceptual novelties of our software and individual-based modelling, then demonstrate how to use the resevol package in the manuscript and supporting information.

Our manuscript presents a description of a major new piece of software, which we believe will be widely used by researchers and managers, including future work by the authors already in planning. The resevol package has been downloaded over 4500 times from the Comprehensive R Archive Network (CRAN). In addition to providing new modelling software, our manuscript and R package also introduces a novel methodological and conceptual approach for individual-based models of complex genomes and traits. We show how an evolutionary algorithm can be applied in a bottom up, mechanistic, approach to construct individuals with traits that covary in predictable ways from underlying genomes.

The resevol R package is open-source and available on CRAN and GitHub, and we intend to actively maintain it and use it for addressing major theoretical and applied questions in biopesticide management. We certify that this manuscript is of original work and not under review at any other journal or book. A pre-print version of this manuscript is available on bioRxiv (<https://www.biorxiv.org/content/10.1101/2022.08.22.504740v1>). In the interest of transparency, the entire version controlled history of resevol development (including this manuscript) is published on GitHub (<https://github.com/bradduthie/resevol>).

Our R package includes accompanying documentation for building and install software, using software, and testing the software (see the resevol website, CRAN documentation, and supporting information of this manuscript).

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