resevol: an R package for spatially explicit models of pesticide resistance given evolving pest genomes

A. Bradley Duthie[1,2], et al.

[1] Biological and Environmental Sciences, University of Stirling, Stirling, UK [2] alexander.duthie@stir.ac.uk, Biological and Environmental Sciences 3A149 University of Stirling Stirling, FK9 4LA, UK

Abstract

1. Pesticide resistance is a serious problem.
2. We introduce the resevol R package, which runs individual-based models of pests with quantitative and covarying traits and three mating systems.
3. Simulations are on a landscape where crops and pesticides are changed.
4. We give an example of simulating pests with covarying traits
5. The resevol R package is open source under GNU Public License; source code and documents are freely available on GitHub.

Key words: *pest management*, *food security*, *ecological modelling*

Introduction

- Pest resistance to pesticide is a serious wicked problem that affects food security.
- A quantitative genetic approach to pesticide resistance to maintaining resistance.
- The resevol R package addresses two problems: genetic architecture and landscape selection
- The R package can facilitate general questions and targetted ones

Covarying pest quantitative traits

- The issue is that we want mechanistic, not phenomenological, trait covariances
- Solution is to use a genetic algorithm to find genome structures (Hamblin, 2013)
- Genomes include values that then define a network from alleles to traits
- Example using the `mine_gmatrix` function, and its various arguments

Simulating landscape-level pesticide resistance

- We want to model evolution of pesticide resistance across heterogenous landscape
- Track entire genomes, traits, and yield over time and across space
- Use covarying traits from `mine_gmatrix` to make evolving pests

- Options for 10 crops and 10 pesticides simultaneously, and rotation
- Function `run_farm_sim` runs simulations

Example of individual-based simulations

- Example of evolving species with different crop and pesticide appications

Conclusions

Availability

The resevol R package can be downloaded from CRAN (https://cran.r-project.org/package=resevol) or GitHub (https://bradduthie.github.io/resevol/). The package is open source under GNU Public License.

Conclusions

Acknowledgements

This software was developed as part of the project for Enhancing Diversity to Overcome Resistance Evolution (ENDORSE). The ENDORSE project is a joint Newton funded international partnership between the Biotechnology and Biological Sciences Research Council (BBSRC) in the UK and the São Paulo Research Foundation (FAPESP) in Brazil under BBSRC award reference BB/S018956/1 and FAPESP award reference 2018/21089-3. ENDORSE is a partnership among Universidade Estadual Paulista (UNESP), the University of Stirling (UoS), and the Centre for Agricultural and Biosciences International (CABI).

References

Hamblin, S. (2013). On the practical usage of genetic algorithms in ecology and evolution. *Methods in Ecology and Evolution*, 4(2):184–194.