

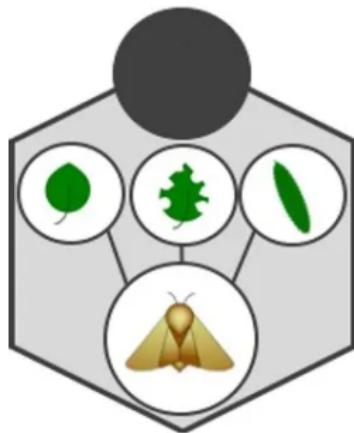
resevol: an R package for spatially explicit models of pesticide resistance given evolving pest genomes

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<http://bradduthie.github.io/talks/resevol.pdf>

Pesticide resistance evolution

Impact on agriculture



- ▶ Resistance wicked & widespread¹
- ▶ Obstacle to food security²

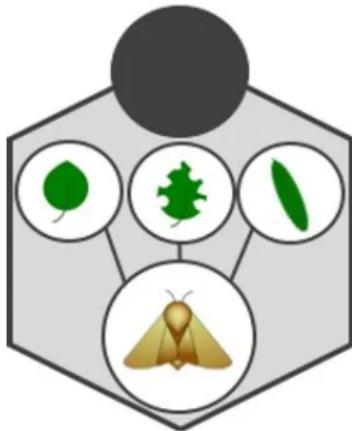
¹Gould et al. 2018. *Ecol. Appl.* 13:1791-1805.

²Bradshaw et al. 2016. *Nat. Commun.* 7:12986.

³Carroll et al. 2014. *Science* 346:1245993.

⁴Saikai et al. 2021. *Pest Manag. Sci.* 77:273-284.

Pesticide resistance evolution



Impact on agriculture

- ▶ Resistance wicked & widespread¹
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Manage resistance evolution

- ▶ Weaken selection for resistance³
- ▶ Varying pesticide application⁴

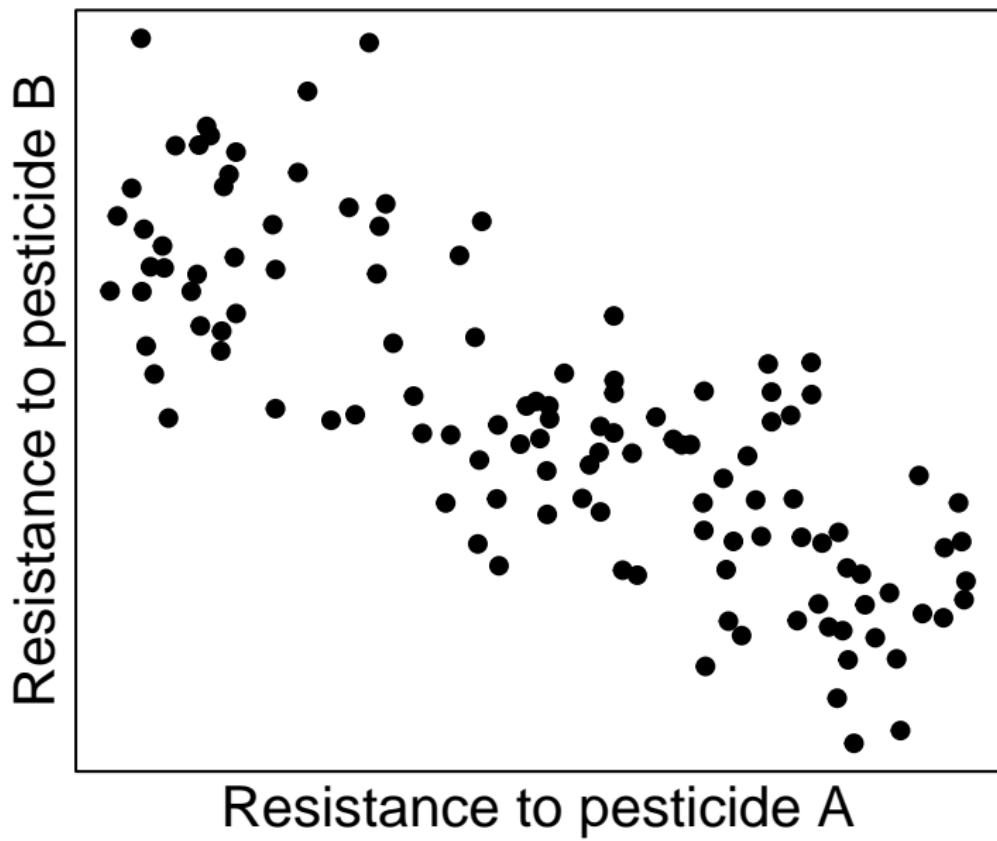
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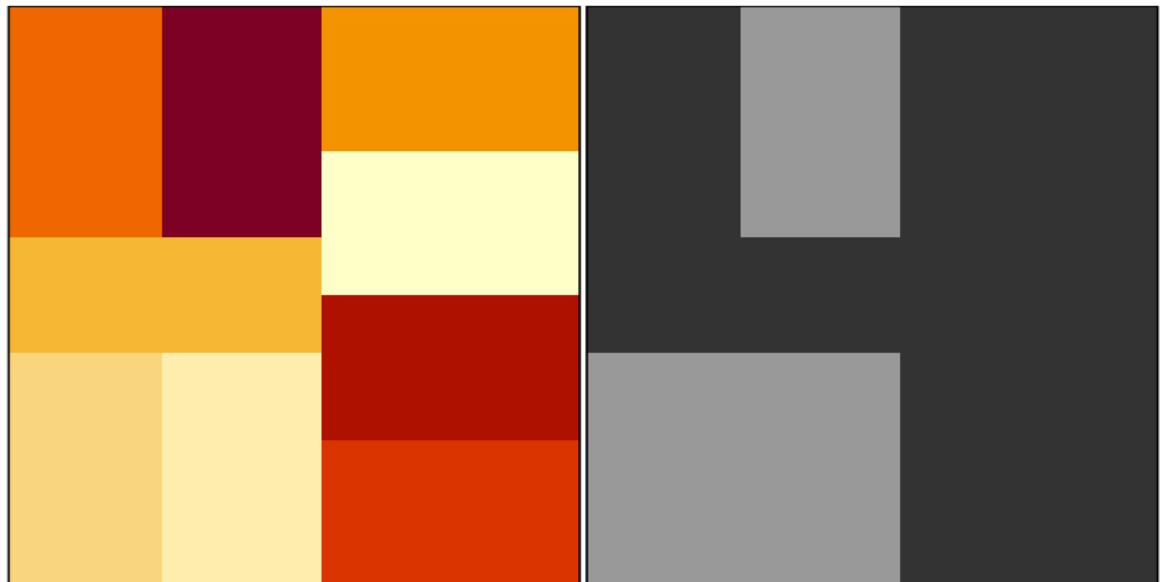
⁴Saikai et al. 2021. *Pest Manag. Sci.* 77:273-284.

Negatively correlated cross-resistance between pesticides



¹Chapman & Penman. 1979. *Nature* 281:298-299.

Enhancing Diversity to Overcome Resistance Evolution



Unique farms

Pesticide applied

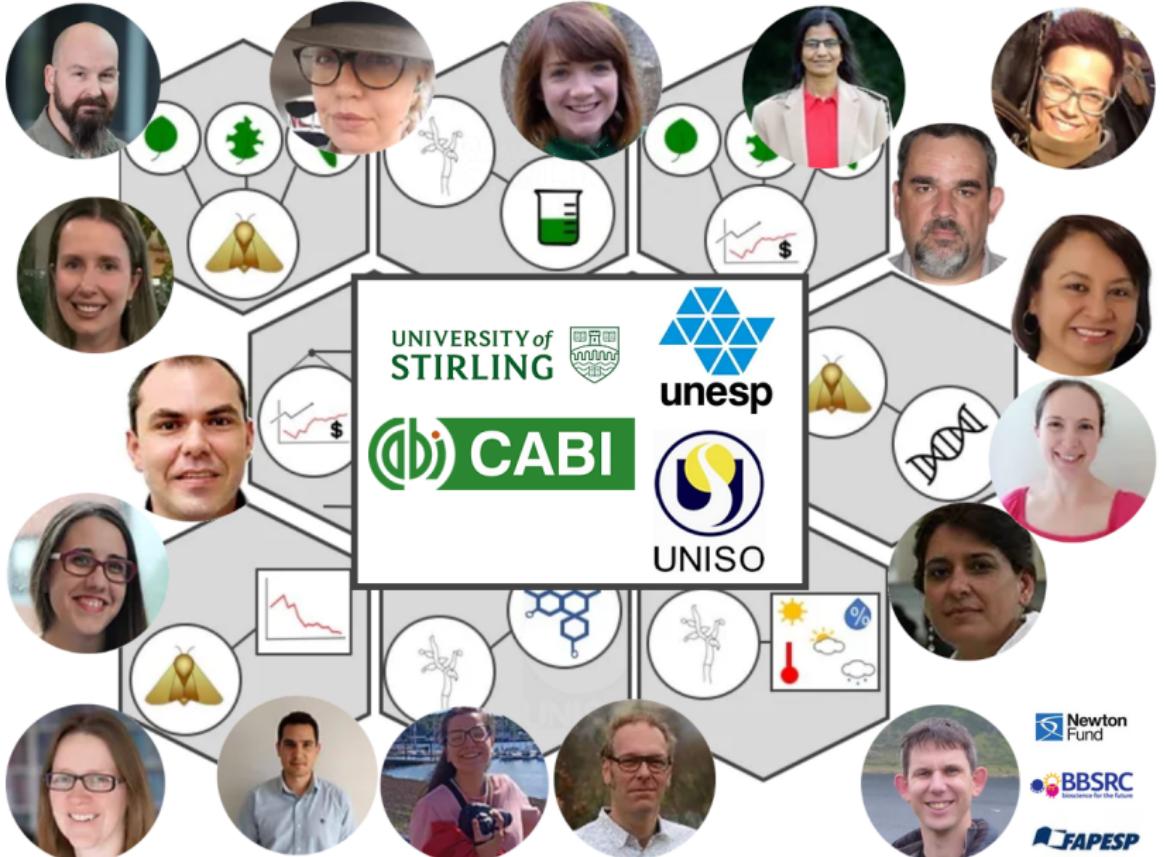




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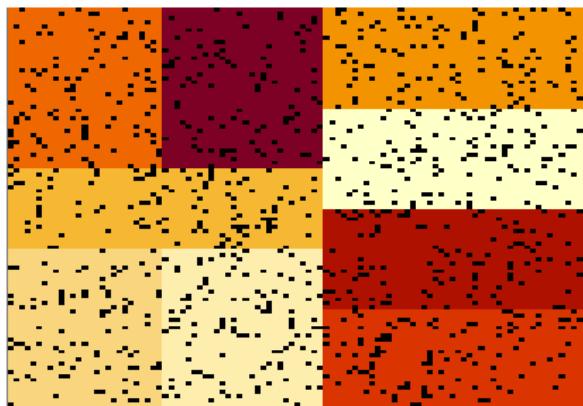
Modelling as a proof of concept before scaling up



¹Image: [Public Domain](#)

Agent-based modelling

Simulate a complex system *in silico* with code



- ▶ Agents as discrete entities
- ▶ Individual variation
- ▶ Spatially explicit landscapes
- ▶ Stochastic processes
- ▶ High model complexity

resevol: An R package for modelling agricultural pests

resevol 0.3.3.0 Get started Reference Articles ▾ Changelog Lab notebook



CRAN 0.3.0.1 downloads 3425 downloads 173/month

Resistance Evolution (resevol) simulation package

The resevol R package is a tool for simulating social-ecological individual-based models (IBMs) for the ecology and evolution of agricultural pest species. Simulations model a spatially explicit landscape broken down into one or more independent farms on which one of up to 10 crops can be grown and one of up to 10 pesticides can be applied. Crop and pesticide application can be rotated during a simulation at different spatial and temporal scales to simulate the effects of heterogeneity of pest environment. Haploid or diploid pest genomes are modelled explicitly with an arbitrary number of loci that map to any number of traits. This mapping of loci to traits can be set with a pre-specified trait correlation structure, which is found using an evolutionary algorithm run using the `mine_gmatrix()` function. Individual pest traits can affect movement, reproduction, feeding, pesticide tolerance, metabolism, and other individual characteristics. Simulations of pest populations dynamics run with the `run_sim_farm()` function can track individual pest locations, pedigree, behaviour, and trait evolution.

Links

[View on CRAN](#)
[Browse source code](#)
[Report a bug](#)

License

GPL (>=2)

Citation

[Citing resevol](#)

Developers

A. Bradley Duthie
Author, maintainer

Rose McKeon
Author, contractor

[More about authors...](#)

¹Duthie AB, McKeon CR (2022). `resevol`: Simulate Agricultural Production and Evolution of Pesticide Resistance. R package version 0.3.3.0, <https://bradduthie.github.io/resevol/>.

resevol: An R package for modelling agricultural pests

Complex individuals

- ▶ Complete genomes
- ▶ Highly polygenic traits
- ▶ Set trait covariances
- ▶ Flexible life-history
- ▶ Flexible mating system

¹Duthie AB, McKeon CR (2022). resevol: Simulate Agricultural Production and Evolution of Pesticide Resistance. R package version 0.3.3.0, <https://bradduthie.github.io/resevol/>.

²Duthie, AB, R Mangan, CR McKeon, MC Tinsley, LF Bussière. 2022. resevol: an R package for spatially explicit models of pesticide resistance given evolving pest genomes. bioRxiv 2022.08.22.504740; doi: <https://doi.org/10.1101/2022.08.22.504740>

resevol: An R package for modelling agricultural pests

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Dynamic landscapes

- ▶ Custom land dimensions
- ▶ Custom pesticide rotation
- ▶ Custom crop rotation
- ▶ Individual farms tracked
- ▶ Raster landscape maps

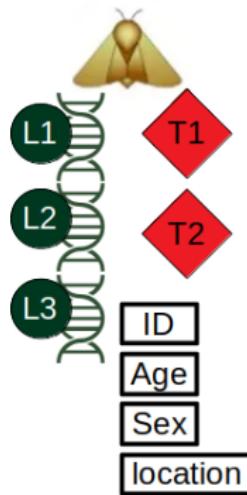
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resevol: An R package for modelling agricultural pests

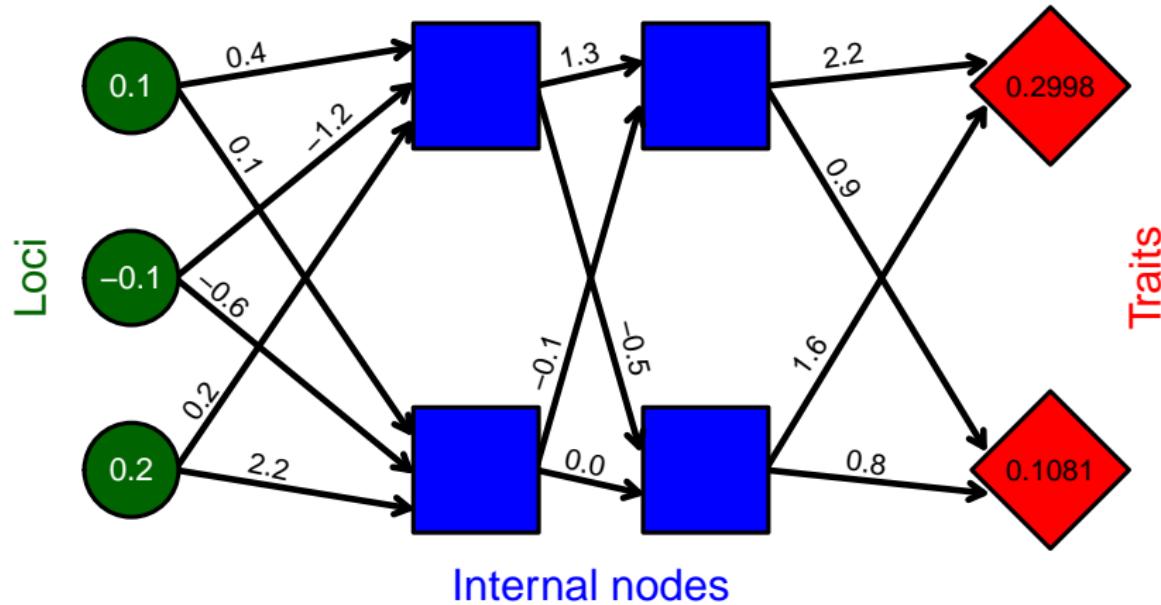
Complex individuals

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¹Image: Public domain

A genetic architecture for pre-specified trait covariances

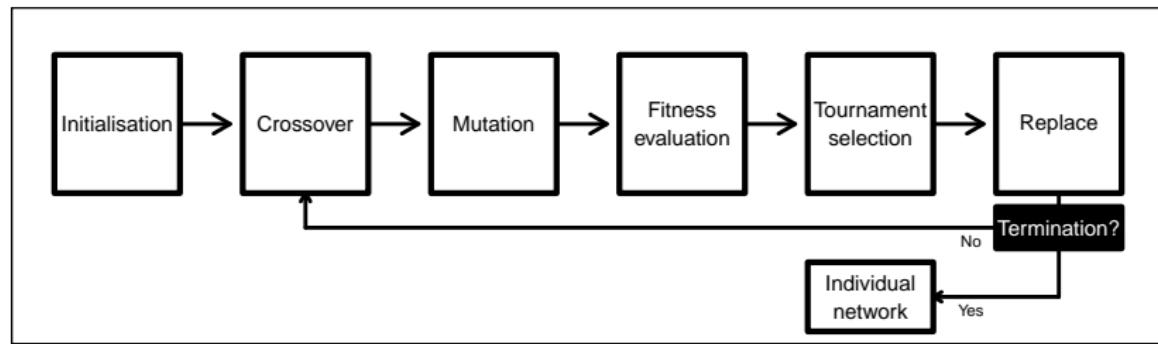


¹resevol R package vignette:

https://bradduthie.github.io/resevol/articles/evolutionary_algorithm.html

Evolutionary algorithm to find genetic architecture

Initialise a population of multiple potential networks from loci to traits.



Evolve values between nodes, mapping loci to traits.

¹resevol R package vignette:

https://bradduthie.github.io/resevol/articles/evolutionary_algorithm.html

Evolutionary algorithm to find genetic architecture

```
gmt <- matrix(data = c( 1.0, -0.5, -0.5, 2.0),  
               nrow = 2);
```

```
mg  <- mine_gmatrix(gmatrix = gmt,  
                     loci = 3,  
                     indivs = 2000, npsize = 12000,  
                     max_gen = 5400, sampleK = 1200,  
                     chooseK = 6, layers = 4,  
                     mu_pr = 0.2, pr_cross = 0.2,  
                     mu_sd = 0.004, term_cri = -8);
```

Evolutionary algorithm to find genetic architecture

**Pre-specified
covariances**

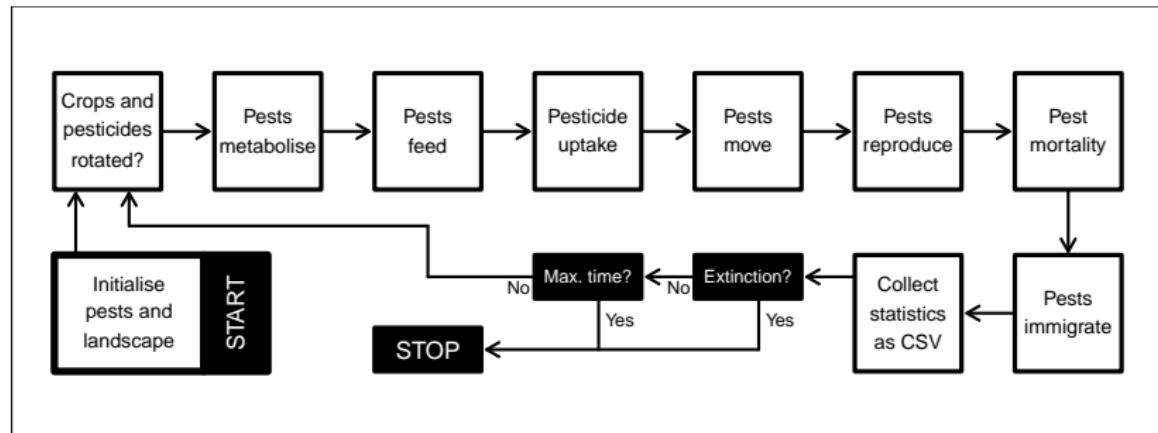
$$\begin{bmatrix} 1.0 & -0.5 \\ -0.5 & 2.0 \end{bmatrix} \quad (1)$$

**Covariances
produced**

$$\begin{bmatrix} 1.002 & -0.498 \\ -0.498 & 1.998 \end{bmatrix} \quad (2)$$

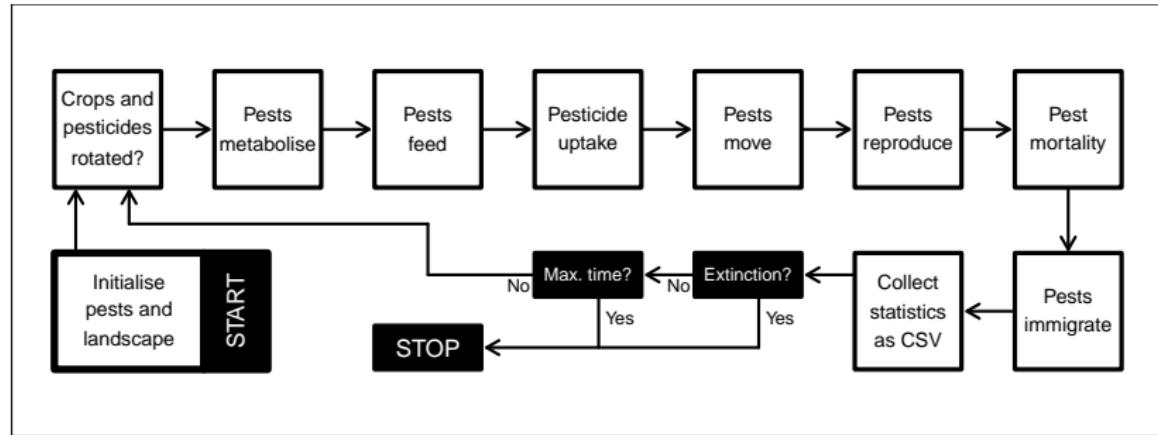
Pest life-history events defined within an age range

Within a time step, order of events are specified.



Pest life-history events defined within an age range

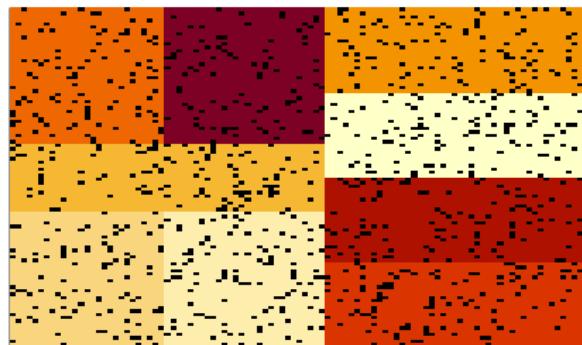
Within a time step, order of events are specified.



Specific events can be restricted to age ranges:

Feed: 0-2, Move: 3-8, Mate: 7-9

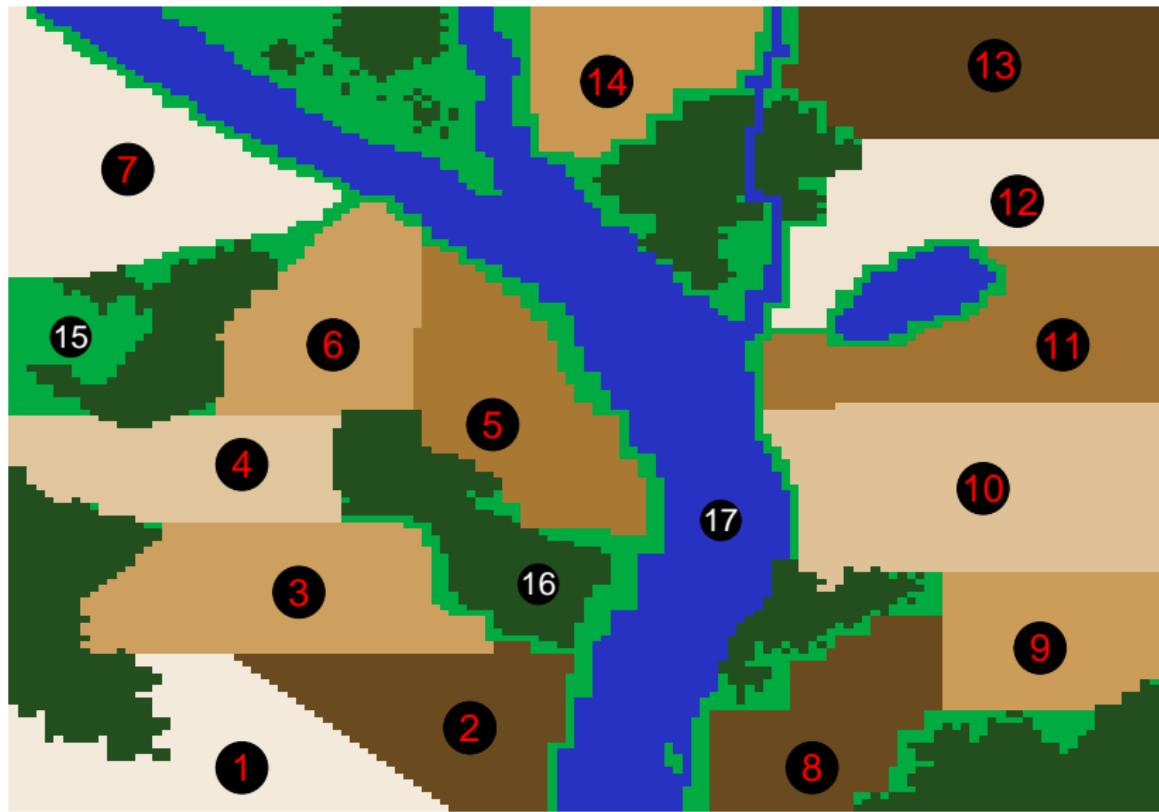
Constructing a landscape: Default options



- ▶ Specify 'farms', 'xdim', 'ydim'.
- ▶ Shortest splitline algorithm
- ▶ Land edge: torus, leaky, reflect

Each farm can use up to one crop and one pesticide, and the timing and rotation rules for crops and pesticide allow any Markov process.

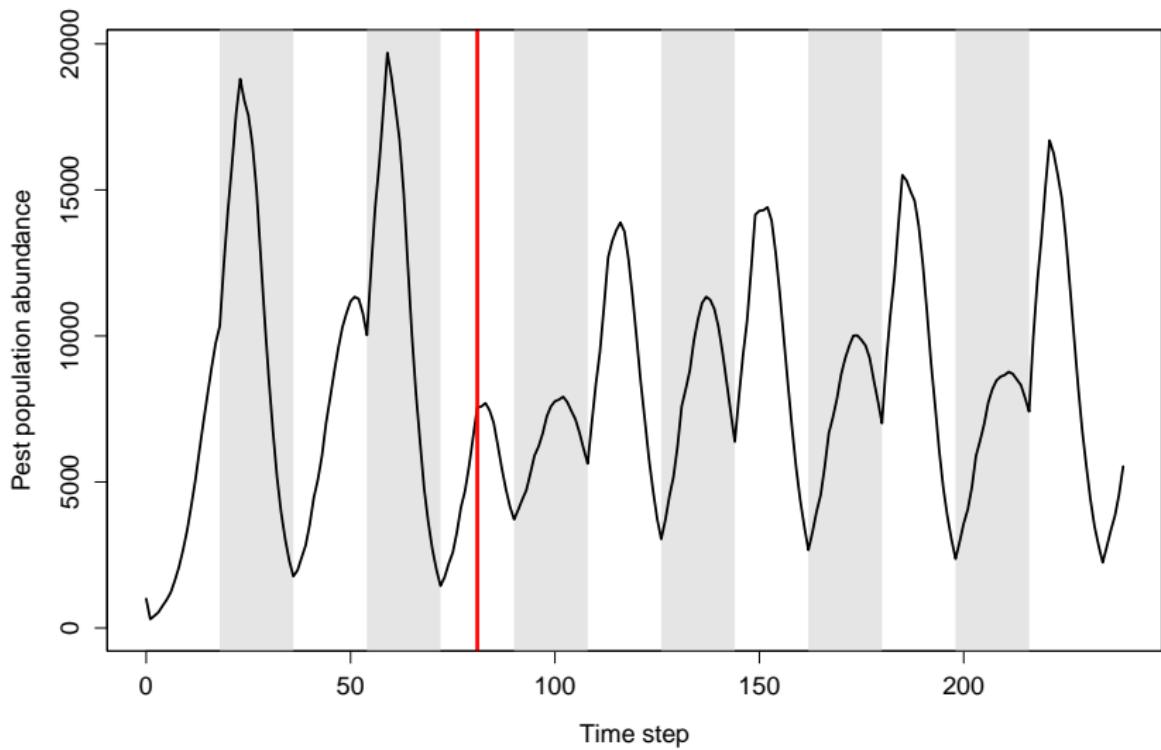
Constructing a landscape: Advanced options



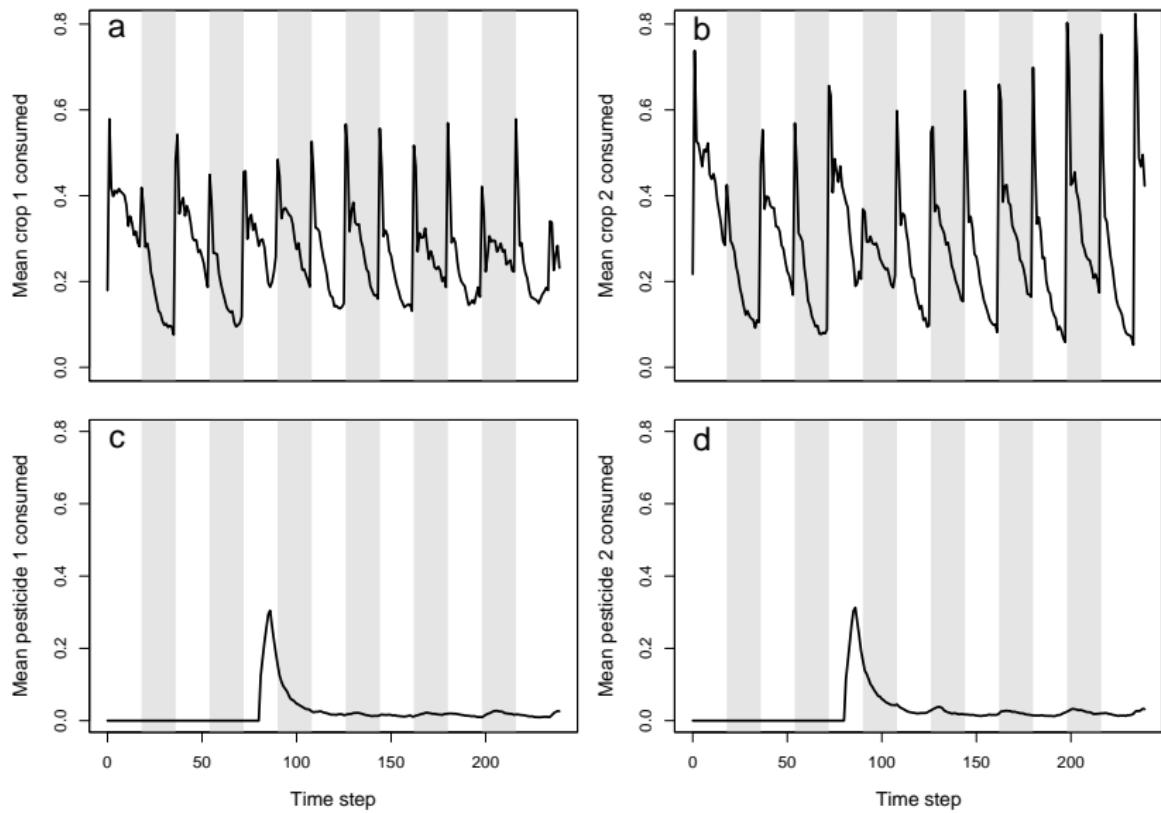
Running a simulation in resevol

```
run_farm_sim(mine_output = mg, repro = "asexual",
              pesticide_number = 2, time_steps = 160,
              farms = 9, pesticide_init = "random",
              pesticide_consume = c("T1", "T2"),
              pesticide_rotation_time = 16, xdim = 64,
              pesticide_rotation_type = 3, ydim = 64,
              pesticide_tolerated_surv = 0, max_age = 4,
              pesticide_per_cell = 1, crop_number = 1,
              crop_rotation_time = 16, crop_per_cell = 4,
              food_consume = 1, food_needed_surv = 1,
              reproduction_type = "food_based",
              food_needed_repr = 1, land_edge = "torus",
              min_age_feed = 0, max_age_feed = 2,
              min_age_move = 3, max_age_move = 4,
              min_age_reproduce = 4, print_gens = FALSE,
              max_age_reproduce = 4, rand_age = TRUE,
              age_pesticide_threshold = 2,
              immigration_rate = 10, move_distance = 2,
              print_last = TRUE, trait_means = c(0.1, 0.1));
```

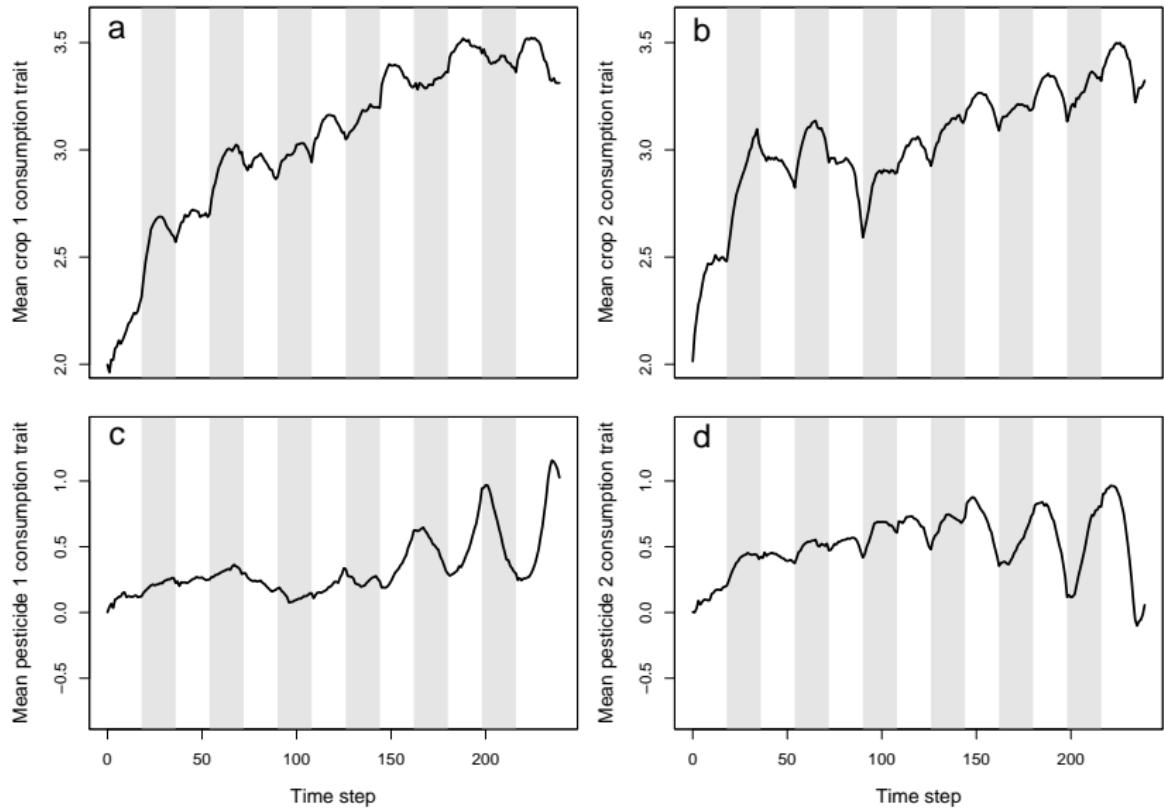
Simulating ecology, evolution, crop yields



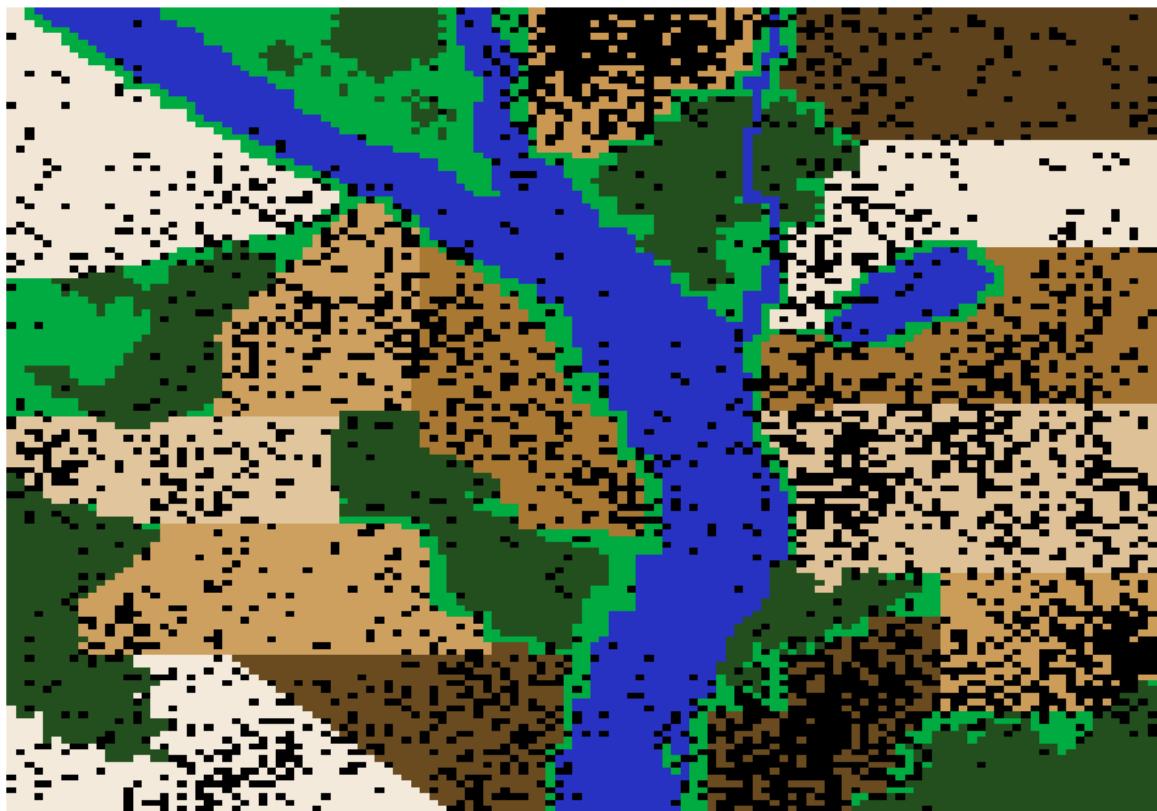
Simulating ecology, evolution, crop yields



Simulating ecology, evolution, crop yields



Simulating ecology, evolution, crop yields



The resevol R package: summary

- ▶ Rapidly develop and simulation models of pest ecology and resistance evolution
- ▶ Introduces a novel approach to modelling complex pest genetic architecture
- ▶ Flexible pest life-histories, mating systems, trait covariances
- ▶ Highly customisable, detailed landscapes
- ▶ Free to use¹, open source² (GPL >= 2), documented^{1,3}

¹Website: <https://bradduthie.github.io/resevol/>

²Code: <https://github.com/bradduthie/resevol>

³Lab Notebook: <https://bradduthie.github.io/resevol/notebook/>