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

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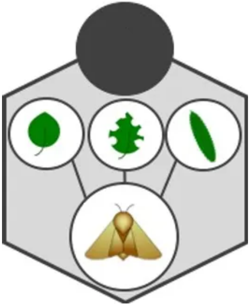
http://bradduthie.github.io/talks/BES2022.pdf

Pesticide resistance evolution



Impact on agriculture

- Resistance wicked & widespread[1]
- Obstacle to food security[2]

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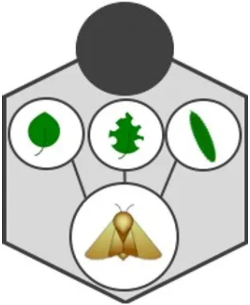
[1] Gould et al. 2018. *Ecol. Appl.* 13:1791-1805.
[2] Bradshaw et al. 2016. *Nat. Commun.* 7:12986.
[3] Carroll et al. 2014. *Science* 346:1245993.
[4] Saikai et al. 2021. *Pest Manag. Sci.* 77:273-284.
[5] Boots, M. 2011. *Am. Nat.* 178:214-220.
[6] Via, S. 1986. *Pesticide resistance*. 222-235.

Pesticide resistance evolution



Impact on agriculture

- Resistance wicked & widespread[1]
- Obstacle to food security[2]

Manage resistance evolution

- Vary biopesticide application[3,4]
- Polygenic resistance traits[5]
- Negative cross-resistance[6]

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[1] Gould et al. 2018. *Ecol. Appl.* 13:1791-1805.
[2] Bradshaw et al. 2016. *Nat. Commun.* 7:12986.
[3] Carroll et al. 2014. *Science* 346:1245993.
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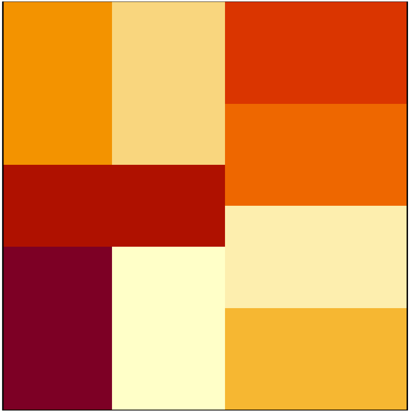
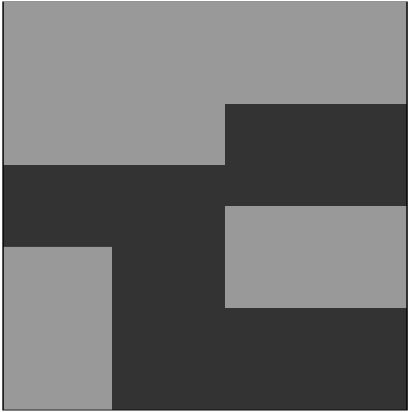
[6] Via, S. 1986. *Pesticide resistance.* 222-235.

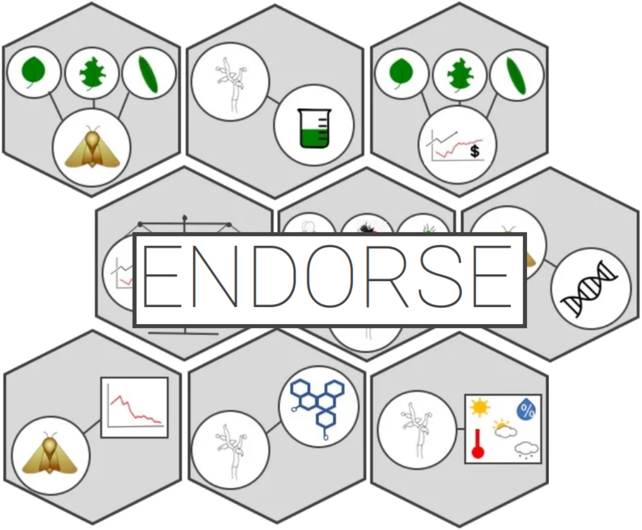
Agricultural heterogeneity to overcome resistance evolution



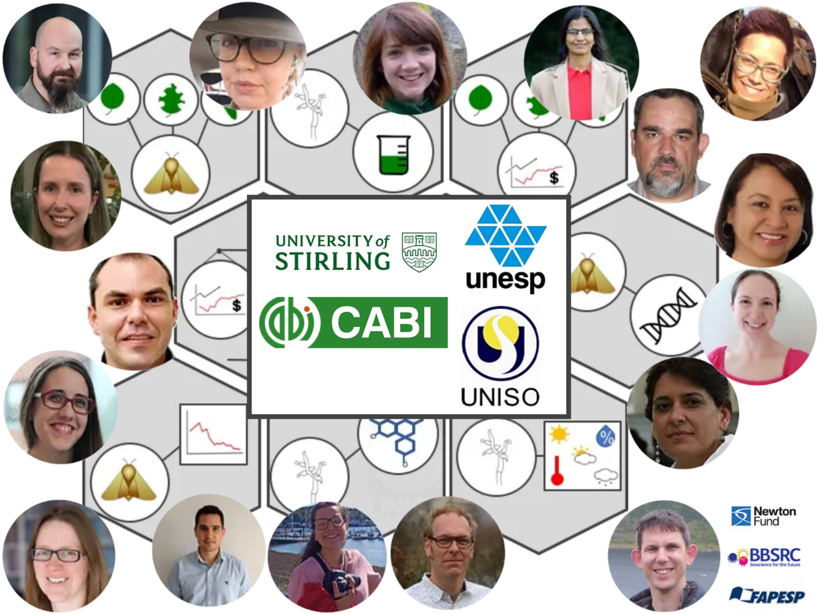
Unique farms



Biopesticide applied



ENDORSE



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BBSRC bioscience for the future

FAPESP

Modelling as a proof of concept before scaling up

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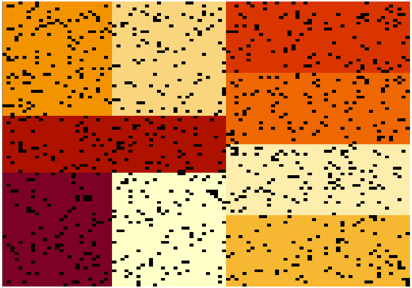
[1] Image: Public Domain

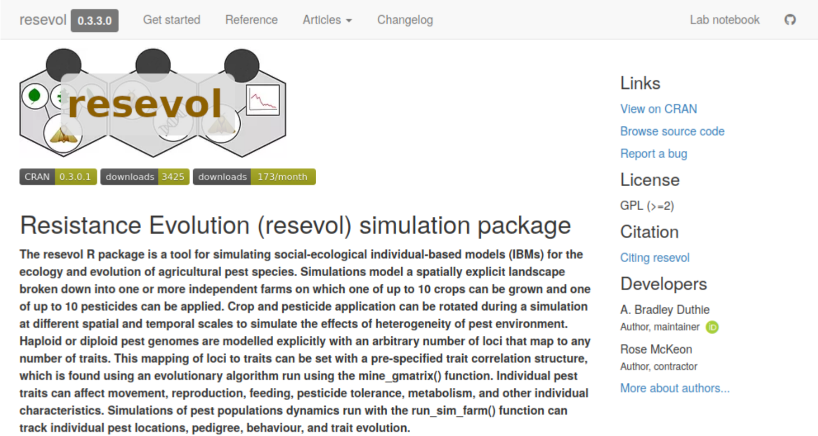
Agent-based modelling

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



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...

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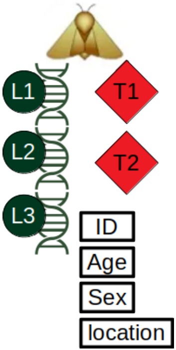
[1] Duthie AB, McKeon CR (2022). resevol: Simulate Agricultural Production and Evolution of Pesticide Resistance. R package version 0.3.3.0, https://bradduthie.github.io/resevol/.

resevol: An R package for modelling agricultural pests

Complex individuals

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



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[1] **Image**: Public domain

resevol: An R package for modelling agricultural pests

Complex individuals

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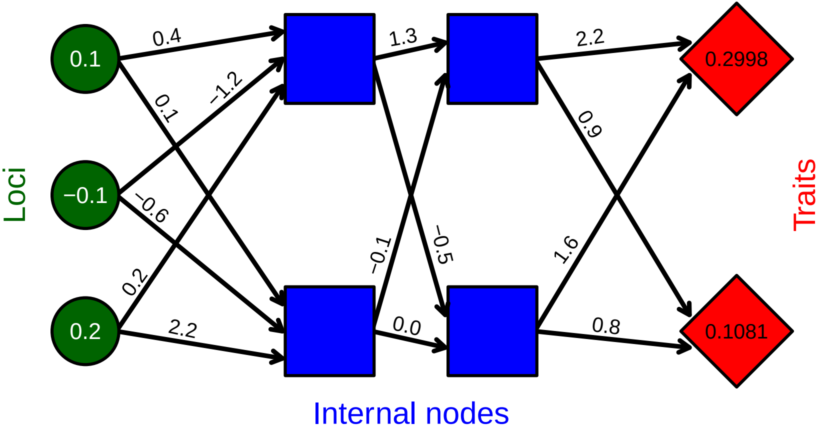
[1] Duthie AB, McKeon CR (2022). resevol: Simulate Agricultural Production and Evolution of Pesticide Resistance. R package version 0.3.3.0, https://bradduthie.github.io/resevol/.

[2] Duthie, 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

A genetic architecture for pre-specified trait covariances



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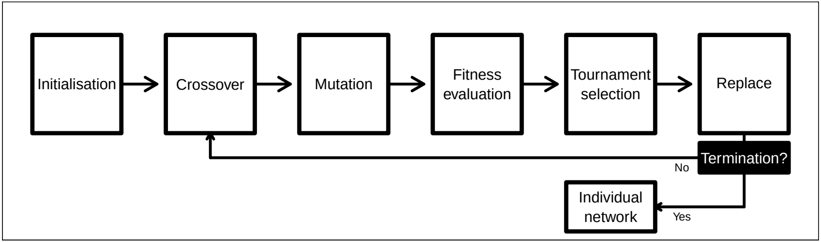
[1] resevol R package vignette: https://bradduthie.github.io/resevol/articles/evolutionary_algorithm.html

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.

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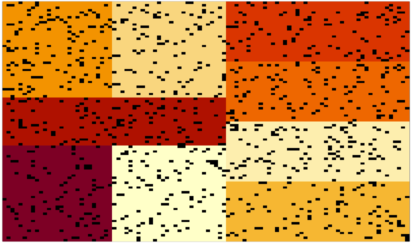
[1] resevol R package vignette: https://bradduthie.github.io/resevol/articles/evolutionary_algorithm.html

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);
```

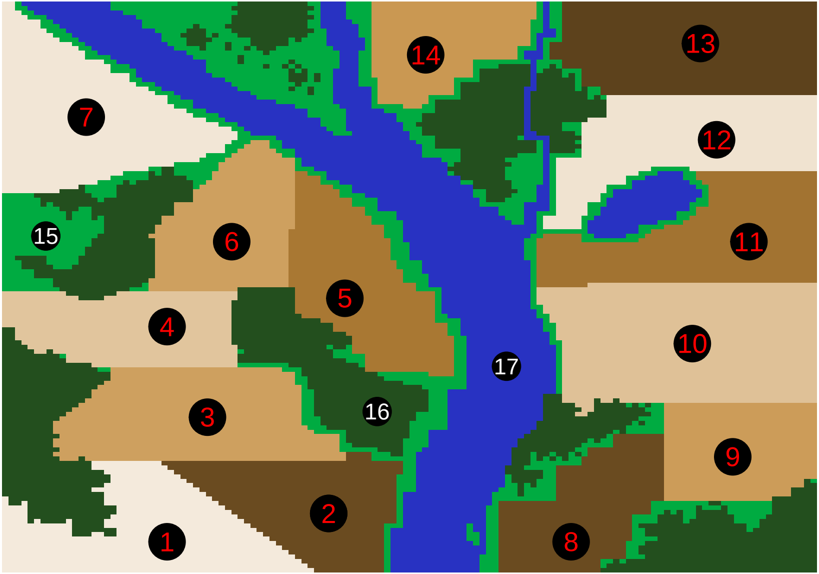
Constructing a landscape: Default options



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

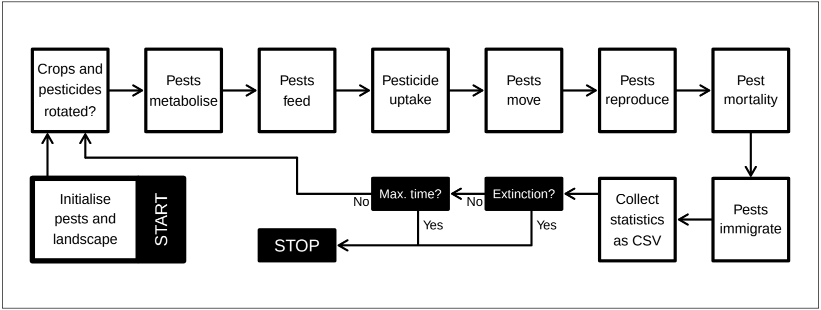
Each farm can use up to one crop and one pesticide, and the timing and rotation rules for crops and pesticide allow any Markov process.

Constructing a landscape: Advanced options



Pest life-history events defined within an age range

Within a time step, order of events are specified.



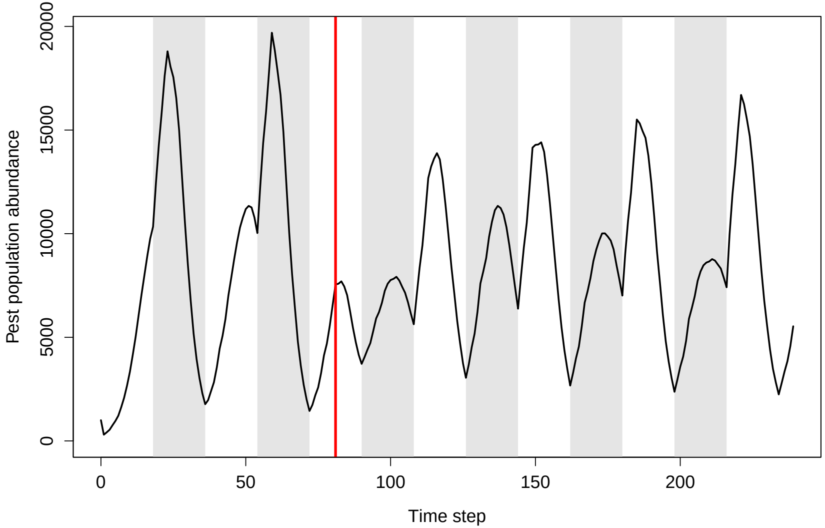
Specific events can be restricted to age ranges:

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

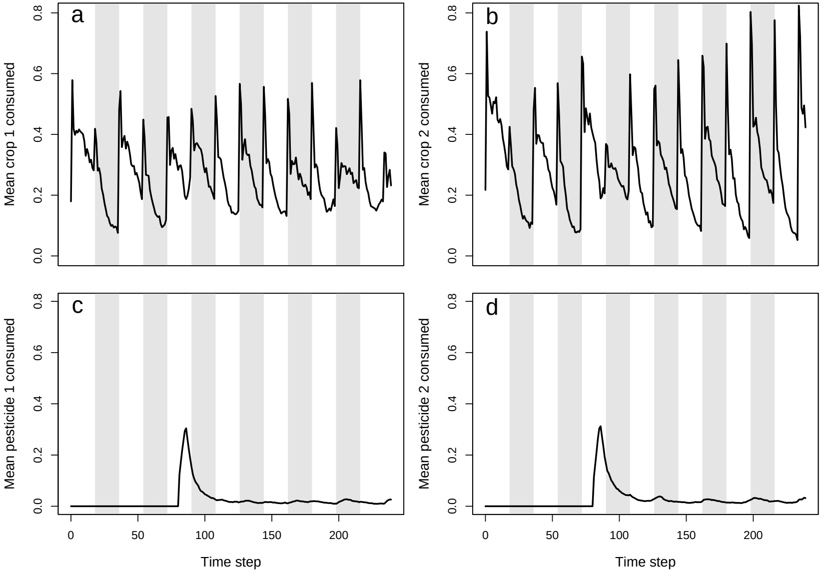
Running a simulation in resevol

```
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));
```

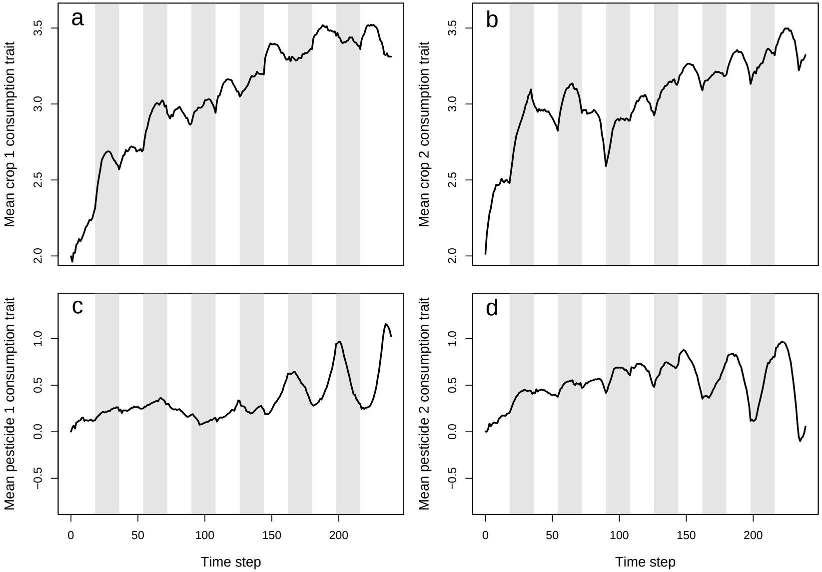
Simulating ecology, evolution, crop yields



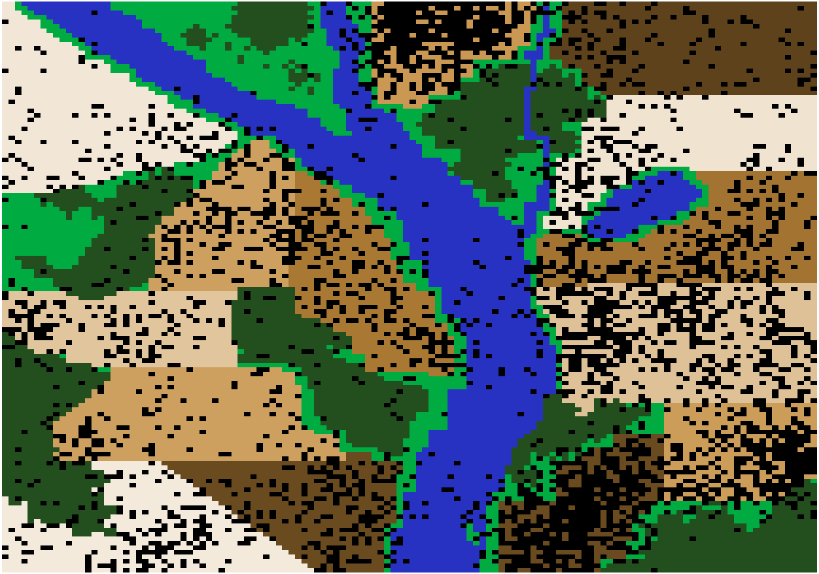
Simulating ecology, evolution, crop yields



Simulating ecology, evolution, crop yields



Simulating ecology, evolution, crop yields



The resevol R package: summary

- Simulations of pest ecology, resistance evolution, and agricultural production
- Covarying polygenetic traits
- Flexible pest life-histories, mating systems, traits
- Highly customisable, detailed landscapes
- Free to use[1], open source[2] (GPL $>=$ 2), documented[1,3], actively maintained[4]

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[1] **Website**: https://bradduthie.github.io/resevol/

[2] **Code**: https://github.com/bradduthie/resevol

[3] **Lab Notebook**: https://bradduthie.github.io/resevol/notebook/

[4] **Email**: alexander.duthie@stir.ac.uk **Mastodon**: @bradduthie@ecoevo.social