Introduction to individual-based modelling using R

https:
//stirlingcodingclub.github.io/individual_based_modelling

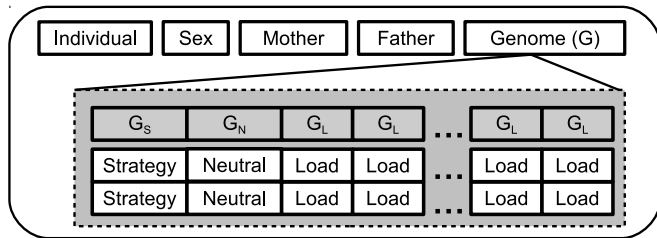Brad Duthie

20 April 2022

Individual-based modelling: what is it?

▶ Simulate a system *in silico*, using computer code

[1]Duthie, A. B., & Reid, J. M. (2016). *Am. Nat.* 186, 651-667.

Individual-based modelling: what is it?

- Simulate a system *in silico*, using computer code

- Individuals are represented as discrete entities

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Individual-based modelling: what is it?

Fig. 1. Interactions among plants, obligate pollinators, and obligate exploiters for a single set of parameter values.

▶ Processes are often stochastic (events probabilistic)

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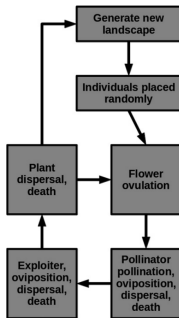
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▶ Can test ideas by simulating across many parameters

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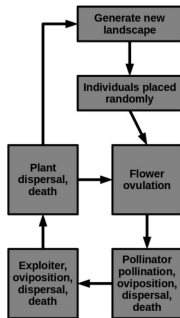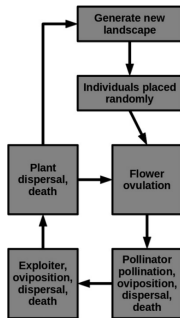
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Fig. 1. Interactions among plants, obligate pollinators, and obligate exploiters for a single set of parameter values.

▶ Processes are often stochastic (events probabilistic)

▶ Can test ideas by simulating across many parameters

▶ Highly mechanistic models are possible

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Advantages & disadvantages of using IBMs

Advantages

1. Very easy to model individual variation (genetic, phenotypic, environment, etc.)

2. Key biological processes are inherent to the model (e.g., drift, mutation, demography)

3. Models can often be more detailed and therefore more targeted

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Disadvantages

1. Computational power can be limiting

2. Sometimes difficult to see the link between model assumptions and model predictions (i.e., difficult to interpret results)

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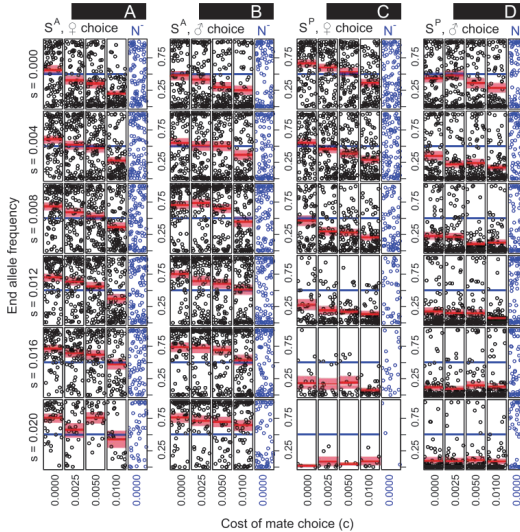
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Getting started using R for IBMs

- ▶ **Objective**: Learn how to start writing IBMs from a basic knowledge of R coding

- ▶ **Notes**: Walk through all of the code required to get started with a basic predator-prey model

- ▶ **Caveat**: Code in the notes is not optimised for speed

- ▶ **Languages**: Other languages such as C, C++, or NetLogo are also worth considering

# One way to model individuals in an IBM

Rows are individuals & columns are individual characteristics

ind_ID	x_loc	y_loc	body_mass	age
1	3	7	36.60	5
2	3	3	31.20	1
3	3	5	45.89	3
4	8	2	29.61	2
5	8	1	44.43	4
6	2	8	46.65	6
7	2	4	43.33	5
8	4	6	36.52	4

The process of modelling is then to do something to the individuals
and their characteristics – have them interact, change, be removed,
have more added. Models are as complex as we are willing to code.

Individual-based models are often spatially explicit
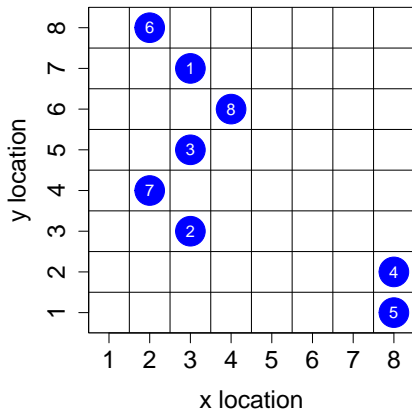
- ▶ Individual locations can be mapped to a landscape, with rules for movement
- ▶ Movement entails rules for changing x and y locations
- ▶ Landscape need not be represented in code, but can be to define landscape properties

Simulate individuals over multiple time steps

Define individuals

```
inds       <- array(data = 0, dim = c(5, 3));
inds[, 1] <- 1:5;
inds[, 2] <- sample(x = 1:8, size = 5, replace = TRUE);
inds[, 3] <- sample(x = 1:8, size = 5, replace = TRUE);
```

Move individuals to the right 5 times

```
ts         <- 0;
time_steps <- 5;
while(ts < time_steps){
    inds[, 2] <- inds[, 2] + 1;
    ts    <- ts + 1;
}
```

Working through the IBM notes

https://stirlingcodingclub.github.io/individual_based_modelling/ibm_notes.html

- ▶ Walks through R code for modelling individual movement, birth, death, and predation over time

- ▶ Meant to be a starting point for further development

- ▶ Ask questions in Twitch chat and in the GitHub Repository issues page