

[DPPS-303] Forward-time Simulations in Ecology and Evolution

Olivier Cotto
Frédéric Guillaume
Max Schmid

Tvärminne Zoological Station – University of Helsinki

March 2023

Contact: frederic.guillaume@helsinki.fi
Viikki, Biocenter 3 – 5717

Aims of the course

After this course, you will be able to:

- explain the purposes and mechanisms of forward-time individual-based simulations,
- run simulations with Nemo (and some SLiM),
- navigate and use the Unix computational environment productively,
- plan and implement a simulation-based project according to a research question,
- evaluate simulation software according to your project needs.

Organization of the course

Lectures:

- 1 Setup and intro to Nemo
- 2 Basic forward-time genetics in Wright-Fisher populations
- 3 Evolutionary dynamics with selection non-Wright-Fisher populations
- 4 Quantitative traits and local adaptation in variable environments
- 5 Eco-evolutionary dynamics in stage-structured populations
- 6 Complex traits: phenotypic plasticity, pleiotropy and linkage
- 7 Species interaction: basic resource competition
- 8 Running simulations on a cluster with nemosub

Resources:

- GitHub repository: <https://github.com/fredgui/Course-ForwardTimeIndividualBasedSimulations>

Individual-based models

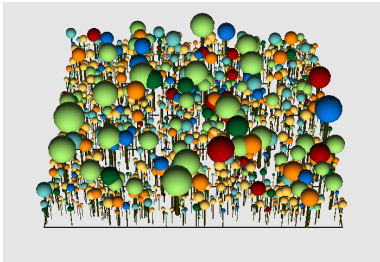
Individual-based models are stochastic simulation models where:

- Each individual is explicitly represented.
- Each individual is defined by its state variables (e.g., sex, age, location, phenotype, genes).
- Individuals interact with each other following simple rules (e.g., mating, movement, predation).
- The resulting dynamics is studied at the system, or population level.
- The system dynamics depend on simple interaction rules among agents and on the “individuality” of the agents (reductionist).
- Often applies to stochastic systems with non-linear dynamics which cannot be understood from summary statistics.
- We study the **emerging properties** of the system in a given time frame.

Applications in Ecology and Evolution

Ecology

- Population dynamics
- Community dynamics
- Forest Succession (Gap) Models
- ...

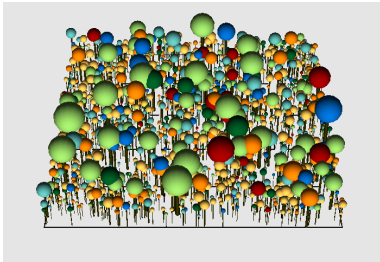


Huthan, Wikipedia, CC-by-sa 4.0

Applications in Ecology and Evolution

Ecology

- Population dynamics
- Community dynamics
- Forest Succession (Gap) Models
- ...



Huthan, Wikipedia, CC-by-sa 4.0

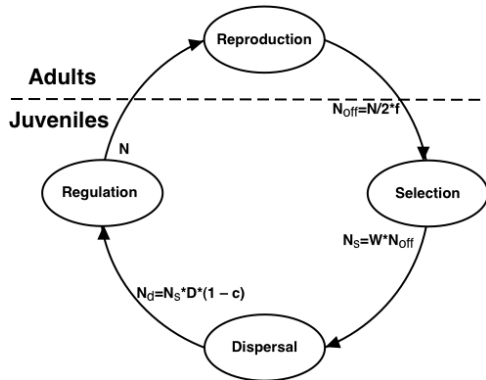
Evolution

- Population genetics
- Evolutionary game theory
- Life-history evolution
- Eco-evolutionary dynamics
- ...

Forward-time individual-based simulations

How do they work?

- iteration of a life cycle from T_0 to T_t
- simulate a *whole population* with N individuals
- evolve the population from T_0 to T_t
- individuals thus change over time
- individuals may persist for more than one iteration (generation/year) or not
- we monitor the state of the population and of the individuals over time



What are they good for?

- Test theory predictions, releasing simplifying assumptions
- Generate new theoretical results for complex systems
- Generate data under known conditions to test analysis pipelines or statistical methods
- Test explanatory hypotheses by matching simulated with empirical data

Introducing Nemo and Slim (briefly)

NEMO:

BIOINFORMATICS APPLICATIONS NOTE Vol. 22 no. 20 2006, pages 2556–2557
doi:10.1093/bioinformatics/bti415

Genetics and population analysis

Nemo: an evolutionary and population genetics programming framework

Frédéric Guillaume^{1,2,*} and Jacques Rougemont³

Received: 9 April 2020 | Accepted: 24 June 2020

DOI: 10.1111/2041-210X.13460

RESEARCH ARTICLE

Methods in Ecology and Evolution 

NEMO-AGE: Spatially explicit simulations of eco-evolutionary dynamics in stage-structured populations under changing environments

Olivier Cotto¹  | Max Schmid²  | Frédéric Guillaume² 

SLiM:

SLiM: Simulating Evolution with Selection and Linkage

Philipp W. Messer¹

Department of Biology, Stanford University, Stanford, California 94305

SLiM 3: Forward Genetic Simulations Beyond the Wright–Fisher Model

Benjamin C. Haller^{*1} and Philipp W. Messer^{*1}

¹Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, NY

What are we going to simulate?

- Neutral genetic variation in simple population genetics models (population history)
- Selection at many loci (e.g., background selection)
- Selection at many phenotypes (quantitative genetics)
- Complex genotype-phenotype maps with dominance, pleiotropy, epistasis
- Demographic stochasticity (non-equilibrium populations)
- Non-overlapping generations (age-structured populations)
- Stage-structured populations with competition (density-dependence)
- Spatially explicit simulations with many populations (landscape genetics)
- Eco-evolutionary dynamics in non Wright-Fisher populations
- and more...