

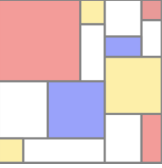
SLiM: An Evolutionary Simulation Framework

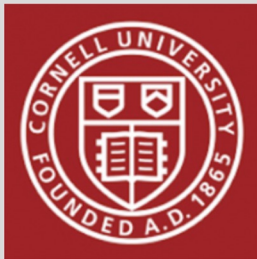
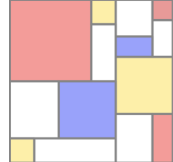
CompBio Skills Seminar
4/25/24

Introduction

Advantages:

- Flexibility
- Performance
- Interactive GUI





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Messer Lab – SLiM

About SLiM

SLiM is an evolutionary simulation framework that combines a powerful engine for population genetic simulations with the capability of modeling arbitrarily complex evolutionary scenarios. Simulations are configured via the integrated Eidos scripting language that allows interactive control over practically every aspect of the simulated evolutionary scenarios. The underlying individual-based simulation engine is highly optimized to enable modeling of entire chromosomes in large populations. We also provide a graphical user interface on macOS, Linux, and Windows, for easy simulation set-up, interactive runtime control, and dynamical visualization of simulation output.

A 4–5 day SLiM Workshop is now available online. The SLiM Workshop is also offered in person from time to time; see the SLiM Workshops subsection below for more information.

Downloads (version 4.2.1)



[macOS Installer](#)



[Source Code](#)



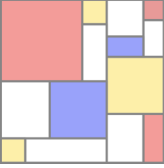
[SLiM Manual](#)



[Eidos Manual](#)



[Ref Sheets](#)

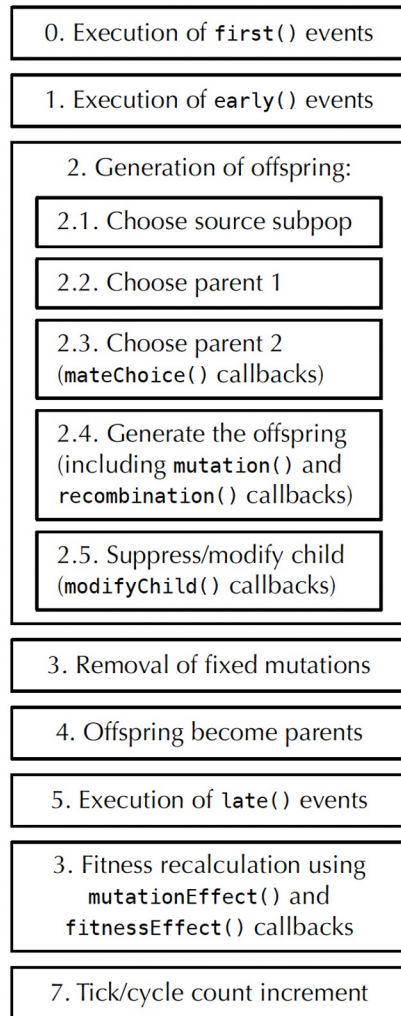


Installing on Windows machines

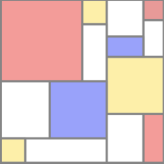
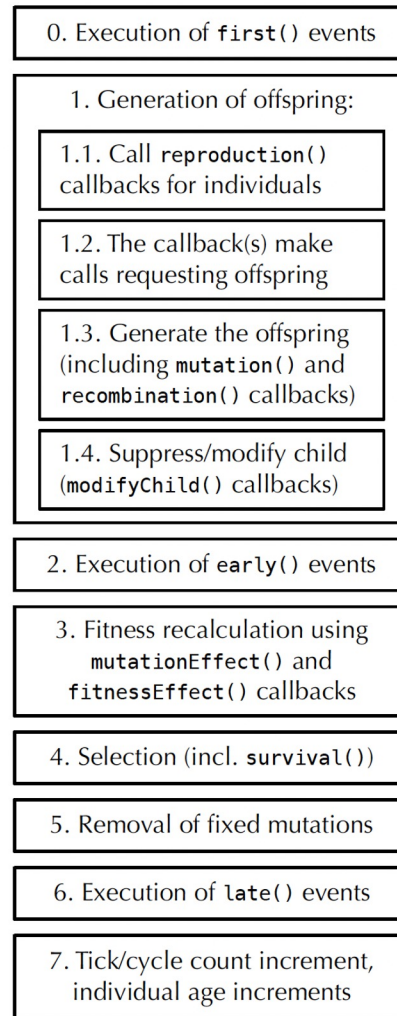
- Requires MSYS2 Software Distribution and Building Platform for Windows (<https://www.msys2.org/>)
- Click on 'MSYS2 MSYS' in the Start menu
- Type 'pacman -S mingw-w64-x86_64-slim-simulator' in the opened command prompt

→ This should install SLiM and the SLiMgui

The WF model's tick cycle

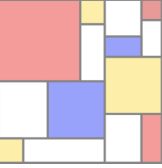


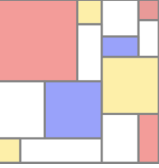
The nonWF model's tick cycle



WF vs non-WF models

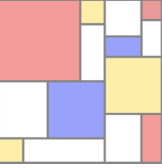
- WF is the 'default' mode, non-WF is used to explicitly model various 'advanced' scenarios





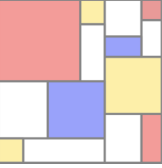
WF vs non-WF models

- WF is the 'default' mode, non-WF is used to explicitly model various 'advanced' scenarios
- In general, non-WF models are more individual-based, more explicit (more control), more biologically realistic but more complex



WF vs non-WF models

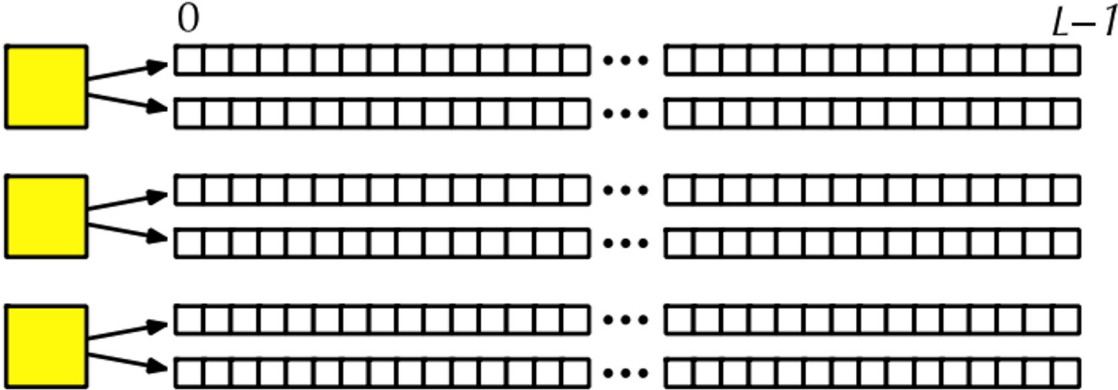
- WF is the ‘default’ mode, non-WF is used to explicitly model various ‘advanced’ scenarios
- In general, non-WF models are more individual-based, more explicit (more control), more biologically realistic but more complex
- These models vary in the following ways:
 - Age structure/overlapping generations
 - Offspring generation
 - Population regulation
 - Fitness
 - Migration
 - Subpopulation splits

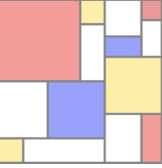


Conceptual overview

Individuals and genomes:

- **Individuals** are diploid by default, thus each have two **Genomes**

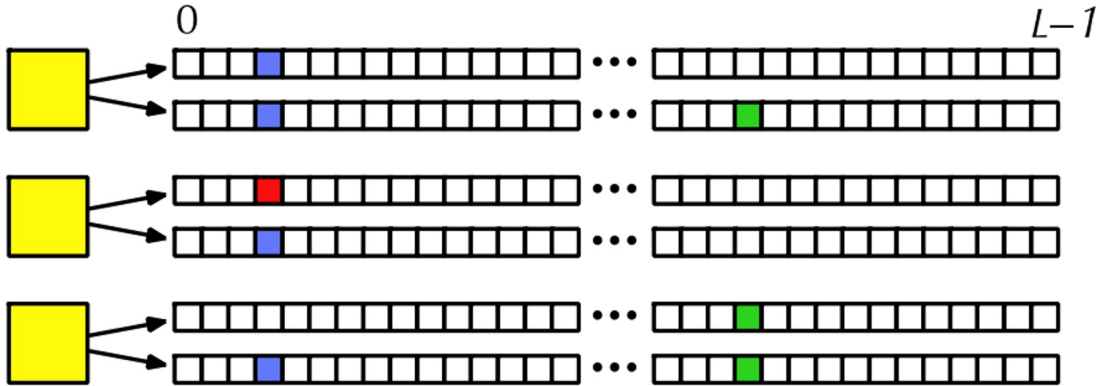




Conceptual overview

Mutations and substitutions:

- Each instance of mutation (different colors) are references to the same **Mutation** object
- Each **Mutation** instance stores a base position, selection coefficient s , and a dominance coefficient h

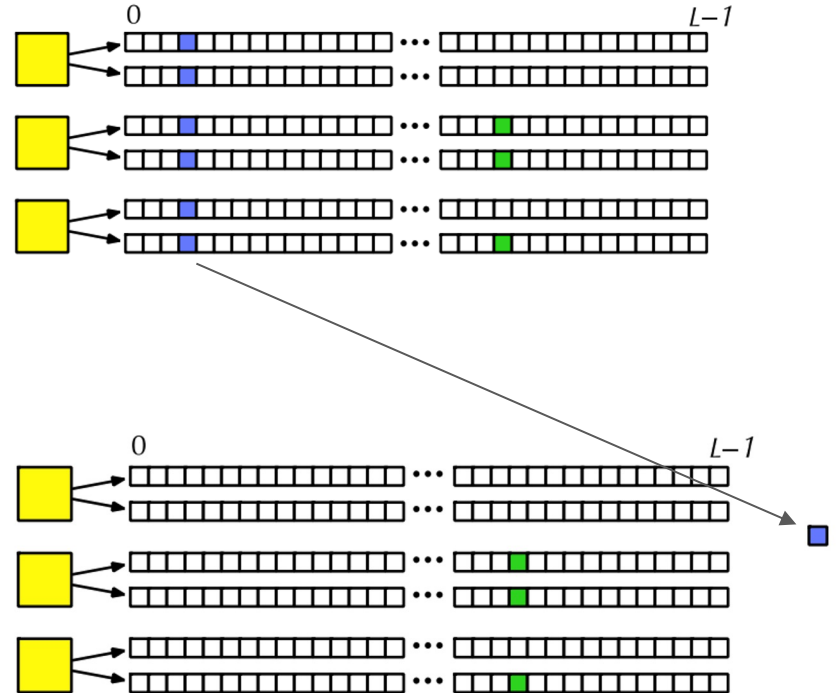


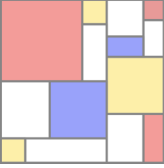
Conceptual overview



Mutations and substitutions:

- When fixed in a population, a mutation is removed and stored as a *substitution* object (default behavior)





Conceptual overview

Genomic elements, genomic element types, mutation types, and the chromosome:

- The **Chromosome** contains genomic elements (**GenomicElement**), which each have a genomic element type (**GenomicElementType**)

Chromosome: a mosaic of genomic elements



Genomic element types

non-coding



exon



intron



Mutation types

neutral



beneficial



deleterious

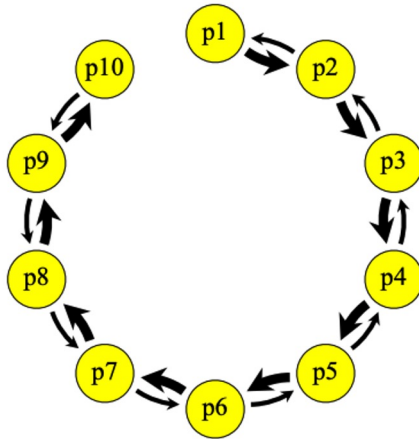


Conceptual overview

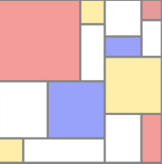


Subpopulations and migration:

- Mating occurs within **Subpopulations**; ie. they are reproductively isolated from other subpopulations
- This allows you to model gene flow, eg. the ‘stepping-stone’ river system model below

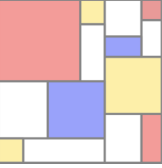


Conceptual overview



Subpopulations and migration:

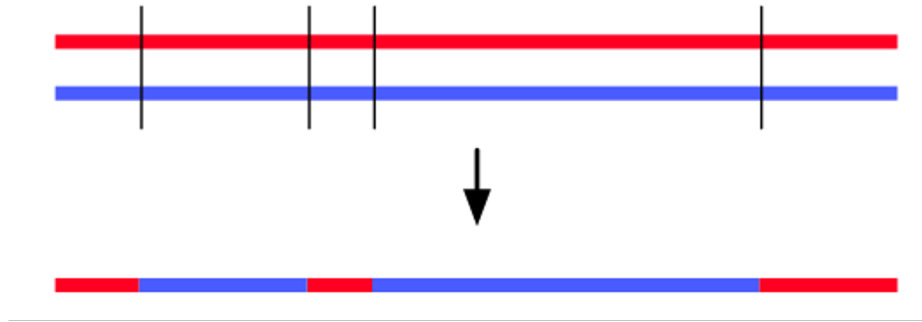
- Using spatial layers, you can also model spatial competition or spatial mate choice preference



Conceptual overview

Recombination and gene conversion:

- “Crossover breakpoints” model: crossover only, no gene conversion



- “Double-stranded break (DSB)” model: gene conversion

Fitness



WF models

- *Relative* fitness- population size is set by the model
- fitness = probability an individual will reproduce in next generation

non-WF models

- *Absolute* fitness- fitness composition in populations actively influences their size
- fitness = probability that an individual will survive to reproduction (in next generation)

Both calculate fitness per individual like this: $(1+s)^*(1+hs)^*(1+hs)^* \dots$

