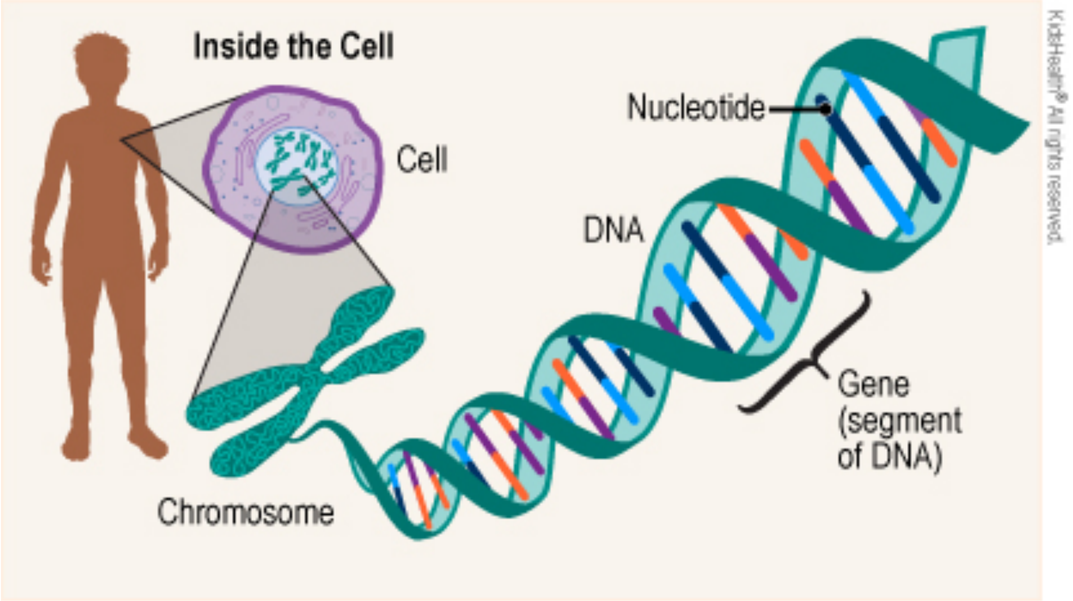
Getting Complicated with SLiM

Getting Complicated

- Evolutionary biology often deals with genetics
- This can get very complicated



SLiM: An Evolutionary Simulation Framework

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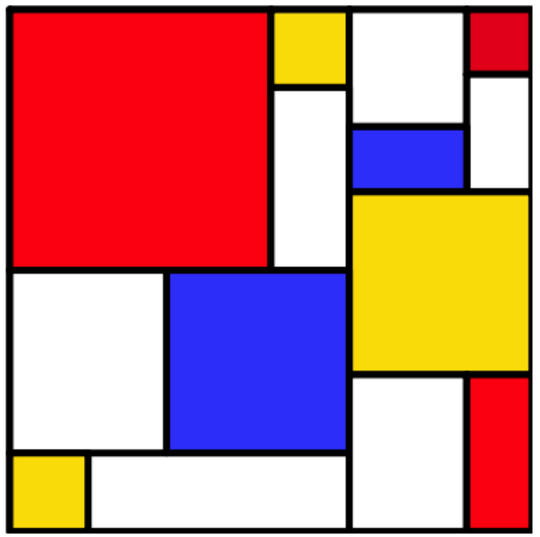


SLiM = Forward Genetic Simulator

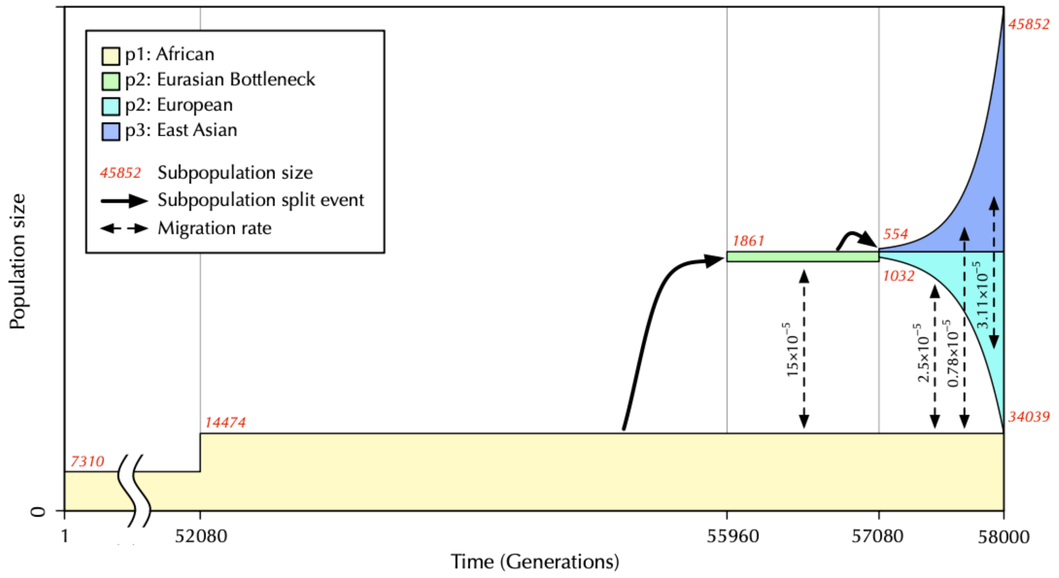
- **Forward**
  - Simulated processes going forward in time
  - Unlike coalescent simulators
- **Genetic**
  - Explicit loci on a chromosome
- **Simulator**
  - Individual based modeling, not analytical solutions

What can SLiM do?

Examples from the SLiM workshop (http://benhaller.com/workshops/workshops.html)

The Gravel model (5.4)

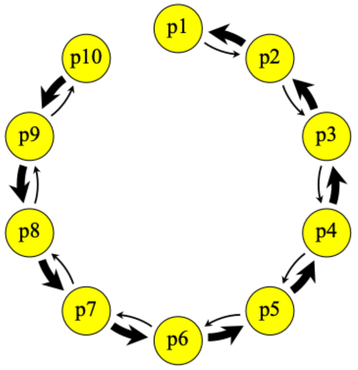
- Simulating human evolutionary history
- Demographic events, exponential growth

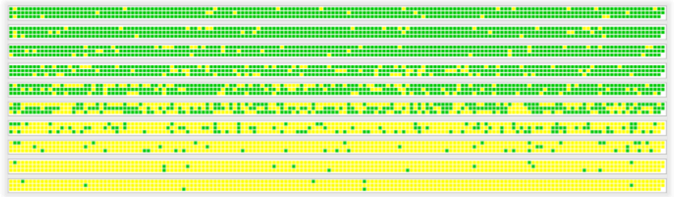


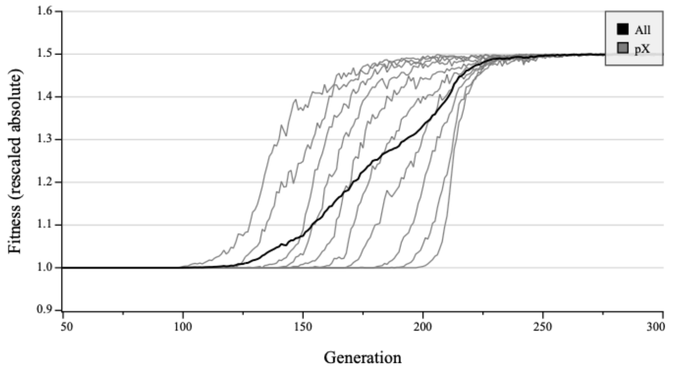
What can SLiM do?

Introgression & sweeps (9.7)

- Introgression of a single introduced mutation
- Ten subpopulations connected by migration



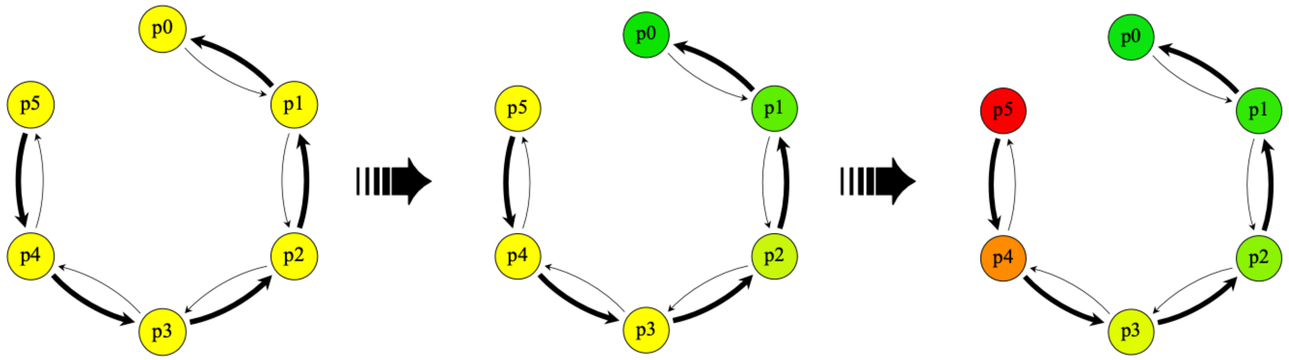




What can SLiM do?

Gene drives (12.3)

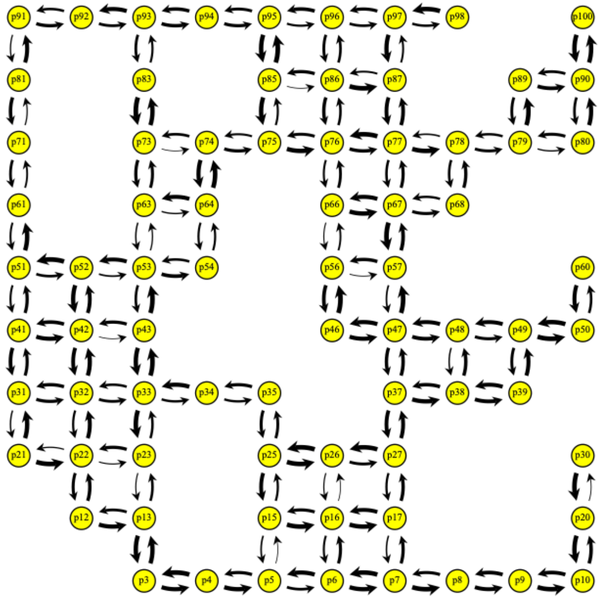
- Simulating CRISPR gene drive
- Fixes despite negative fitness effects
- Fixes despite going against migration



What can SLiM do?

Metapopulations (5.3.4)

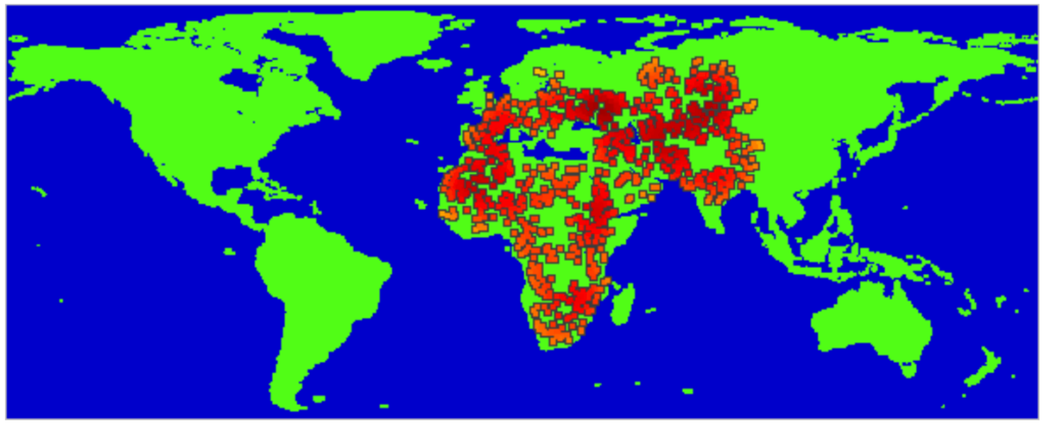
- Many subpopulations connected by migration
- The connection pattern can be spatial, or not



What can SLiM do?

Continuous space (15.10)

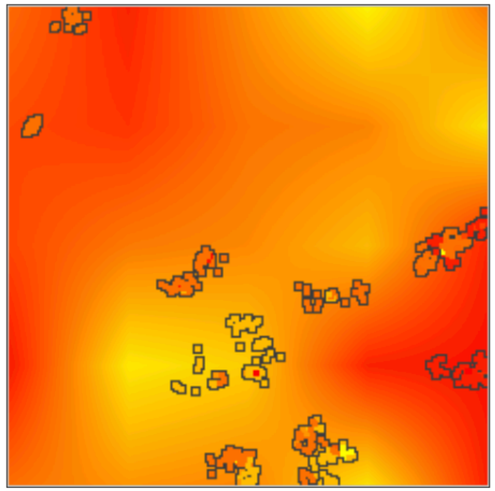
- Individuals live in a continuous 2-D space
- A landscape map of the world is used
- Population expansion out of Africa



What can SLiM do?

Local adaptation (15.11)

- Individuals live in a continuous 2-D space
- A map defines a heterogeneous environment
- Adaptation to the local environment results



What can SLiM do?

Nucleotide-based models (18.1)

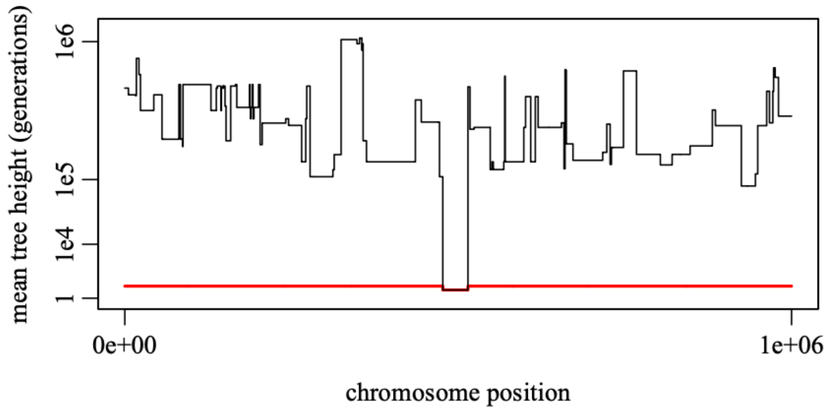
- Track the nucleotide sequence of every genome
- Mutations have an associated nucleotide
- Mutation rates are sequence-dependent
- Realistic gene conversion, including gBGC

```
GAATGTCGGTTAGAGCAACCTAGCTTCTCAGATCGCAATA
GAATGTCCGTTAGAGCAACCTAGCTTCTCAGATGGCTATA
GAATGTCCGTTAGAGCAACCTAGCTTCTCAGATGGCCATA
GAATGTCGGTTAGAGCATCCTAGCTTCTCAGATCGCAATA
GAATGTCGGTTAGAGCAACCTAGCTTCTCAGATCGCAATA
GAATGTCCGTTAGAGCAACCTAGCTTCTCAGATGGCAATA
GAATGTCGGTTAGAGCATCCTAGCCTCTCAGATGGCAATA
GAATGTCGGTTAGAGCATCCTAGCTTCTCAGATCGCAATA
```

What can SLiM do?

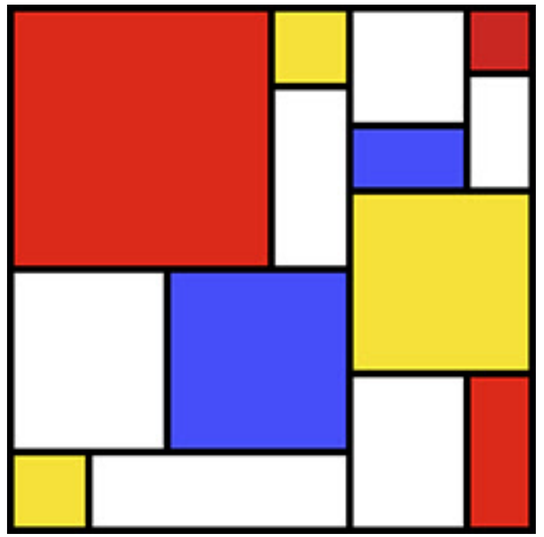
Tree sequences & ancestry (17.10)

- Tracking the ancestry tree at every position
- Mean tree height is a proxy for diversity at a site
- After a sweep, diversity is lowest near the sweep
- Recapitation constructs neutral burn-in history



How to Simulate in SLiM

- Start with SLiM GUI
- Do production runs on a cluster



SLiM Organization

- Different Classes
- Individual has genome
  - Genome has mutations
  - Different mutation types
  - Different genomic elements
  - Also can be in XYZ space

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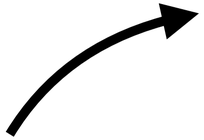

Subpopulations
- Migration

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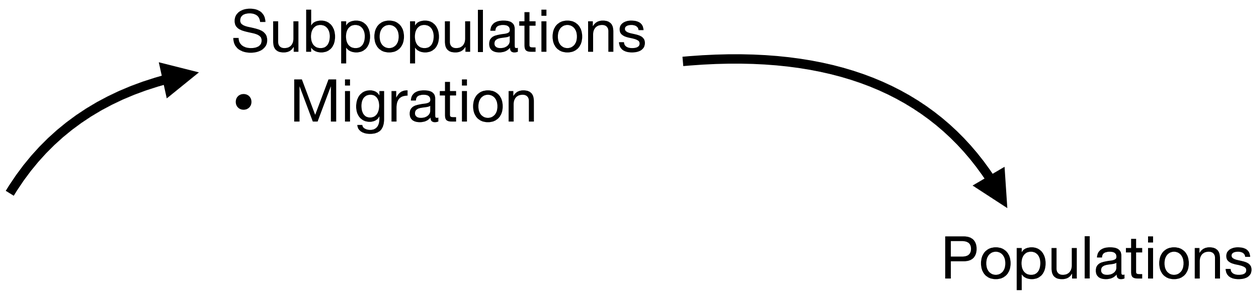

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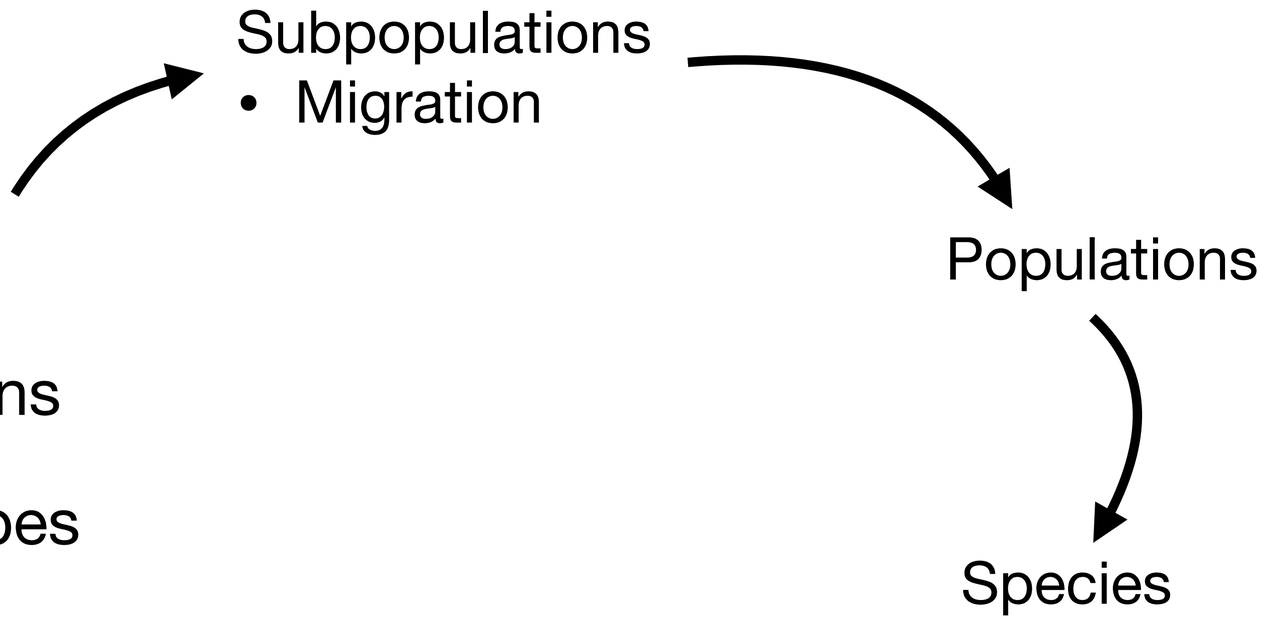

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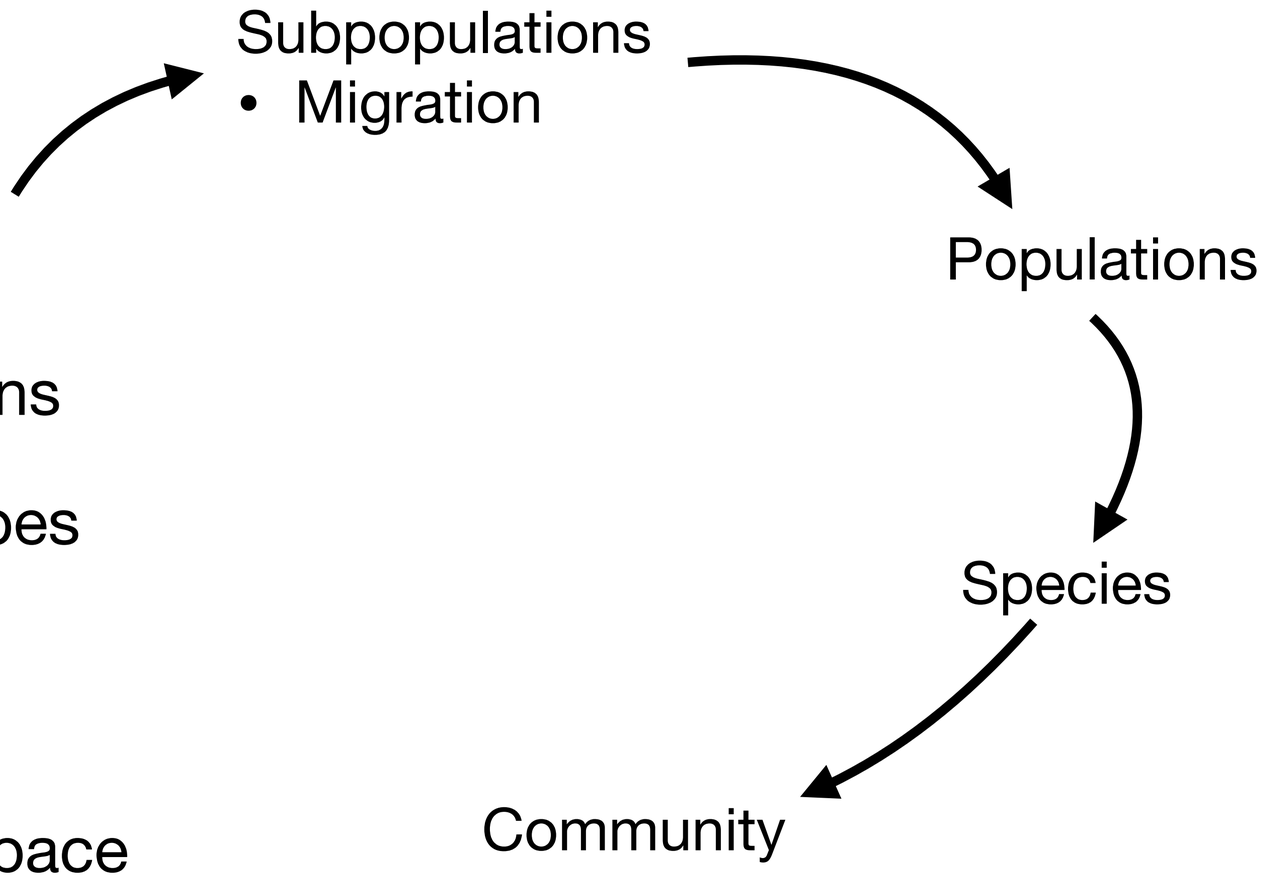
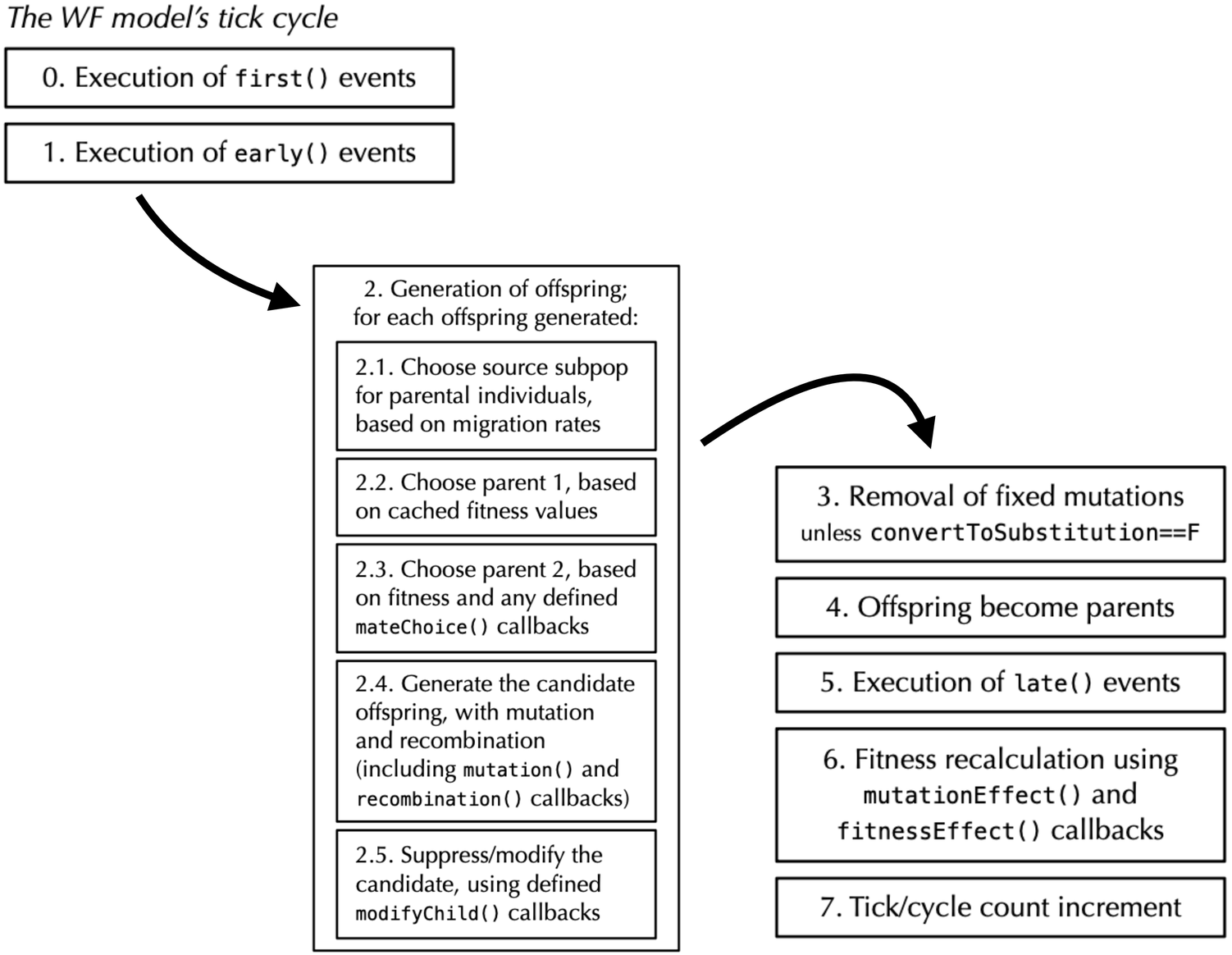
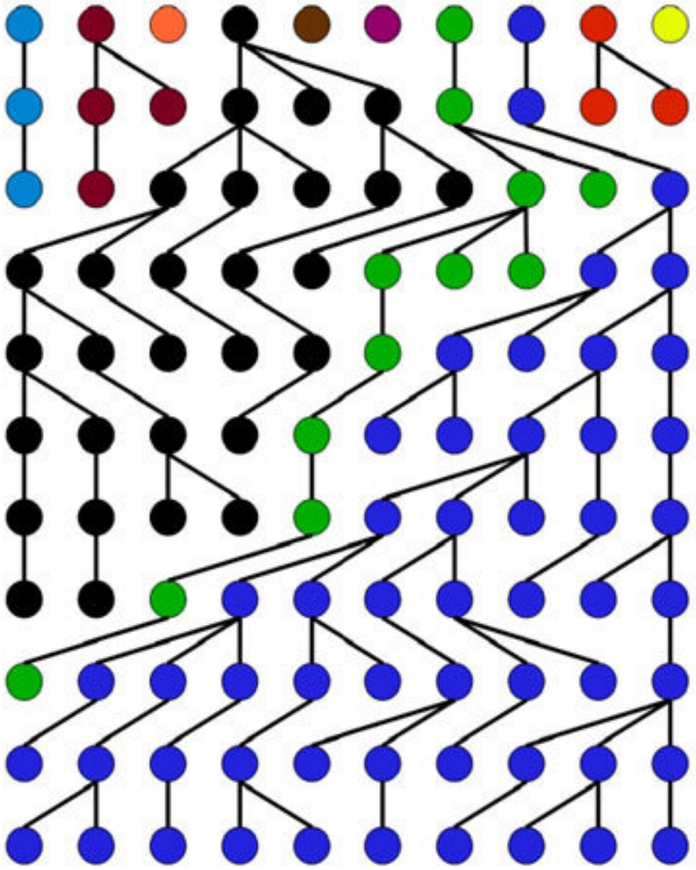


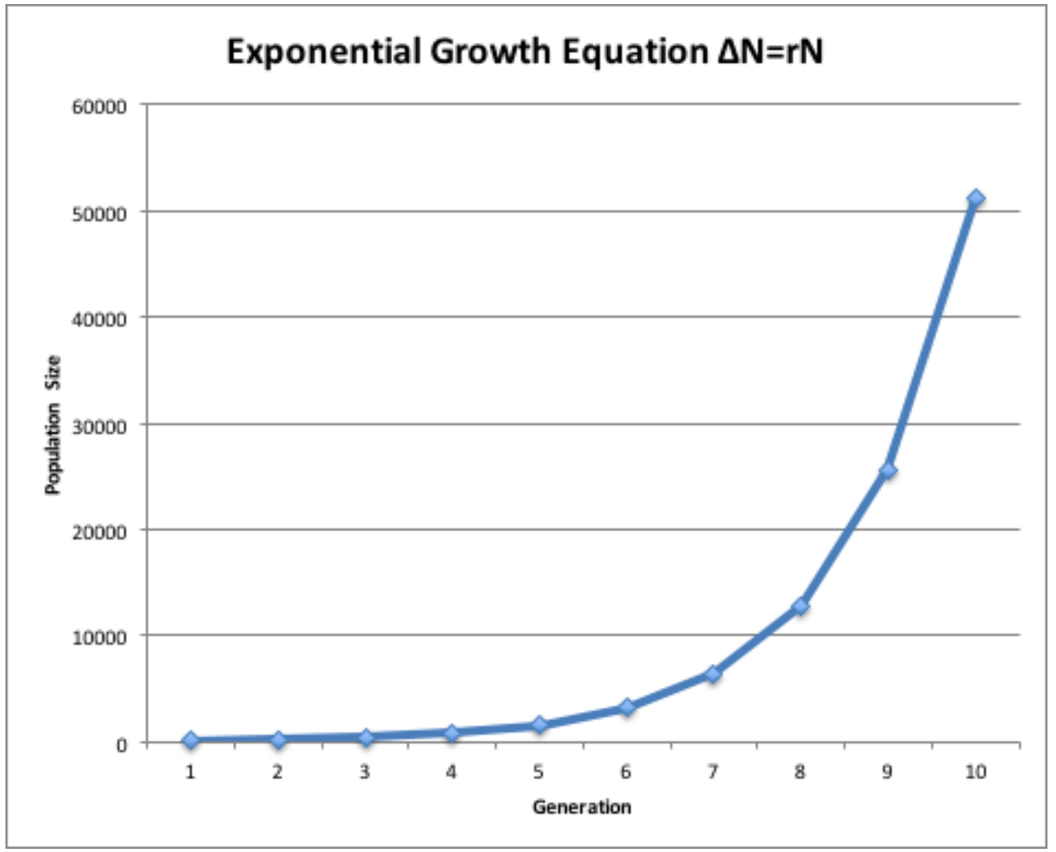
SLiM Ticks

- Unit of time
- Within a generation
- First, early, and late



Wright-Fisher vs Non-Wright-Fisher





Resources for learning SLiM

- The SLIM manual (available when you download slim)
- The eidos manual
- The built in manuals are much better for searching functions
- The recipes
- The SLiM workshop - http://benhaller.com/workshops/workshops.html