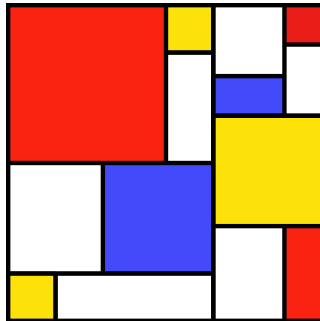


# SLiM

## Workshop Series



#15: non-Wright–Fisher models

# WF versus nonWF

- SLiM supports two different model types:
  - **WF**: Wright–Fisher
  - **nonWF**: non-Wright–Fisher
- Differences:
  - generation cycles
  - offspring generation
  - population regulation
  - age structure
  - fitness models
  - demography
  - mate choice
  - migration

# WF

1. Execution of `early()` events

2. Generation of offspring:

2.1. Choose source subpop

2.2. Choose parent 1

2.3. Choose parent 2  
(`mateChoice()` callbacks)

2.4. Generate the offspring  
(including `mutation()` and  
`recombination()` callbacks)

2.5. Suppress/modify child  
(`modifyChild()` callbacks)

3. Removal of fixed mutations

4. Offspring become parents

5. Execution of `late()` events

6. Fitness value recalculation  
using `fitness()` callbacks

7. Generation count increment

## WF Models

- Population size is a parameter
- Population regulation is automatic
- Fitness affects mating probability
- Selection is soft (relative fitness)
- Non-overlapping generations
- No age structure
- Migration is due to parameters

# nonWF Models

- Population size is emergent
- Population regulation is scripted
- Fitness affects viability/survival
- Selection is hard (absolute fitness)
- Generations can overlap
- Age structure is emergent
- Migration is scripted

## nonWF

1. Generation of offspring:

1.1. Call **reproduction()** callbacks for individuals

1.2. The callback(s) make calls requesting offspring

1.3. Generate the offspring (including **mutation()** and **recombination()** callbacks)

1.4. Suppress/modify child (**modifyChild()** callbacks)

2. Execution of **early()** events

3. Fitness value recalculation using **fitness()** callbacks

4. Viability/survival selection

5. Removal of fixed mutations

6. Execution of **late()** events

7. Generation count increment, individual age increments

# WF

# nonWF

1. Execution of **early()** events

2. Generation of offspring:

2.1. Choose source subpop

2.2. Choose parent 1

2.3. Choose parent 2  
(**mateChoice()** callbacks)

2.4. Generate the offspring  
(including **mutation()** and  
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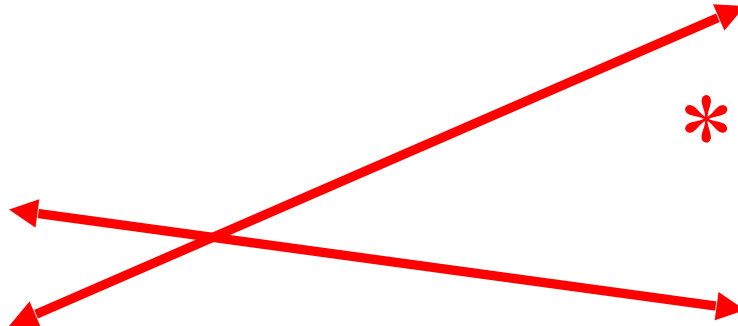
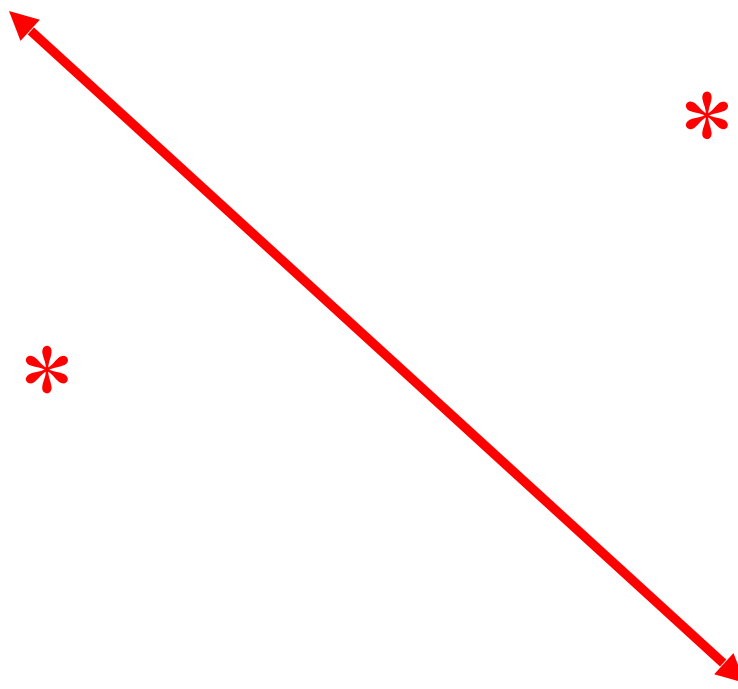
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4. Viability/survival selection

5. Removal of fixed mutations

6. Execution of **late()** events

7. Generation count increment,  
individual age increments



# nonWF Models

- Need to declare the model as nonWF
  - `initializeSLiMModelType("nonWF")`
- Need to consider substitution explicitly
  - `convertToSubstitution` defaults to F
- Need a `reproduction()` callback
  - generates offspring for one *focal individual*
  - does so by calling `addCrossed()` etc.
- Need to impose population regulation
  - typically density-dependence in `early()`

# The initialize() callback

```
// set up a simple neutral nonWF simulation
initialize() {
    initializeSLiMModelType("nonWF");
    defineConstant("K", 500); // carrying capacity

    // neutral mutations, which are allowed to fix
    initializeMutationType("m1", 0.5, "f", 0.0);
    m1.convertToSubstitution = T;

    initializeGenomicElementType("g1", m1, 1.0);
    initializeGenomicElement(g1, 0, 99999);
    initializeMutationRate(1e-7);
    initializeRecombinationRate(1e-8);
}
```

- Calls `initializeSLiMModelType("nonWF")`
- Defines a carrying capacity, K
- Sets `convertToSubstitution=T` for m1

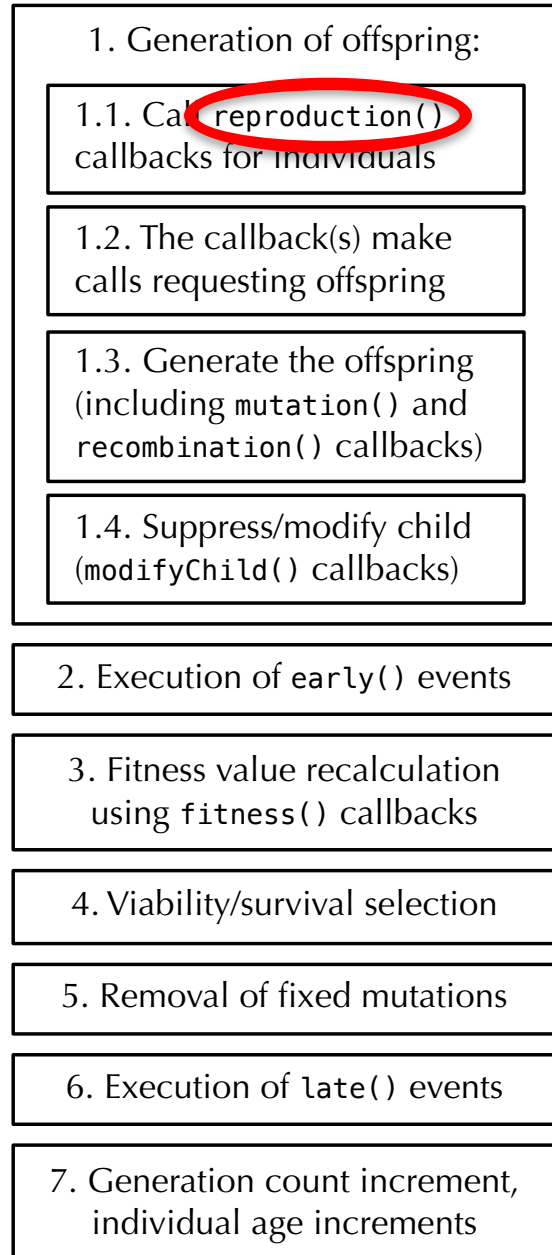
# The reproduction() callback

```
// each individual reproduces itself once
reproduction() {
    subpop.addCrossed(individual, p1.sampleIndividuals(1));
}
```

- Required in nonWF models
- Called during offspring generation
- Called once for each *focal individual*
- Does all reproduction for that individual
- Replaces the mateChoice() callback
- Partly replaces modifyChild()



The sequence of events within one generation in nonWF models.



# reproduction() callbacks

```
reproduction([<subpopID>[, <sex>]])  
{  
    ...  
}
```

- apply to *one or all* subpops
- apply to *one or all* sexes
- **pseudo-parameters:**
  - individual
  - genome1
  - genome2
  - subpop
- no return value

# Population regulation

```
// provide density-dependent selection
early() {
    p1.fitnessScaling = K / p1.individualCount;
}
```

- There is no set population size
- Population size is regulated by **mortality**
- Mortality depends upon **fitness**
- Various mechanisms can operate:
  - resource availability
  - territorial behavior
  - predation
  - natural disasters

# A complete nonWF model

```
// set up a simple neutral nonWF simulation
initialize() {
    initializeSLiMModelType("nonWF");
    defineConstant("K", 500); // carrying capacity

    // neutral mutations, which are allowed to fix
    initializeMutationType("m1", 0.5, "f", 0.0);
    m1.convertToSubstitution = T;

    initializeGenomicElementType("g1", m1, 1.0);
    initializeGenomicElement(g1, 0, 99999);
    initializeMutationRate(1e-7);
    initializeRecombinationRate(1e-8);
}

// each individual reproduces itself once
reproduction() {
    subpop.addCrossed(individual, p1.sampleIndividuals(1));
}

// create an initial population of 10 individuals
1 early() {
    sim.addSubpop("p1", 10);
}

// provide density-dependent selection
early() {
    p1.fitnessScaling = K / p1.individualCount;
}

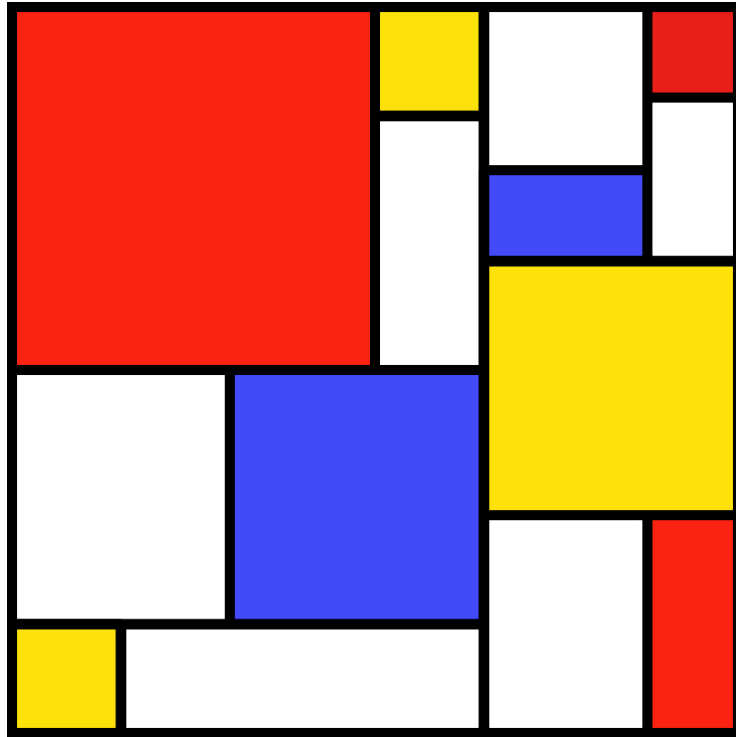
2000 late() { sim.outputFixedMutations(); }
```

# Fitness in nonWF models

- In WF models:
  - fitness is *relative*, selection is *soft*
  - fitness influences **mating success**

# Fitness in nonWF models

- In WF models:
  - fitness is *relative*, selection is *soft*
  - fitness influences **mating success**
- In nonWF models:
  - fitness is *absolute*, selection is *hard*
  - fitness influences **mortality**
  - survival probability is capped at 100%
  - beneficial mutations behave unexpectedly!



SLiM Workshop Exercise #15