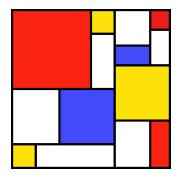
SLiM

Workshop Series



#10: Callbacks I (fitness())

- 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

The WF Generation Cycle

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The WF Generation Cycle

- a set of standard behaviors:
 - generation start
 - mate choice / reproduction
 - parental mortality
 - fitness value recalculation
 - generation end

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The WF Generation Cycle

- a set of standard behaviors:
 - generation start
 - mate choice / reproduction
 - parental mortality
 - fitness value recalculation
 - generation end
- modified by callbacks
 - script providing new behavior

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The WF Generation Cycle

Callbacks:

- early() events
- mateChoice() callbacks
- mutation() callbacks
- recombination() callbacks
- modifyChild() callbacks
- late() events
- fitness() callbacks
- interaction(), reproduction()

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early() events

- called *early* in each generation
- often used to:
 - set up demographic parameters
 - prepare state for mating
 - make a plan for the generation

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late() events

```
late()
{
    ...
}
```

- called *late* in each generation
- often used to:
 - modify the offspring state
 - run behavioral interactions
 - prepare for fitness calculations
 - produce custom output

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fitness() callbacks

- called during fitness calculation
- override default fitness
- often used to:
 - produce spatial variation
 - produce temporal variation
 - produce epistatic interactions
 - produce frequency dependence
 - make a mutation type neutral
- fitness(NULL) callbacks

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fitness() callbacks

```
fitness(<mutTypeID> [, <subpopID>])
{
    ...
}
```

- apply to one mutation type
- apply to one or all subpops
- called once for:
 - each focal mutation,
 - in each focal individual
 - allows individual effects
- return a fitness effect

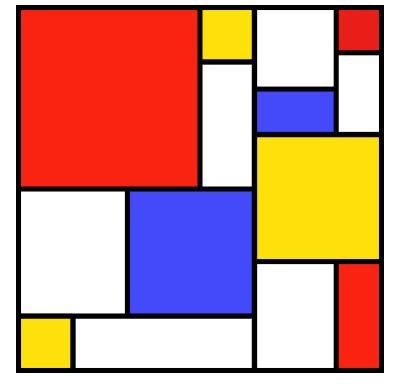
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fitness() callbacks

- there is a focal mutation
- it is in a focal individual
- how does the callback know?
- pseudo-parameters:
 - mut
 - homozygous
 - individual
 - genome1
 - genome2
 - subpop
 - relFitness

Fitness calculation

- Fitness values in SLiM:
 - evaluated per individual, per mutation
 - homozygous: T if homozygous, F if heterozygous
 - relFitness has the default fitness value:



SLiM Workshop Exercise #10