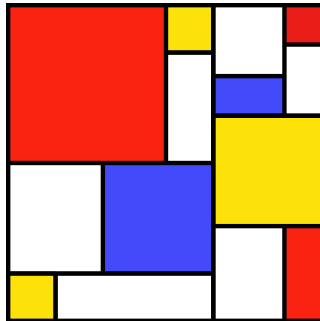


SLiM

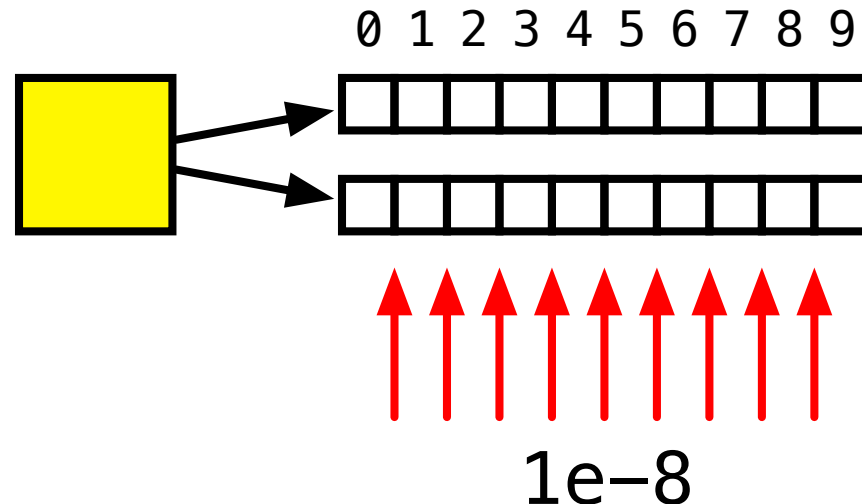
Workshop Series



#6: Recombination

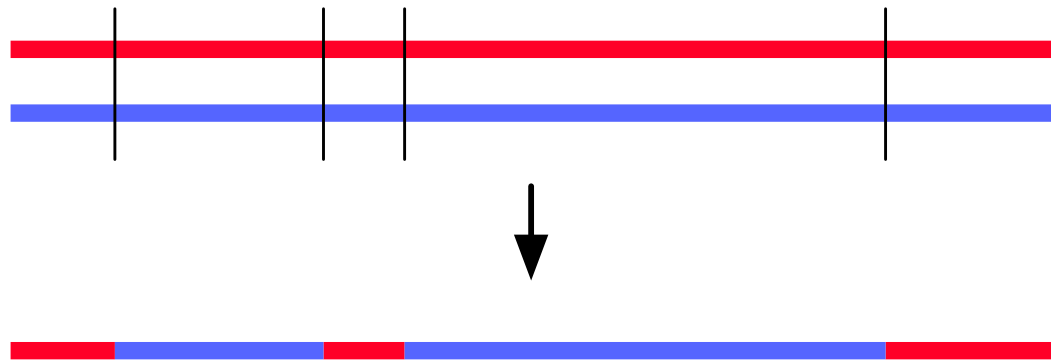
Recombination

- Can be given a uniform rate:
 - `initializeRecombinationRate(1e-8)`
- *Probability* / base / generation



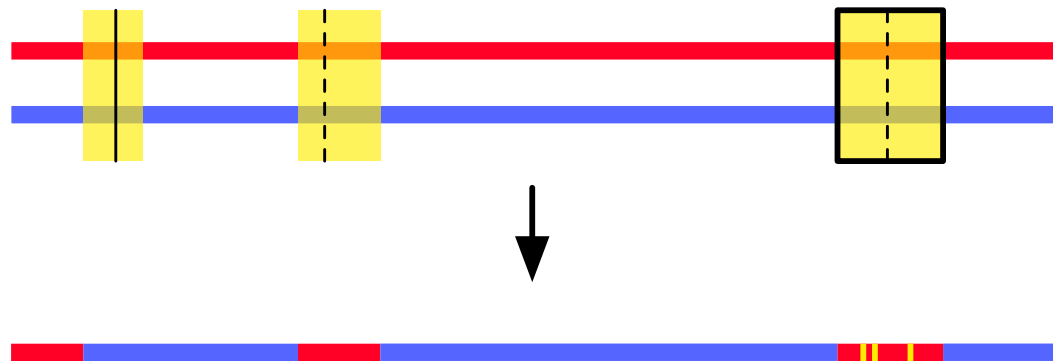
The Crossover Breakpoints Model

- During gamete generation:
 - breakpoints are drawn by probability
 - a simple crossover model is the default



The DSB Model

- Each breakpoint initiates *gene conversion*
 - DSBs can be crossovers or non-crossovers
 - gene conversion tracts can be simple or complex
 - heteroduplex mismatch repair, GC biased repair



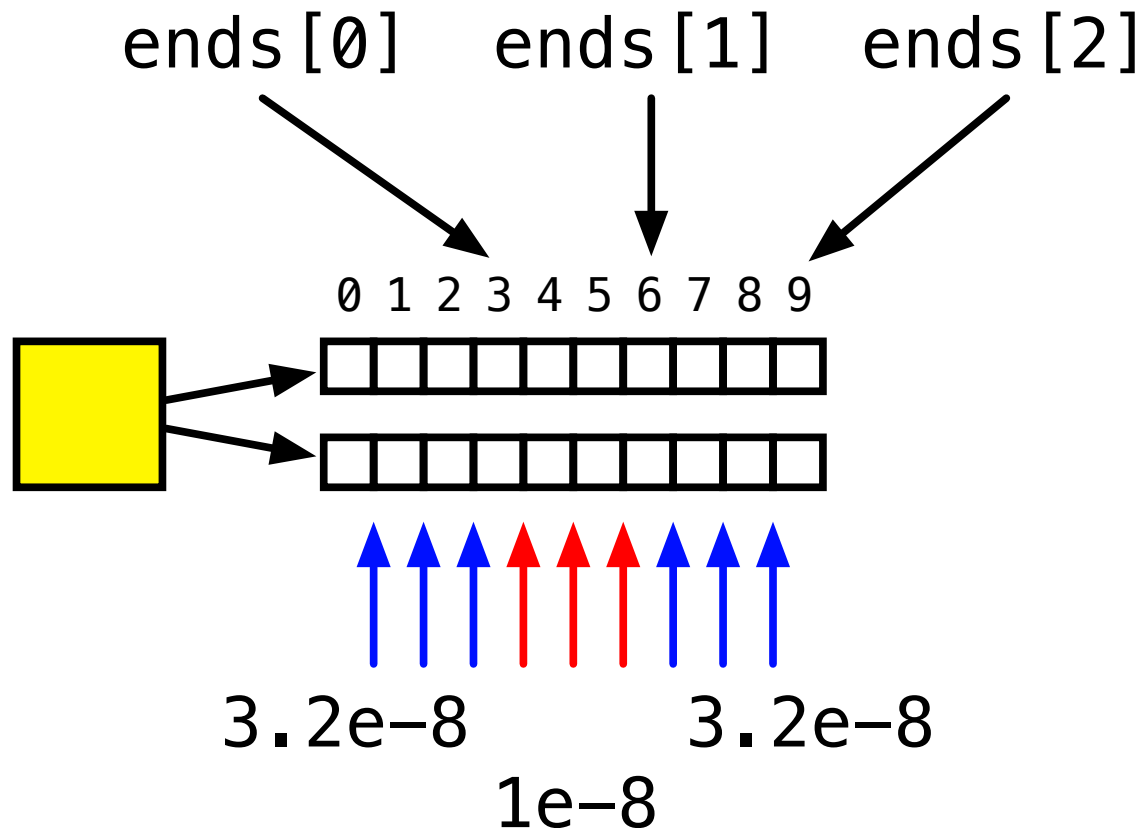
Recombination Rate Maps

- Can also be given vectors of *rates* and *ends*:

```
(void)initializeRecombinationRate(numeric rates,  
    [Ni ends = NULL], [string$ sex = "*"])
```

- Rates apply until the **left edge** of each end

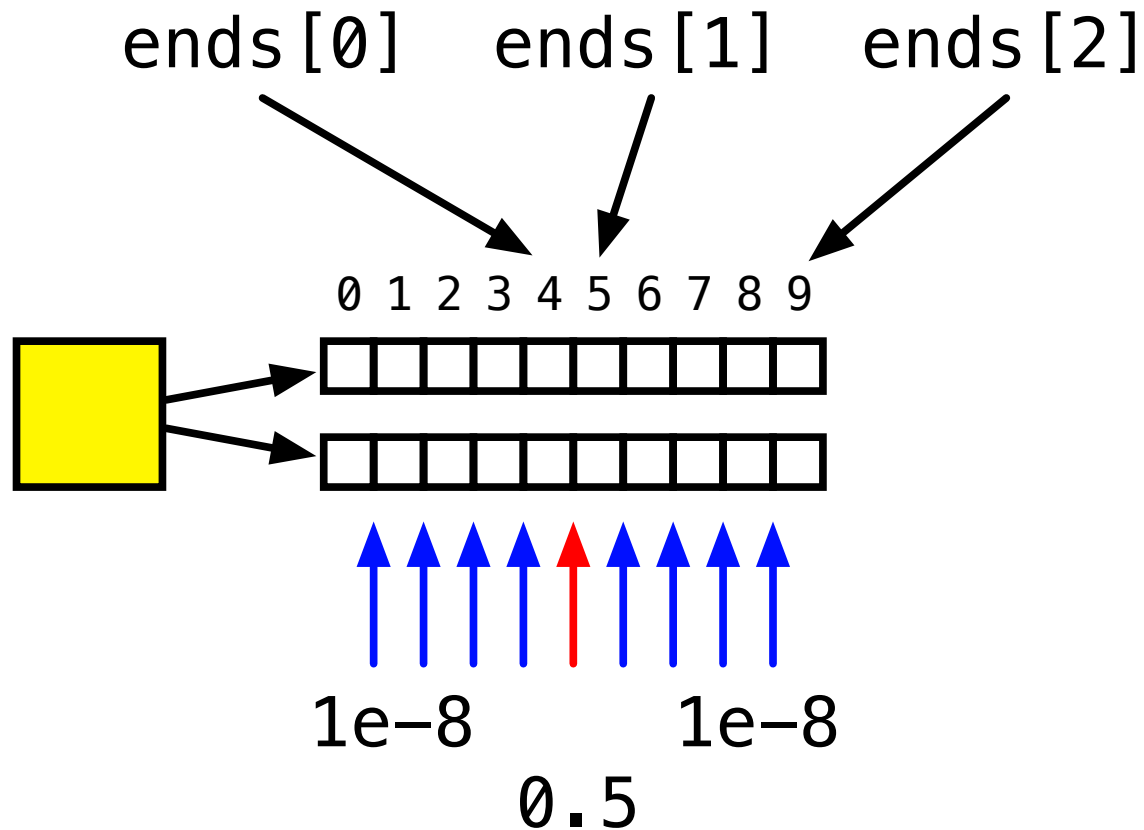
```
initializeRecombinationRate(  
    rates = c(3.2e-8, 1e-8, 3.2e-8),  
    ends = c(3, 6, 9));
```



Multiple Chromosomes

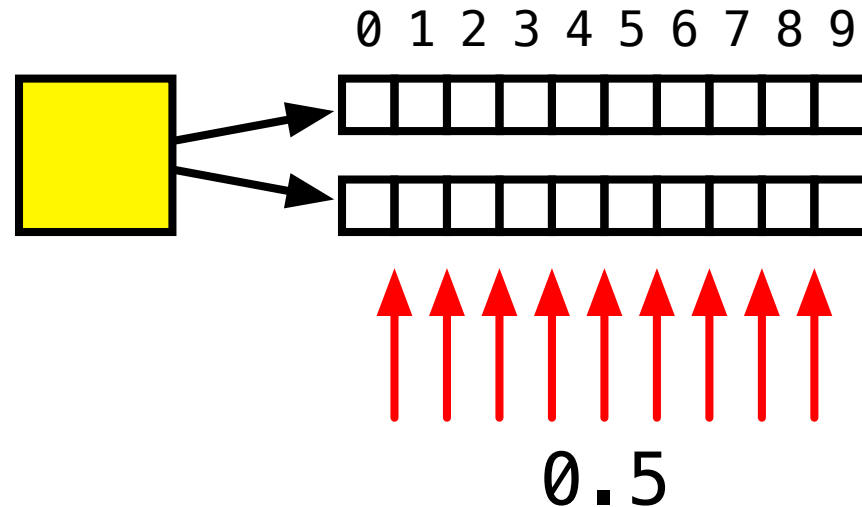
- SLiM models a single chromosome
- A rate of **0.5** makes regions **unlinked**
- You can model >1 “*effective chromosome*”

```
initializeRecombinationRate(  
    rates = c(1e-8, 0.5, 1e-8),  
    ends = c(4, 5, 9));
```



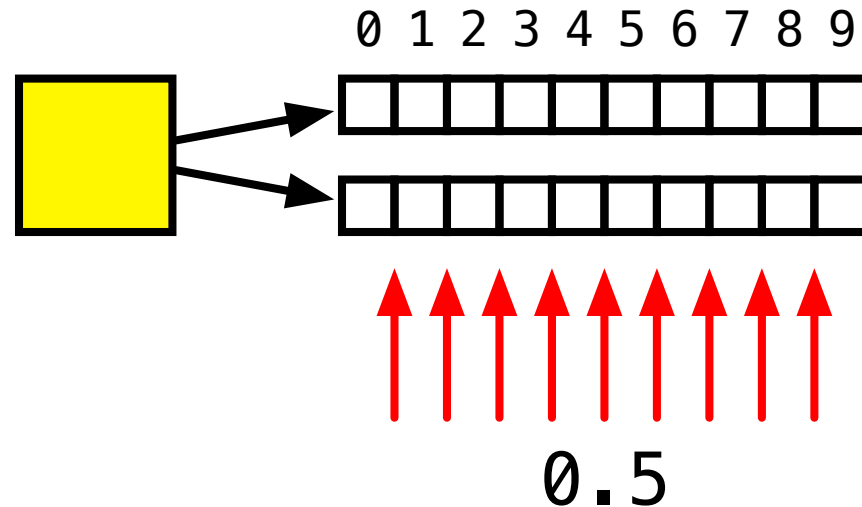
Unlinked Loci

- A rate of **0.5** makes regions **unlinked**
- Model any number of unlinked loci

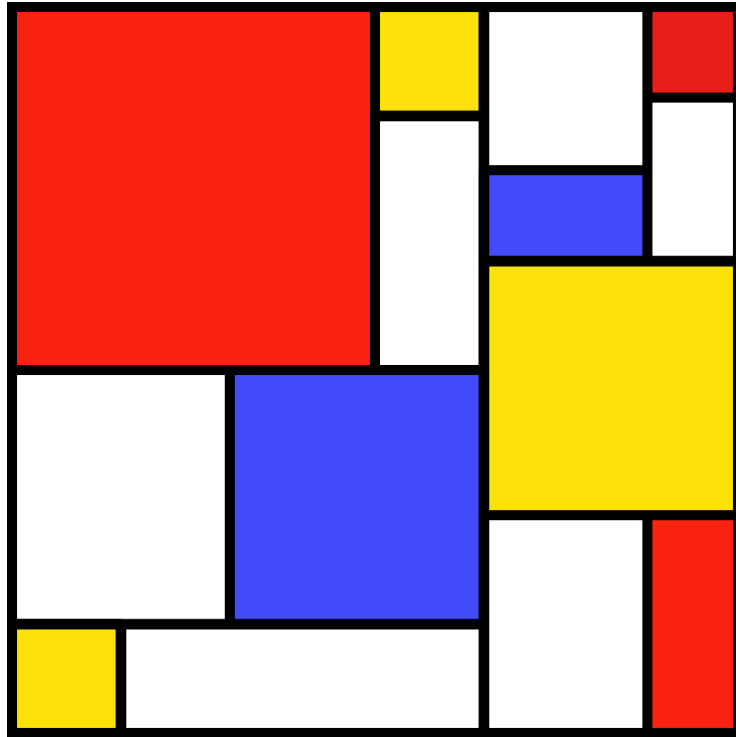


Unlinked Loci

- A rate of **0.5** makes regions **unlinked**
- Model any number of unlinked loci



- Performance can be an issue!



SLiM Workshop Exercise #6