

Third R Project.

For this final R project, we are going to do one more simulation. We will simulate three-point test crosses.

In particular, imagine an individual mouse with the following genotype:

*S W E/s w e*

for the genes Split, Waltzer and Ebony.

You will cross this individual to an individual homozygous for each of the mutant, recessive alleles:

*s w e/s w e*.

Your task will be to simulate 1000 progeny outcomes with arbitrary genetic distances and levels of interference. You will need to simulate the biological process, not just generate the expected values mathematically.

*Note: As you might recall, generating these numbers by FIRST calculating the non-crossover parental proportion, then the single crossover proportion, followed by the double crossover proportion is extremely tricky. You have to do it in reverse.*

To generate expected proportions: Based on the genetic distance between the two markers, AND the level of interference, determine the expected proportion of doubles. Then, considering how many doubles you have obtained, allocate the remaining recombinant proportion to the single class for each of the two spans (ie, between S and W, and W and W), ensuring the genetic distance is accounted for. Remember, genetic distance in a span is measured with the single crossovers in that span AND the double crossovers that have a recombination event also in that span. Once the expected single and double class proportions are determined, allocate the remaining proportion to the parental class.

**The trick here is to first figure out the expected proportions, and then simulate counts from these expected proportions. How to you do that? That is the key. But one suggestion is that you generate random numbers and compare the random numbers to the expected proportions. This can be used to determine if a "gamete" is in a particular class, then do this again 999 more times.**

You don't need to automate the output, but an output would look like this:

```
S W E: ###  
S w E: ###
```

To submit.

1. Submit your code. Your code should be flexible so that to modify it, you only have to change three numbers for 1,2,3 and 4 : Distance from *S* to *W*, *W* to *E* and the Interference number.
2. Submit values for the 8 genotypes under the following conditions:
  - Distance from *S* to *W*: 23 cM
  - Distance from *W* to *E*: 9 cM
  - Interference = 0
3. Submit values for the 8 genotypes under the following conditions:
  - Distance from *S* to *W*: 23 cM
  - Distance from *W* to *E*: 9 cM
  - Interference = 0.5
4. Submit values for the 8 genotypes under the following conditions:
  - Distance from *S* to *W*: 23 cM
  - Distance from *W* to *E*: 9 cM
  - Interference = 1