HEREDITY **PSOW** **D3.2 INHERITANCE**

Gene Linkage Simulation

Introduction

Genes that are on the same chromosome are said to be linked and do not typically undergo independent assortment. However, linked genes can become unlinked during meiotic division if chiasmata form between them and cause crossing over. This is a random occurrence that does not occur with every meiotic division.

Aim

To determine the relationship between the distance between linked genes and frequency of recombination

Method

1. To simulate crossing over during meiosis, access the gene linkage simulation at the following website: https://www.labxchange.org/library/items/lb:LabXchange:013a7416:lx_simulation:1?fullscreen=true
2. Select either simulation 1 or 2 and then change the gene map distance between gene 1 and gene 2
3. Run the simulation for the following map distances: 0, 20, 40, 60, 80 and 100 centiMorgans (cM)
4. Record the frequency of recombinant phenotypes as a proportion of the total to work out percentage

Results

Distance (cM)	0	20	40	60	80	100
Number of recombinants						
Total size of population						
Percentage recombination						

Discussion

1. Determine the value of the correlation coefficient for map distance and percentage recombination

2. Explain the difference between a correlation coefficient (r) and a coefficient of determination (r^2)