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CS 172

Project Proposal

Genetic Cross Program

For my final project, I wish to make a program able to conduct theoretical genetic crosses, both simple Mendelian crosses, and several types of non-Mendelian crosses. It will take input from the user of parent genotypes, then output the genotypic and phenotypic ratios for the progeny. This program will also allow the user to enter the number and phenotypes obtained in the progeny from a genetic cross, and tell the user if the cross’s results fit those predicted. Or, if it is statistically impossible for this to happen by conducting a chi-squared test, it will state so. Then it will output a report containing a Punnett square of the theoretical cross, and the genotypic and phenotypic ratios. If progeny numbers are entered, it will also output the results of the chi-squared test.

Challenges associated with this project will be the number of classes needed to house information inputted by the user, and how I wish to break up the classes for the different genetic crosses. I will need a class for loci on the chromosomes, what they code for, and any dominance relations involved. I will also need a class to store parent organisms for conducting crosses, and a class or classes for different crosses to be conducted. If there is time, I will expand the parent and cross classes to be able to handle situations with linkage for genes, which means I will most likely have to create a separate class for linked chromosomes to store the arrangement of genes and map distances for the loci therein. Then, I would need to add the ability for the program to handle linked genes, which means that I will need to work in an owned/is owned by relationship in the parent class or loci class for other loci. Or, I will add in methods for the cross classes I develop to test for linkage when progeny numbers are entered from a two-point or three point-test cross, and if a linkage test is passed, it will generate the theoretical genetic map for up to three genes in a linkage group and add this to the report to be generated in a text file.

To begin to create this program, I will need to create a comprehensive UML diagram with clear ownership, and keep careful track of which methods will need to call on objects from other classes. I will also need to make sure that the program has a chi-squared table stored in some way, probably in the form of a multi-dimensional static array in one of the classes, to compute the p-values for the crosses I will be conducting. Finally, I will probably need to make extensive use of vectors to function as resizable arrays for storing organisms and their genotypes, to allow for the selection of loci for the crosses.