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CS 172

Final Project Specification: Genetics Program

*Problem Definition:* This program will provide Punnett squares, and predicted ratios of phenotypes and genotypes for monohybrid crosses involving discontinuous traits (either present of absent) with two alleles only, for organisms with a XX-XY sex determination system. It will only work with traits on autosomal loci, or loci on the X chromosome.

It will conduct the following seven cross types: Sex-linked and autosomal complete dominance crosses, and autosomal incomplete and codominance crosses. It will also conduct sex-influenced and sex-limited crosses, and will conduct crosses where the trait has a maternal effect involved.

*Requirements:*

This will require the following classes: A base class for loci with subclasses of Sex-Linked Loci, Sex-Influenced Trait, and Sex-Limited Trait, a class for organisms, and a class for crosses.

*Assumptions:* This program makes many assumptions, and it will not account for interaction between genes of any kind, or incomplete expressivity or penetrance (so, it is assumed that if an organism has a given genotype, it will always display the given phenotype, and all organisms will display the phenotype to an identical degree). It also will not allow for any differences in sex chromosome number, disjunction in gamete generation (meiosis failure to have the chromosomes properly divide), or lethal genotypes.

*UML Diagram:*



