

Population Genetics Simulation of Transcription Factor Binding

Please develop a working program that begins to develop a platform to simulate transcription factor binding to its cognate binding sites in a diploid organism. The program should involve stochastic simulation of a problem, and differential binding of at least two transcription factor variants to at least two binding site variants. You will want to think about how binding should relate to fitness, multiple loci being regulated, how to incorporate multiple binding sites in a haplotype, mutation, recessive/dominance relationships and the effect of population size. You should have a working program written in C/C++ and/or Perl that solves at least part of the problem, and a good written explanation of how you would continue to program if given the opportunity. We do not want to see any pseudo-code or python!