Homework May 12, 2015 (to be returned on May 19)

Run a computer simulation to reproduce the result shown during the lectures about the final heterozygosity as a function of the distance from the selected locus, as measured by the ratio s/r (selection over recombination rates). It is reminded that selection acts only on locus A (selection coefficients: 1, 1 - hs, 1 - s for A_1A_1, A_1A_2, A_2A_2 , respectively) while the second diallelic locus B is taken neutral. The frequency p_1 of the selected allele A_1 is initially 1/2N (N being the population size) and sweeps then to high values (stochastic fluctuations are neglected). Run the simulation up to high values of p_1 , e.g. $p_1 \ge 0.9999$, and measure the heterozygosity $2p_2q_2$. Suppose additivity h = 1/2 for simplicity. Try different values of the population size N = 1,000; 5,000; 10,000 and selection coefficient $s = 10^{-4}, 10^{-3}, 10^{-2}$ and see how much that changes the graph, always using r/s as measure of the distance.