Lilelihood approach of the fitness per genotype

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https://en.wikipedia.org/wiki/Normal_distribution https://en.wikipedia.org/wiki/Gamma_distribution

Genotypes and selection model

Given two loci, A and B, with alleles A and a, and B and b, there must be nine possible gammetes. If the A allele and B allele are selected with coefficients s_A and s_B , and we assume no dominance and no epistasis, we can write the average fitness per genotype. For simplicity we use an haploid model, which would be similar to the diploid homozygotes case:

$$\begin{array}{c|cccc} & B & b \\ \hline A & 1 + s_B + s_A + (s_B \times s_A)\kappa & 1 + s_A \\ a & 1 + s_B & 1 \end{array}$$

And a likelihood (perhaps overdispersed poisson) can be proposed for the fitness function

$$w = 1 + s_1 + s_2 + \kappa(s_1 \times s_2) \tag{1}$$

$$fiw = 1 + \sum_{j=1}^{p} s_j + \kappa \prod_{i=1}^{p} s_i$$
 (2)

(3)

Another genotype selection model

$$\begin{array}{c|cccc} & B & b \\ \hline A & (1+s_B)(1+s_a)^{\kappa} & 1+s_A \\ a & 1+s_B & 1 \end{array}$$

In this case when $\kappa > 1$, then there is some type of epistasis.

$$w = \prod_{i=1}^{p} (1 + s_i)^{\kappa} \tag{4}$$