



HARDY-WEINBERG

The Hardy-Weinberg Theorem is a powerful model for assessing whether populations are at equilibrium or if allele and/or genotypic frequencies are changing and, hence the population is evolving. Remember that expected values are $AA = p^2$, $Aa = 2pq$, and $aa = q^2$

Enter the number of each genotype (AA, Aa, and aa) observed.

EvolutionSolution calculates the total number of individuals sampled, the frequency of each allele ($A = p$, $a = q$) and the frequency of heterozygotes; the expected genotypic frequencies and number of individuals for each genotype expected under Hardy-Weinberg conditions; the chi-square test statistic to test if the observed number of heterozygotes deviates statistically significantly from the expected number of heterozygotes; F , the inbreeding coefficient, which measures the reduction in heterozygosity within nonrandomly mating populations compared to randomly mating populations; and the expected genotypic values, taking into account the inbreeding coefficient.

FORWARD MUTATION

The Hardy-Weinberg equilibrium can be relaxed to accommodate forward mutation. That is where one allele, say A , is allowed to mutate into another allele, a , but the a allele cannot mutate to A . We can use this simple form of mutation to estimate what the allele frequency will be in the next generation, p' , given initial allele frequency, p , and the rate of mutation, μ . The change in allele frequency from one generation to the next is represented as Δp .

Enter the initial allele frequency, p and the mutation rate, μ .

EvolutionSolution calculates the frequency in the allele in the next generation, p' , as well as any change in Δp .

FITNESS

Fitness can be simply defined as the differential survival of genotypes. We represent the fitness of each genotype as w_{AA} , w_{Aa} and w_{aa} . The mean fitness of a population, \bar{w} , then depends on the genotypic frequencies (p^2 , $2pq$, and q^2) and their respective fitness.

Enter the relative fitness values for each of the genotypes and the allele frequency, p .

EvolutionSolution calculates the frequency of q ($=1-p$) and the mean fitness of the population, \bar{w} . The change in allele frequency, Δp , is dependent on the initial frequencies of p and q , differences in relative fitnesses and the mean fitness of the population. The equilibrium value of p , \hat{p} , is dependent on the fitness of the various genotypes but independent of the allele frequencies.

INBREEDING DEPRESSION

The relative fitness of populations can be measured in many ways, for example the number of eggs per clutch or the number of seeds that germinate. Inbreeding depression, δ , is estimated as a relative measure of the fitness of selfed individuals, w_S compared to the fitness of outcrossed individuals, w_O . Said another way inbreeding depression can be thought of as the reduction of a specific fitness component of an inbred population, w_S , compared to the mean for that same fitness component in a completely outcrossing population, w_O . We can see that when w_S and w_O are similar (e.g., both populations are producing about the same number of fruits per plant, say), that δ will be small. Conversely, as w_S becomes smaller (e.g., inbred plants produce only 1/10 of the number of fruits per plant compared to the uncrossing population), the value of δ increases.

Enter the mean fitness values for the inbred population, w_S , and the outcrossed population w_O .

EvolutionSolution calculates the inbreeding depression coefficient, δ , automatically.

HERITABILITY: BROAD-SENSE

Broad-sense heritability, H^2 , is defined as the ratio of the total genetic variance to the total phenotypic variance. In turn, the phenotypic variance can be further divided into environmental and genetic components. In order for a trait to have a high heritability, most of the observed variation must have a genetic, rather than a phenotypic, basis. If most of the variation is due to the environment, then heritability will approach zero. The higher the heritability of a trait, the more similar offspring are to their parents.

Enter values for genetic variance and environmental variance.

EvolutionSolution will calculate the total phenotypic variance and the broad-sense heritability.

HERITABILITY: NARROW-SENSE

The genetic variance, σ^2_g , can be further partitioned into the additive genetic variance, σ^2_a , and the dominance variance, σ^2_d . The additive genetic variance measures the difference between the means of the homozygous genotypes, AA and aa . Dominance variance measures the on degree of dominance of the alleles. It is the additive genetic variance that contributes to the response to selection. Narrow-sense heritability, h^2 , is defined as the ratio of the additive genetic variance to the total phenotypic variance.

Enter values for the additive genetic variance and the total phenotypic variance.

EvolutionSolution will calculate the narrow-sense heritability, h^2 .

SELECTION

Artificial selection can produce dramatic results in a short amount of time if the traits being selected for have a high heritability. We can determine the mean value of a trait for a population before selection, μ ; the mean value of individuals selected to breed (above a specific truncation value), μ_s ; and the mean value of the population after selection, μ' . We can define the selection differential as $S = \mu_s - \mu$ and the response to selection as $R = \mu' - \mu$.

Narrow sense heritability, h^2 , can also be defined as the ratio of the response to selection, R , to the selection differential, S .

Enter the mean value of a trait for a population before selection, μ , the mean value of individuals selected to breed, μ_s , and the mean value of the population after selection, μ' .

EvolutionSolution calculates the selection differential, the response to selection, and the narrow-sense heritability.



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