

1- Answer:

$$f(A_1) = 0.2929; f(A_2) = 0.2599; f(A_3) = 0.4472 \text{ (30 points, 10 each)}$$

Solution:

$$f(A_1) = p; f(A_2) = q; f(A_3) = r$$

$$r^2 = 0.2 \Rightarrow r = \sqrt{0.2} = 0.4472$$

$$q^2 + 2qr = 0.3 \Rightarrow q^2 + 0.8944q - 0.3 = 0 \Rightarrow q = 0.2599 \text{ (Also } -1.1543, \text{ unacceptable)}$$

$$p = 1 - q - r = 0.2929$$

2- Answer: $F_I = 0.3125$ (30 points)

Solution:

The equation to calculate F for X-link genes is still $F = \sum_i (1 + F_{A,i}) \left(\frac{1}{2}\right)^{n_i-1}$ with the following adjustments:

No male-to-male steps are allowed in a path

n_i : number of female-to-child steps in a path (there is only one option to pass an X-linked allele from male to female)

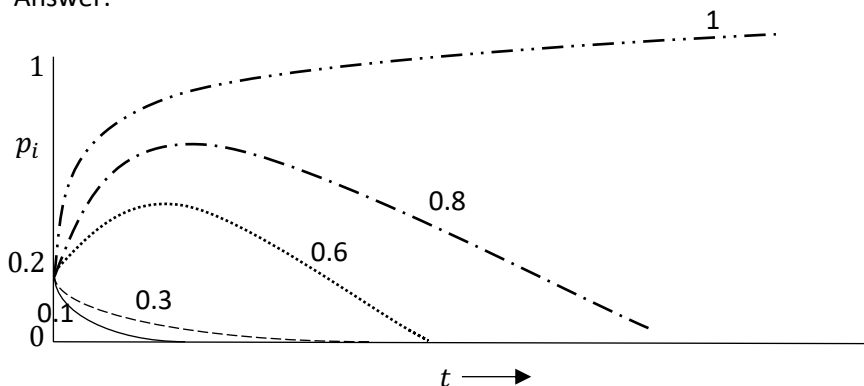
$F_{A,i}$: Inbreeding coefficient of the common ancestor of path i . Inbreeding coefficient does not have any real biological meaning for an X-linked gene in a male individual because it has only one allele, but for the sake of pedigree analysis, we can assume $F_{A,i}$ to be 1 for a male ancestor because a male ancestor always gives the same X-linked allele to all his offspring; and therefore, behaves as if he had two IBD alleles.

Only legitimate path in the given pedigree: $IG\textcolor{red}{E}HI$

$$F_E = \frac{1}{4}$$

$$F_I = \left(1 + \frac{1}{4}\right) \left(\frac{1}{2}\right)^2 = 0.3125$$

3- Answer:



Solution: As the provided equations suggest, p_A will increase for alleles that have higher than average fitness. At generation zero, $\bar{w} = \sum f_i w_i = 0.2(0.1 + 0.3 + 0.6 + 0.8 + 1) = 0.56$ (all alleles have equal frequency). So, the alleles with w of 0.6, 0.8 and 1 start to increase in frequency. The alleles with w 0.1 and 0.3 will fall in frequency (the $w = 0.1$ alleles with a steeper slope) until they approach zero and go extinct. Note that the change in allele frequencies will change \bar{w} generation by generation. The increase in the proportion of high-fitness alleles increases the population average fitness. When it reaches a value greater than 0.6, the allele with $w = 0.6$ will now start to drop in frequency and

eventually go extinct. The 0.8 and 1 alleles continue to rise. At some point, \bar{w} will reach 0.8 and the $w = 0.8$ allele will decrease in frequency after that point as well and go eventually extinct. Only the allele with the highest frequency will keep rising continuously until it reaches $f = 1$ and get fixed in the population.

Note: The sum of the 5 five allele frequencies at each time must add up to 1, but this is difficult to ensure when drawing the curves by hand. Points should be given if:

$w = 0.1$ and 0.3 : Always decrease and eventually reach 0 (20 points, 10 each)

$w = 0.6$ and 0.8 : First increase, then decrease till they reach 0 (20 points, 10 each)

$w = 1$: Always increase till it reaches 1 (10 points)

4- Answer:

Completed sweep: B; Partial sweep: C; Balancing selection: A. (10 points each)

Solution: A complete selective sweep means that descendants of the high-fitness allele will propagate and reach high frequencies through the generations much faster than the expectation by drift. Therefore, going back in time, the present-day alleles will reach their common ancestor faster, leading to a coalescent tree with shorter branches (B). A partial sweep will show the same pattern but only for a fraction of alleles: descendants of the beneficial allele. The time to most recent common ancestor of this group and the rest of the alleles (represented by the left branch in C) will be close to expectation by drift. Balancing selection, which likes to preserve variation, maintains two or more lineages of alleles in the population for a long time and prevents them from getting lost, resulting in longer coalescent branches (A).

5- Answer:

a) Nonsynonymous (10 points)

b) The χ^2 independence test (10 points)

c) $\chi^2 = 8.1978$ (5 points); $df = 1$ (5 points); $p = 0.004194$ (5 points); Null hypothesis IS rejected. (5 points)

d) $\omega = 8.647$ (5 points)

e) Positive selection (15 points)

Solution for e: Under neutral evolution, there is no reason to believe that syn and nsyn mutations should behave differently. Therefore, under pure drift, $\omega = 1$. Positive selection in one population increases the number of fixed differences between populations while mildly reducing the remaining variation (polymorphism) in the population where selection has happened. As nonsynonymous changes are more likely to affect fitness, positive selection will result in an excess of fixed nonsynonymous differences (nsyn divergence) and a dearth of nonsynonymous polymorphisms compared to the expectation from neutral evolution, thus producing values of $\omega > 1$. Values of $\omega < 1$ indicate purifying selection because in this scenario, nsyn mutations are still introduced into the population and can exist in low frequencies (polymorphism), but they can hardly reach high frequencies and get fixed (reduced nsyn divergence).