

WORKSHEET — POPULATION GENETICS

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The probability of any given gene can range from 0 to 1. If there are two or more possibilities, the sum of all probabilities must equal 1. The Hardy-Weinberg Law, published in 1908, is based on several assumptions--it is true only if a) no mutations occur, b) there is random breeding, c) each pair produces a number of offspring, and d) the population is sufficiently large. For some gene with alleles A and a, the probability or frequency of allele A can be represented by **p** and the probability or frequency of a can be represented by **q**, and since these are the only two possibilities, $p + q = 1$. Remembering that an organism has two alleles for each gene, the possible genotypes are AA, Aa, or aa. Since the genotype AA is made up of two A alleles, the probability of that genotype is the probability of A times the probability of A, or p^2 . Likewise, the probability of aa is q^2 . Remember that there are two ways to get Aa: either Aa or aA, so the probability of genotype Aa is $2pq$. Since the sum of the probabilities for all possible outcomes must be equal to 1, this means that $p^2 + 2pq + q^2 = 1$ and you may recall from algebra that $p^2 + 2pq + q^2 = (p + q)^2$.

EXAMPLE:

For PTC (phenylthiocarbamide) paper, about 70% of the population can taste the paper (the dominant trait) and about 30% cannot. This means that genotypes TT and Tt make up about 0.70 of the population and genotype tt makes up about 0.30 of the population. We know that the probability of tt is q^2 , so we can say that $q^2 = 0.30$ and thus, $q = 0.548 = 0.55$. Since $p + q$ must = 1, then $p = 1 - q = 1 - 0.55 = 0.45$, and $p^2 = 0.20$. Also, $2pq = 2 \times 0.55 \times 0.45 = 0.50$. Note that $p^2 + 2pq + q^2 = 0.20 + 0.50 + 0.30 = 1$. The probability of a dominant phenotype (T-) equals the sum of all possible ways to have a dominant genotype; probability of T- = probability of TT + probability of Tt, or $0.20 + 0.50 = 0.70$ (to double check, note that this is equal to the 70% statistic noted above). Suppose you want to determine the probability of two tasters having a child who is a non-taster. For the child to be a non-taster, his/her genotype must be tt, and the only way this could be is if both parents are genotype Tt. Out of all people with dominant phenotypes (T-) $0.20/0.70 = 2/7$ of them have the genotype TT and $0.50/0.70 = 5/7$ of them have genotype Tt. Thus, the probability of both parents being Tt, is $5/7 \times 5/7$. If both parents are Tt, then from a regular Punnett square, remember that the probability of them having a tt child is $1/4$. This means that the probability of two tasters having a non-taster child is $5/7 \times 5/7 \times 1/4 = 0.128$ or 12.8%.

NON-RANDOM BREEDING:

The Hardy-Weinberg Law can also be used to determine if breeding is, indeed, random.

EXAMPLE:

For the human MN blood group, a person can have either type M (genotype MM) or type MN (genotype MN) or type N (genotype NN). From a population in Australia there were 320 type M people, 800 type MN, and 880 type N, so:

320	MM	, therefore 640 M alleles
800	MN	, therefore 800 M alleles and 800 N alleles
880	NN	, therefore 1760 N alleles

2000 people, therefore 4000 alleles including 1440 M (= 36% or 0.36) and 2560 N (= 64% or 0.64) alleles. Thus, $p = 0.36$ and $q = 0.64$. If p and q have these values and there is random breeding, $p^2 = 0.13$, $2pq = 0.46$, and $q^2 = 0.41$. In a population of 2000 individuals we should then expect to see $0.13 \times 2000 = 260$ type M, $0.46 \times 2000 = 920$ type MN, and $0.41 \times 2000 = 820$ type N people. A χ^2 comparison with the actual numbers indicates that there is not random breeding (or the two sets of numbers would be more nearly the same):

O	E	(O-E) ² /E	
320	260	13.846	
800	920	15.652	df = 3 - 1 = 2, so χ^2_{tab} at .05 level = 5.991
880	820	4.390	
		$\Sigma = 33.888$	$= \chi^2_{calc}$, which is greater than χ^2_{tab} , so the null hypothesis can be rejected--there is not random breeding.

As an example of non-random breeding, consider plants that are self-pollinating. In this case, AA can only mate with AA, Aa can only mate with Aa (producing AA, Aa, and aa offspring), and aa can only mate with aa. Thus, over time, the number of AA and aa individuals in the population increase relative to the number of Aa individuals.

SEX-LINKED GENES:

The Hardy-Weinberg Law can also be used in cases of sex-linked genes.

EXAMPLE:

In humans, red-green colorblindness is a sex-linked recessive trait. A colorblind male has the genotype X^bY and a normal male has the genotype X^BY, thus the genotype and phenotype frequencies are equal. Females could be X^BX^B (normal), X^BX^b (carrier), or X^bX^b (colorblind),

thus the normal Hardy-Weinberg Law applies. If 10% (0.10) of the males are colorblind and 90% (0.90) are normal, then $p = 0.90$ and $q = 0.10$ because each male has only one allele for this gene. From this the phenotype frequencies for the females can be calculated: $p^2 = (0.90)^2 = 0.81$ normal, $2pq = 2 \times 0.90 \times 0.10 = 0.18$ carriers, and $q^2 = (0.10)^2 = 0.01$ colorblind.

MULTIPLE ALLELES:

A slightly more complicated case is that of multiple alleles.

EXAMPLE:

In the human ABO blood group, there are three alleles for this gene: I^A, I^B, and i. A person can have any two of the three alleles, so I^AI^A or I^Ai make type A blood, I^BI^B or I^Bi make type B blood, I^AI^B makes type AB blood, and ii makes type O blood. Let p represent the frequency of I^A, q represent the frequency of I^B, and r represent the frequency of i. Remember that $p + q + r = 1$. The Hardy-Weinberg Law says that at equilibrium, $(p + q + r)^2 = p^2 + q^2 + r^2 + 2pq + 2pr + 2qr = 1$ where p^2 is the probability of I^AI^A and $2pr$ is the probability of I^Ai (thus probability of type A = $p^2 + 2pr$), q^2 is the probability of I^BI^B and $2qr$ is the probability of I^Bi (thus probability of type B = $q^2 + 2qr$), r^2 is the probability of ii (thus probability of type O = r^2), and $2pq$ is the probability of I^AI^B (thus probability of type AB = $2pq$). If out of 2000 people, 37.8% are type A, 14.0% type B, 4.5% type AB, and 43.7% type O, then $r^2 = 0.437$ so $r = 0.661$. Temporarily "ignoring" I^B, the frequency of type A blood + frequency of type O blood = $p^2 + 2pr + r^2 = (p + r)^2$. We know that there are 37.8% with type A blood ($p^2 + 2pr$) and 43.7% with type O blood (r^2), so $(p + r)^2 = 0.378 + 0.437 = 0.815$. Then $p + r = \sqrt{0.815} = 0.903$, so $p = 0.903 - r = 0.903 - 0.661 = 0.242$. Also, the frequency of type B + frequency of type O = $q^2 + 2qr + r^2 = (q + r)^2 = 0.140 + 0.437 = 0.577$, so $(q + r) = \sqrt{0.577} = 0.760$. Therefore, $q = 0.760 - r = 0.760 - 0.661 = 0.099$. To check, $p + q + r = 0.242 + 0.099 + 0.661 = 1.0$, so that is correct. Also, $p^2 + q^2 + r^2 + 2pq + 2pr + 2qr = 0.059 + 0.010 + 0.437 + 0.048 + 0.320 + 0.131 = 1.0$, so that is correct.

MULTIPLE GENES:

The Hardy-Weinberg Law also applies for multiple genes--either linked or non-linked.

EXAMPLE:

For a gene with alleles A and a, $p_A^2 + 2p_Aq_a + q_a^2 = 1$ and for some other gene with alleles B and b, $p_B^2 + 2p_Bq_b + q_b^2 = 1$. If, for example, it is desired to find the frequency of AaBb, multiply the frequencies needed ($2p_Aq_a \times 2p_Bq_b$). If $p_A = 0.2$ ($q_a = 0.8$) and $p_B = 0.1$ ($q_b = 0.9$), then the probability of AaBb should be $2 \times 0.2 \times 0.8 \times 2 \times 0.1 \times 0.9 = 0.058$.

EFFECTS OF MUTATION:

The effects of mutation can also be calculated. If mutations of allele A to allele A' (not necessarily A to a--could be a to A) recur at a given rate, and if this is the only mutation of A that takes place, then the frequency of A can go from 100% down to 0% while the frequency of A' goes from 0% to 100%. We can symbolize the mutation rate as **u**, and for this example, let it be 1×10^{-6} . There is a concept that is sort of like the idea of half-life in radioactive isotopes--the number of generations (**t**) needed to reduce the frequency of A to 0.5 of its original value. The equation for this is $t = -(\ln 0.5)/u$, where $\ln 0.5 = -0.693$, so if $u = 1 \times 10^{-6}$, $t = 0.693/(1 \times 10^{-6}) = 6.93 \times 10^{16} = 6.93 \times 10^2 = 693,000$ generations. Thus, if p_A starts out at 0.96, after 693,000 generations, p_A will be 0.48 and after another 693,000 generations (= 1,386,000 total) it will be 0.24.

If the reverse mutation also occurs, eventually, the population will reach an equilibrium point where the rates of the two mutations are equal, where the gain from mutations to an allele is the same as the loss from mutations from that allele.

EXAMPLE:

For a gene with alleles A and a, p is the frequency of A and q is the frequency of a. Let **u** be the rate of mutation from A → a and **v** be the rate of mutation from a → A. For allele a, the net rate of change in frequency, $\Delta q = \text{gain} - \text{loss} = up - vq$. When equilibrium is established, $\text{gain} = \text{loss}$, or $\Delta q = 0$ and $up = vq$. Thus:

$$vq = up = u(1 - q) = u - uq$$

$$vq + uq = u$$

$$q(u + v) = u$$

$$q = u/(u + v)$$

To distinguish this as being the equilibrium value of q, it is written as \hat{q} . Similarly, $\hat{p} = v/(u + v)$.

EFFECTS OF MIGRATION:

The effects of migration can also be calculated. If immigration is sporadic, we say there is gene exchange between populations. If it happens more often, there is gene flow.

EXAMPLE:

If we let q_0 be the q value of the original population under consideration for a certain gene, q_m be the q value for the migratory population, q_i be the frequency after immigration has taken place and **m** be the number of migrants (assuming the population remains constant in size), then $q_i = mq_m + (1 - m)q_0 = mq_m - mq_0 + q_0 = m(q_m - q_0) + q_0$. When the original population and the population after immigration are considered, $\Delta q = q_i - q_0 = m(q_m - q_0)$. Thus, the effect

of immigration on the population depends on the number of individuals that migrate and the Δq between the migrating population and the original population. Note that if $q_0 = q_m$, then $\Delta q = 0$, but if they are different, then the number of individuals that migrated is also important.

NATURAL SELECTION:

Natural selection affects different genotypes (AA, Aa, aa) differently--selection will be for or against each one of these genotypes. Let w = adaptive value and s = selection coefficient, such that $w + s = 1$. Note that as w increases, s decreases and visa versa. These values are assigned to each genotype (irrespective of the other genotypes). $W = 1$ if the genotype is the most adaptive (able to adapt to new conditions). If w is less than 1, there is selection against that genotype. Also, the larger s is, the more selection will take place. For example, if we have:

$$w = \begin{matrix} AA & Aa & aa \\ 1.00 & 1.00 & 0.99 \end{matrix}$$

then there is selection against aa, so for every 100 AA individuals produced, only 99 aa are produced. Note also that in this example, for aa, $s = 1 - w = 0.01$. In another example:

$$w = \begin{matrix} AA & Aa & aa \\ 0.90 & 0.90 & 0.10 \end{matrix}$$

there is a selection coefficient of 0.01 against both dominant phenotypes.

Three different cases are possible:

CASE 1--SELECTION AGAINST DOMINANT:

If the initial value of p (p_i) = 0.8, the initial value of q (q_i) = 0.2, and $s = 0.1$, over the course of a number of generations, p will decrease until it becomes 0 and q will increase until it reaches 1. How long this takes depends on what s is--if $s = 1$, then AA and Aa will not produce any offspring. For example, a population could have:

$$w = \begin{matrix} AA & Aa & aa \\ 0.90 & 0.95 & 1.00 \\ s = 0.10 & 0.05 & 0 \end{matrix}$$

CASE 2--SELECTION AGAINST RECESSIVE:

In this case, the general formula would be:

$$w = \begin{matrix} AA & Aa & aa \\ 1.00 & 1.00 & 1-s \end{matrix}$$

In the simplest (most extreme) example, $s = 1$ so $w = 0$ for aa. If you would start with a population that is 51% A- and 49% aa, then $q_i = \sqrt{0.49} = 0.70$, and $p_i = 0.30$, so $p^2 = 0.09$, $2pq = 0.42$, and $q^2 = 0.49$. If all of the aa genotypes die or become sterile for whatever reason, the proportions of AA and Aa remaining in the population become: for AA, $0.09/(0.09 + 0.42) = 17.6\%$ and for Aa, $0.42/(0.09 + 0.42) = 82.3\%$. The possible matings between the remaining Aa and Aa individuals would be:

	AA (0.176)	Aa (0.823)
AA (0.176)	AA x AA	AA x Aa
Aa (0.823)	Aa x AA	Aa x Aa

The probabilities of each of these matings occurring are:

$$\begin{aligned} AA \times AA &= 0.176 \times 0.176 = 0.031 \\ AA \times Aa &= 0.176 \times 0.823 \times 2 = 0.290 \\ Aa \times Aa &= 0.823 \times 0.823 = 0.677 \end{aligned}$$

The possible progeny from each of these matings would be:

	AA	Aa	aa
AA x AA	0.031	0	0
AA x Aa	$0.5 \times 0.290 = 0.145$	$0.5 \times 0.290 = 0.145$	0
Aa x Aa	$0.25 \times 0.677 = 0.169$	$0.5 \times 0.677 = 0.338$	$0.25 \times 0.677 = 0.169$

Thus, at this point, $q_f^2 = 0.169$, $q_f = 0.41$ (remember, we started out with $q_i = 0.70$), which is only 59% of the original value--the frequency of a has decreased nearly 1/2 in only one generation. If $s = 1.00$

against aa and we start with $q_i = p_i = 0.50$, the following chart can be constructed:

gen	q_i	$q^2(aa)$	$p^2(AA)$	$2pq(Aa)$	ratio of Aa:aa	prop. of Aa left	prob. of Aa x Aa	prob. aa off (q^2)	q_i
1	0.50	0.25	0.25	0.50	2:1	0.67	0.44*	0.11*	0.33*
2	0.33	0.11	0.44	0.44	4:1	0.50	0.25	0.06	0.25
3	0.25	0.06	0.56	0.38	6:1	0.40	0.16	0.04	0.20
4	0.20	0.04	0.64	0.32	8:1	0.33	0.11	0.03	0.17
5	0.17	0.03	0.69	0.28	10:1	0.29	0.08	0.02	0.14
n	$\frac{1}{(n+1)}$	$\frac{1}{(n+1)^2}$	$\frac{n^2}{(n+1)^2}$	$\frac{2n}{(n+1)^2}$	2n:1	$\frac{2}{n+2}$	$\frac{4}{(n+2)^2}$	$\frac{1}{(n+2)^2}$	$\frac{1}{n+2}$

*Since the probability of Aa = $.50/(.25 + .50) = \mathbf{b}$, then the probability of Aa x Aa = $\mathbf{b} \times \mathbf{b} = 4/9$. Thus, the probability of an aa offspring is $\frac{1}{4} \times \frac{4}{9} = 1/9$, and $q = \sqrt{1/9} = \mathbf{a}$.

Note especially the column for the ratio of Aa:aa. This means that for every aa that dies or becomes sterile, there are 2n number of Aa produced that could have aa offspring (for example, for the 100th generation, 200 Aa are produced for every aa), thus the more generations that occur, the less effective continued selection actually is. If however, $s = 0.10$ against aa, then:

gen	p_i	q_i	$p^2(AA)$	$2pq(Aa)$	$q^2(aa)$	$p^2 \times 1$ (A) gametes from AA	$2pq \times 1$ (A&a) gametes from Aa	$q^2(1-s)$ (a) gametes from aa
1	0.500	0.500	0.2500	0.5000	0.2500	0.2500	0.25 + 0.25	$.25 \times .9 = 0.225$
2	0.513	0.487	0.2632	0.4997	0.2372	0.2632	0.4997 (1/2 ea)	0.2134
3	0.525	0.475	0.2761	0.4987	0.2252	0.2761	0.4986 (1/2 ea)	0.2027
gen	tot gametes = $1 - sq^2$	# of A gametes	# of a gametes			fract. of A gametes (p_i)	fract. of a gametes (q_i)	
1	0.9750	0.5000	0.4750			0.5128	0.4872	
2	0.9763	0.5130	0.4633			0.5254	0.4745	
3	0.9775	0.5255	0.4520			0.538	0.4624	

Note that with this smaller value for s , less selection takes place. The general expressions for the gametes produced are:

AA genotypes contribute $p^2 \times 1$ of the gametes, all of which are A.
 Aa genotypes contribute $2pq \times 1$ of the gametes, which are half A and half a.
 aa genotypes contribute $q^2 \times (1-s)$ of the gametes, all of which are a.

The total number of gametes produced is, then, $(p^2 + 2pq) + q^2(1-s)$, which in this example is $.250 + .500 + .225 = .975$. Since $p = q - 1$, then

$p^2 = (1 - q)^2 = 1 - 2q + q^2$
 $2pq = 2q(1 - q) = 2q - 2q^2$
 thus, $p^2 + 2pq = (1 - 2q + q^2) + (2q - 2q^2) = 1 - q^2$
 so, $(p^2 + 2pq) + q^2(1 - s) = (1 - q^2) + (q^2 - sq^2) = 1 - sq^2$. Thus, q for the next generation ($n + 1$) can be calculated from the number of a gametes produced divided by the total number of gametes produced or:

$$[q_n^2(1 - s) + 0.5 \times (2p_n q_n)] / (1 - sq_n^2) = q_{n+1}$$

which for the first row of the above table, would be $(.225 + .250) / (.975) = .4872$.

We can, then, calculate the change in q (Δq) as a result of selection:

$$\begin{aligned} \Delta q &= q_{n+1} - q_n \\ &= (q_n^2 - sq_n^2 + p_n q_n) / (1 - sq_n^2) - q_n \\ &= \{ [q_n^2 - sq_n^2 + (1 - q_n)(q_n)] - q_n(1 - sq_n^2) \} / (1 - sq_n^2) \\ &= (q_n^3 - sq_n^2 + q_n - q_n^2 - q_n + sq_n^3) / (1 - sq_n^2) \\ &= (sq_n^3 - sq_n^2) / (1 - sq_n^2) \\ &= -sq_n^2(1 - q_n) / (1 - sq_n^2) \end{aligned}$$

So, for the above example,

gen	$q =$	$\Delta q = q_f - q_i$
1	0.500	-0.0128
2	0.487	-0.0125
3	0.475	-0.0121

CASE 3--SELECTION AGAINST BOTH HOMOZYGOTES:

In this example, Aa is superior to either AA or aa, and this is called **overdominance** or **balanced polymorphism**. An example of this would be the gene for sickle-cell anemia and resistance to malaria in humans. Thus:

$$w = \begin{matrix} AA & Aa & aa \\ 1 - s_A & 1.00 & 1 - s_a \end{matrix}$$

After a generation of selection, there will be $p^2(1 - s_A)$ from AA + $2pq$ from Aa + $q^2(1 - s_a)$ from aa gametes produced. For example, if $p_i = q_i = 0.50$, $s_A = 0.20$, and $s_a = 0.80$ and $w_a = 0.40$, then:

gen	p_i	q_i	p^2	q^2	$2pq$	$p^2(1-s_A)$	$q^2(1-s_a)$	total	# A	# a	% of A	% of a
1	0.50	0.50	0.25	0.25	0.500	0.2000	0.1000	0.800	0.450	0.350	56.250	43.750
2	0.56	0.44	0.32	0.19	0.492	0.2531	0.0766	0.822	0.499	0.323	60.740	39.260
3	0.61	0.39	0.37	0.15	0.477	0.2952	0.0616	0.834	0.534	0.300	64.004	35.996

Eventually, the population will reach equilibrium, this being determined by s_A and s_a , so: $\hat{p} = s_a / (s_A + s_a)$ and $\hat{q} = s_A / (s_A + s_a)$. To continue the above example: $\hat{p} = 0.6 / (0.2 + 0.6) = 0.75$ and $\hat{q} = 0.2 / (0.2 + 0.6) = 0.25$.

EFFECTS OF MUTATION AND SELECTION TOGETHER:

Several interactions between these two factors are possible. For

1. $w = \begin{matrix} AA & Aa & aa \\ 1-s & 1-s & 1 \end{matrix}$ and $A \xrightarrow{u} a$ selection & mutation work in same direction
2. $w = \begin{matrix} 1-s & 1-s & 1 \end{matrix}$ and $A \xrightarrow{u} a$ selection & mutation working against each other--eventually, equilibrium will be established
3. $w = \begin{matrix} 1 & 1 & 1-s \end{matrix}$ and $A \xrightarrow{u} a$ selection & mutation working against each other here too

In this third example, selection is against the recessive, but mutation is toward it. Recall that, due to mutation, $\Delta q = up - vq$ and because of selection, $\Delta q = sq^2(1 - q)/(1 - sq^2)$. Equilibrium will be reached when $\Delta q_{mut} = \Delta q_{sel}$ or:

$$up - vq = sq^2(1 - q)/(1 - sq^2)$$

$$u(1 - q) - vq = sq^2(1 - q)/(1 - sq^2)$$

Note that as q approaches 0, qv approaches 0 (because, in this case, v is so small, too) and $1 - sq^2$ approaches 1, thus if q is nearly 0,

$$\frac{u(1 - q)}{1 - sq^2} \approx \frac{sq^2(1 - q)}{1 - sq^2}$$

So $\hat{q}^2 = u/s$ and $\hat{q} = \sqrt{u/s}$. If the aa genotype is lethal, $s = 1.00$ so $\hat{q} = \sqrt{u}$.

There are also several cases of mutation from recessive to dominant with selection against the dominant. A **semidominant lethal** refers first to the expression of the gene and secondly to the vitality of the organism. A gene is **semilethal** if the organism is born alive, lives for a while, then dies. A gene is **subvital** if the organism is not as viable. In general, these can all be expressed as:

$$4. \quad w = \begin{matrix} AA & Aa & aa \\ 1-s & 1 & 1 \end{matrix}$$

Within this are several special cases:

$$4a. \quad w = \begin{matrix} AA & Aa & aa \\ 0 & 1 & 1 \end{matrix}$$

An example of this is brachydactyly in humans (shortfingerness: **brachy** = short, **dactyl** = finger or toe). The homozygote is not viable, but Aa is not affected. Note that the frequency of $A = \hat{p} = \sqrt{v}$.

$$4b. \quad w = \begin{matrix} 0 & 1-s & 1 \end{matrix}$$

An example in humans is achondroplasia (**a** = not, without; **chondro** = cartilage; **plasio** = form, mold, shape). The homozygote is not viable, while the heterozygote has abnormal cartilage and is a dwarf. Note that $\hat{p} = v/s$.

$$4c. \quad w = \begin{matrix} 0 & 0 & 1 \end{matrix}$$

Neither the homozygote nor the heterozygote live. The homozygote is lethal and the heterozygote is born alive but soon dies. In humans, this is represented by retinoblastoma (**retina** = a net, the retina of the eye; **blasto** = a bud, sprout; **-oma** = tumor, swelling), a condition in which the retinas develop fatal tumors just after birth (not fatal if the eyes are removed to stop the spread of tumors). Note that no Aa genotypes live to reproduce (unless their eyes are removed), thus no AA offspring can be produced, and it is extremely unlikely that a mutation of $a \rightarrow A$ would occur in both parents to form an AA offspring. In this case, then, $\hat{p} = v$ because all born are either Aa or aa . For example, in Michigan from 1936 to 1945, out of 1,054,985 people, only 49 cases of retinoblastoma were reported--this is 49 dominant alleles out of $2 \times 1,054,985$ total alleles, so $v = 49 / (2 \times 1,054,985) = 2.32 \times 10^{-5}$, which, in this case also equals \hat{p} . Since $w = 0$ ($s = 1$) for both AA and Aa , and the only ones to live and reproduce are aa . Thus 100% of the gametes come from aa parents and any A alleles in the population are due totally to mutation. The rate of mutation of a to A is v (and $u = 0$), thus the number of alleles that have mutated (v) is equal to the number of A alleles at equilibrium (\hat{p}). Also, if $\hat{p} = v/s$ and $s = 1$, then $\hat{p} = v$.

PROBLEMS:

1. Consider the gene for Rh factor. Let R be the allele for Rh^+ and r be the allele for Rh^- , such that R^- is Rh^+ and rr is Rh^- . Assume a large population in equilibrium in which 16% of the individuals are Rh^- .

- a. What is the calculated frequency of the r allele? Of the R allele?
- b. What is the calculated frequency of the genotypes in this population?
- c. An Rh^+ man marries an Rh^- woman. What is the probability that the man is heterozygous (Rr)? That he is homozygous (RR)? What is the probability that this couple's first child will be Rh^- ?

2. The MN blood group in humans includes the following genotypes and phenotypes: $MM =$ type M, $MN =$ type MN, and $NN =$ type N.

- a. What is the gene frequency for M and N in a population of people with the following blood types? 40 with type M, 300 with MN, and 660 with N. Is this population breeding at random?
- b. What is the gene frequency for M and N in another population of people with the following blood types: 280 type M, 500 type MN, and 220 type N. Is this population breeding at random?

3. If the frequency of red-green colorblind males in a population is 0.2, what is the frequency of red-green colorblind females in this population? What proportion of the females could have red-green colorblind sons?

4. For the ABO blood group, what blood type percentages would you find in a population in which the frequency of $I^A = 0.1$ and $I^B = 0.4$?

5. Calculate the gene frequencies of I^A , I^B and i for the following population: 490 have type O blood, 150 have type A, 320 type B, and 40 type AB.

6. What will the frequency of the genotype $AaBB$ be at equilibrium if the frequency of a is 0.6 and the frequency of b is 0.2? What genotype will be most frequent in this population?

7. If the mutation rate of K to k is 1.5×10^{-6} , the reverse mutation does not occur, and there is no selective advantage or disadvantage to either allele, what will the gene frequency be after many generations if the initial frequencies are 0.8 K and 0.2 k ?

8. What will the gene frequencies be at equilibrium in a population in which the rate of mutation of M to m is 0.000015 and the rate of the reverse mutation is 0.000030?

9. Consider the following situation:

$$w = \begin{matrix} AA & Aa & aa \\ 1 & 1 & 0.8 \end{matrix}$$

Is selection against the dominant or recessive? What is the value of s , the selection coefficient? What is the value of s in the case of lethals?

10. Consider the following situation:

$$w = \begin{matrix} AA & Aa & aa \\ 0.6 & 1 & 0.8 \end{matrix}$$

What are the values of p and q at equilibrium?

11. In the American white population, the gene frequency for Rh^- (r) is 0.4 as determined by the fact that about 16% of the population is Rh^- . Additionally, about one birth in 250 is a baby who is erythroblastotic (**erythro** = red; **blasto** = a bud, sprout; **-tic** = relation, belonging to, pertaining to the process of; an erythroblast is an immature RBC). This is a disorder characterized by the abnormal presence of erythroblasts in the circulating blood (they are normally found in the bone marrow) usually as a result of trying to compensate for an Rh incompatibility with an Rh^- mother, and thus, affects infants who are heterozygous for Rh factor. Although, if these babies survive to birth they can be given a total blood transfusion to alleviate the symptoms, assume for this problem that these infants do not survive to adulthood.

- a. How many R alleles are found in a population of 1000 newborn babies per generation? How many r alleles?
- b. How many heterozygotes will be eliminated? How many R alleles? How many r alleles?
- c. Under these circumstances, what will tend to happen over a number of generations to the frequencies of R and r ?
- d. What would tend to happen to the frequencies of R and r in a population in which $p_R = 0.4$ and $q_r = 0.6$?

12. Chondrodystrophic (**chondro** = cartilage; **dys** = bad, malicious, hard; **troph** = food, nourish, nourishment) dwarfism (a dominant semilethal) was found to afflict 8 children of 94,075 born to normal parents in Denmark. What is the mutation rate for d to D ?

13. If the rate of mutation from A to a is 0.0000049 and the selection coefficient against a is 0.001, what will be the frequency of the genotype aa at equilibrium? What will be the frequency of gene a ?

