CHAPTER 3

Quantitative Skills in AP Biology

This chapter focuses on some of the quantitative skills that are important in your AP Biology course. These are not all of the skills that you will learn, practice, and apply during the year, but these are the skills you will most likely encounter as part of your laboratory investigations or classroom experiences, and potentially on the AP Biology exam.

Surface Area and Volume

Cells are small because a high surface area to volume ratio allows them to function more efficiently. As a cell increases in size, its volume increases faster than its surface area, which does not allow it to transport substances across the membrane fast enough to get rid of what is unnecessary or obtain substances that are needed. The transport of substances across the membrane is largely driven by diffusion, which puts the size limit on the cell. To accommodate this, cells have adaptations to increase the surface area to volume ratio, such as folding of the cell membrane (e.g., villi in the small intestine).

Example

To calculate the surface area to volume ratio for a spherical cell with a radius of 5 µm, first we calculate the surface area:

$$SA = 4\pi r^2 = 4\pi(5\mu m)^2 = 100\pi\,\mu m^2$$

Next we calculate the volume:

$$V = \frac{4}{3}\pi r^3 = \frac{4}{3}\pi(5\mu m)^3 = \frac{4}{3}\pi(125\mu m^3) = 166.67\pi\,\mu m^3$$

Now that we know the surface area and the volume, we can calculate the ratio:

$$\frac{SA}{V} = \frac{100\pi\,\mu m^2}{166.67\pi\,\mu m^3} = 0.6\,\mu m^{-1}$$

Alternately, we can simplify the formula first and then calculate the ratio:

$$\frac{SA}{V} = \frac{4\pi r^2}{4/3\pi r^3} = \frac{12\pi r^2}{4\pi r^3} = \frac{3}{r} = \frac{3}{5\mu m} = 0.6\,\mu m^{-1}$$

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Example

To calculate the surface area to volume ratio of a cuboidal cell where each side is 5µm, again, let's first calculate the surface area:

$$A = 6a^2 \qquad (where\ a = the\ length\ of\ one\ side\ of\ the\ cube)$$
$$A = 6(5)^2 = 150\,\mu m^2$$

Then we'll calculate the volume:

$$V = lwh = 5\,\mu m \times 5\,\mu m \times 5\,\mu m = 125\,\mu m^3$$

Now let's calculate the surface area to volume ratio:

$$\frac{SA}{V} = \frac{150\,\mu m^2}{125\,\mu m^3} = 1.2\,\mu m^{-1}$$

The spherical cell in these examples is smaller than the cuboidal cell and has a higher surface area to volume ratio, making it more efficient at diffusion than the cuboidal cell.

If you need more information, the following tutorial can help to further explain these concepts:

Khan Academy: Cell size

Water Potential

Water potential measures the tendency of water to move by osmosis from one area to another, and is calculated from two major components, **pressure potential** and **solute potential**. The equation for water potential is

$$\Psi = \Psi_s + \Psi_p$$

where Ψ is the water potential, Ψ_s is the solute potential, and Ψ_p is the pressure potential.

Water will always move from an area of high water potential to an area of low water potential. The value of water potential can be positive, zero, or negative.

The water potential of pure water in an open beaker is zero ($\Psi = 0$) because both the solute potential and pressure potential are equal to zero ($\Psi_s = 0$ and $\Psi_p = 0$). Increasing the amount of solute in water will increase solute potential, which in turn will decrease water potential. An increase in pressure potential (pushing) will increase water potential, while a decrease in pressure potential (pulling) will decrease water potential.

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Example

Suppose you wanted to know whether water would go from an area where $\Psi = -4.2$ to an area where $\Psi = 0$, or vice versa.

Because water flows from areas of high water potential to areas of low water potential, water would go from an area where $\Psi = 0$ to an area where $\Psi = -4.2$.

In an open system, the pressure potential is zero, so the water potential of a solution can be calculated from the solute potential, Ψ_s, using the following formula:

$$\Psi_s = -iCRT$$

where i is the ionization constant, C is the molar concentration of the solution, R is the pressure constant ($R = 0.0831 liter\, bars / mole\, K$), and T is the temperature in kelvins.

Example

Suppose you wanted to know what the water potential is of a 1.5M sucrose solution at 22°C under standard atmospheric conditions. (Note: The ionization constant for sucrose is 1.0 because it does not ionize in water.)

First you would need to calculate the solute potential:

$$\begin{aligned}\Psi_s &= -iCRT \\ &= -(1.0)(1.5\frac{mol}{L})(0.0831\frac{L \bullet bars}{mol \bullet K})(295\,K) \\ &= -36.77 bars\end{aligned}$$

Since the pressure potential is zero, the water potential is equal to the solute potential. Therefore, $\Psi = -36.77 bars$.

If you need more information, the following tutorials can help to further explain these concepts:

Khan Academy: Osmosis

Bozeman Science: Water potential

Hypothesis Testing

Hypothesis testing refers to procedures used by scientists to reject or fail to reject statistical hypotheses. It helps us attend to uncertainty and deal with random error in data collected during an investigation. There are two types of statistical hypotheses:

- **Null hypothesis (H_0):** the hypothesis that there is no difference between two groups of data in an investigation and that the experimental observations are the result of chance

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- **Alternative hypothesis (H_A):** one of several hypotheses that experimental observations are the result of some nonrandom cause

Chi-Square Goodness of Fit Test

The **chi-square test** is a statistical method that is used to determine if there is a significant relationship between two groups of data: observed values are compared to expected (or theoretical) values to determine if any variance from the expected data could be due to chance. It is called a goodness of fit test because we are checking to see if our results match up to a known or theoretical outcome of proportions for multiple categories. The chi-square test tests the null hypothesis. The null hypothesis is the claim against which we are looking for evidence in an investigation, specifically that the population proportions are what we would expect given random chance. For example, if we were rolling a standard six-sided die, our null hypothesis would be that the proportion of 1's, 2's, 3's, 4's, 5's, and 6's would all be 1/6. The alternative hypothesis would be that at least one of these proportions is not equal to 1/6.

The formula for chi-square is

$$\chi^2 = \sum \frac{(o-e)^2}{e}$$

where o is the value of the observed data, and e is the value of the expected data. Sigma (Σ) is an indication that the repeated calculations that follow it should be added together.

The chi-square test is used for count data (i.e., data that is not measured) and is often used to analyze the results of genetic crosses.

Example

If you crossed two pea plants that were heterozygous for yellow seed color (Y = yellow, y = green), you would expect the phenotypic ratio of the offspring in the next generation to be 3:1. This means that if you collected 100 seeds, you would expect 75 yellow seeds and 25 green seeds. This is our null hypothesis: that there is no difference between the phenotypic ratios in our cross and what is expected by Mendelian theory.

If you actually collected 69 yellow seeds and 31 green seeds, is that close enough to what is expected that you can say your results are consistent with the theory—that the deviation in your results is likely due to chance? What if you collected 65 yellow and 35 green seeds?

We can calculate the chi-square value for these data to answer the question:

$$\chi^2 = \sum \frac{(o-e)^2}{e}$$

Categories	o	e	$(o-e)^2/e$
Yellow	69	75	0.48
Green	31	25	1.44

$$\chi^2 = 0.48 + 1.44 = 1.92$$

Now that we know what our chi-square value is, we can compare it to the critical value found in table 3.1.

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Table 3.1: Critical Values of the Chi-Square Distribution

Probability (p)	Degrees of Freedom				
	1	2	3	4	5
0.05	3.84	5.99	7.82	9.49	11.1
0.01	6.64	9.21	11.3	13.2	15.1
0.001	10.8	13.8	16.3	18.5	20.5

- If the chi-square value is lower than the critical value, we will fail to reject our null hypothesis: the data we observed fits well with the data we expected.
- If the chi-square value is higher than the critical value, we will reject our null hypothesis: our observed data does not fit well with our expected data.
- The probability, or p value, is used to tell us how often results like ours could occur under the null hypothesis if only chance is at play.

In order to use the critical value table, we need to know our degrees of freedom, which is the number of categories minus one. For our example, we have 1 degree of freedom because we have two categories. Using the table, we find that the critical value for 1 degree of freedom at a p-value of 0.05 is 3.84. Our chi-square value of 1.92 is less than this critical value, so we fail to reject our null hypothesis. This means that our observed data for this cross is within a 3:1 phenotypic ratio.

We can follow the same logic for the second cross:

$$\chi^2 = \sum \frac{(o-e)^2}{e}$$

Categories	o	e	$(o-e)^2/e$
Yellow	65	75	1.33
Green	35	25	4

$$\chi^2 = 1.33 + 4 = 5.33$$

Our chi-square value of 5.33 is higher than the critical value of 3.84 at $p = 0.05$ and our null hypothesis is rejected. This means that the offspring of the cross in this experiment did not yield a 3:1 phenotypic ratio. This does not mean that if we were to do this cross again we would get the same result: we might get a different result. If that were to happen we would need to repeat our experiment several times so that we have an aggregate of data to analyze. The more data we have, the more confident we can be in our results.

If you need more information, the following tutorial can help to further explain this concept:

Khan Academy: Chi-square distribution introduction

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Mathematical Modeling

Mathematical models can be used to investigate the relationships that occur in nature. The Hardy–Weinberg theorem helps us to understand the relationship between allele frequencies in populations of organisms and evolutionary change, specifically how populations can change over time and what might happen to a population in the future.

Hardy–Weinberg Equilibrium

The **Hardy–Weinberg theorem** states that the allele frequencies of a gene (at a specific locus) in a population will stay the same from one generation to the next as long as the following requirements are met:

- No mutations occur.
- No movement into or out of the population occurs.
- The population is large.
- Mating is random.
- No natural selection occurs.

This means the following factors can disrupt Hardy–Weinberg equilibrium:

- Mutations
- Gene flow
- Genetic drift
- Nonrandom mating
- Natural selection

The changes in the allele frequencies of a population over time can be studied mathematically. Let's start with a gene pool of *A*'s and *a*'s, where *A* is the dominant allele and *a* is the recessive allele.

We can define p as the frequency of *A* and q as the frequency of *a*. Since the total frequencies of all alleles must equal 1, then $p + q = 1$. This means, for example, that if 60% of the alleles in a population are *A*, then the frequency of *A* is 0.6 and the frequency of *a* is 0.4.

The following are all the possible combinations of *A* and *a* in the population: *AA*, *Aa*, *aA*, *aa*. We can use a Punnett square to determine the frequencies of these combinations (i.e., the genotypes in the next generation):

	A (p)	*a* (q)
A (p)	*AA* (p^2)	*Aa* (pq)
a (q)	*aA* (qp)	*Aa* (q^2)

The frequencies of the genotypes in the population must also equal 1. The equation that describes this is

$$p^2 + pq + qp + q^2 = 1$$

This can be simplified to

$$p^2 + 2pq + q^2 = 1$$

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where p^2 is the frequency of the dominant genotype, q^2 is the frequency of the recessive genotype, and $2pq$ is the frequency of the heterozygous genotype. This is the **Hardy–Weinberg equation**.

Using the previous example, if 60% of the alleles in a population are *A*, we can calculate all of the genotypic frequencies:

$$p = frequency\ of\ A = 0.6$$

$$q = frequency\ of\ a = 0.4$$

$$p^2 = frequency\ of\ AA = (0.6)^2 = 0.36$$

$$q^2 = frequency\ of\ aa = (0.4)^2 = 0.16$$

$$2pq = frequency\ of\ Aa = 2(0.6)(0.4) = 0.48$$

Example

If we assume that a population is in Hardy–Weinberg equilibrium for a particular locus, we can apply the Hardy–Weinberg equation to other questions, such as, if an autosomal recessive disease affects three in 100 people of a population, what is the frequency of carriers in the population?

We know that three out of 100 people are affected by an autosomal recessive condition — this is the frequency of *aa*, which is q^2:

$$q^2 = \frac{3}{100} = 0.03$$

If q^2 is 0.03, then we can calculate the frequency of the recessive allele:

$$q = \sqrt{0.03} = 0.173$$

Since $p + q = 1$, we can now use this information to calculate the frequency of the dominant allele:

$$p + q = 1$$
$$p + 0.173 = 1$$
$$p = 1 - 0.173$$
$$p = 0.827$$

Since the disease is autosomal recessive, this means that the heterozygous individuals in the population are carriers of the disease. Now that we know the frequency of each allele in the population, we can calculate the frequency of the carriers:

$$\begin{aligned} frequency\ of\ Aa &= 2pq \\ &= 2(0.827)(0.173) \\ &= 0.286 \end{aligned}$$

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If you need more information, the following tutorial can help to further explain this concept:

Khan Academy: Allele frequency

Population Growth

Populations can experience unlimited growth when resources are abundant, but this is rarely the case in nature.

The change in the size of a population over a given amount of time mostly depends on the number of births and the number of deaths that occur within it. This can be written mathematically as

$$\frac{\Delta N}{\Delta t} = B - D$$

where ΔN is the change in the population, Δt is the change in time, B is the number of births, and D is the number of deaths.

In a given population, the per capita rate of increase, r, can be written as

$$r = \frac{B - D}{N}$$

The equation for the change in population size can now be written as

$$\frac{\Delta N}{\Delta t} = rN$$

Two basic models of population growth are the exponential growth and the logistic growth model:

- **Exponential growth model:** A population increases in size when r is constant and greater than zero:

$$\frac{\Delta N}{\Delta t} = r_{max} N$$

where r_{max} is the maximum per capita rate of increase and N is the size of the population. In other words, the population (usually a small one) grows at a fixed rate.

- Logistic growth model: A population increases in size until r approaches zero as the size of the population reaches its carrying capacity:

$$\frac{\Delta N}{\Delta t} = r_{max} N \frac{(K - N)}{K}$$

where K is the carrying capacity of the population. The **carrying capacity** is the maximum population size that can be supported by a particular environment at a certain point in time without disruption to the habitat.

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Exponential growth example

Suppose a population of 100 bacteria is experiencing exponential growth: The current birth rate is 22 bacteria per day and the current death rate is 15 individuals per day. We want to calculate the growth of this population over 30 days.

First, let's calculate the per capita rate of increase:

$$r = \frac{B - D}{N}$$
$$r = \frac{22 - 15}{100}$$
$$r = 0.7$$

Now, let's calculate the growth rate for day one:

$$\frac{\Delta N}{\Delta t} = rN$$
$$\frac{\Delta N}{\Delta t} = (0.7)(100)$$
$$\frac{\Delta N}{\Delta t} = 70$$

This means that 70 bacteria are added the first day. So, for the second day, we start with 170 bacteria. Using this same equation, we can calculate the size of the population for the next day:

$$\frac{\Delta N}{\Delta t} = rN$$
$$\frac{\Delta N}{\Delta t} = (0.7)(170)$$
$$\frac{\Delta N}{\Delta t} = 119$$

If we repeat this calculation until day 10, we will see the following for our population growth:

Day	Number of Bacteria
0	100
1	170
2	289
3	491
4	835
5	1420
6	2414
7	4103
8	6976
9	11859
10	20160

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If we continued this for the next 30 days, the growth of our population would look like this:

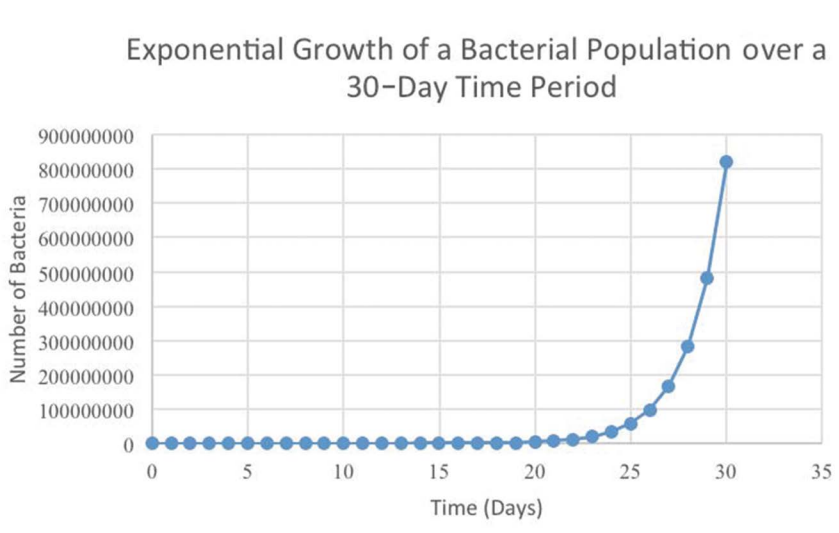

Figure 3.1: Exponential Growth of a Bacterial Population

Logistic growth example

Say that the same population of bacteria from the previous example is experiencing logistic growth at the same rate, but the carrying capacity of the environment is 2000 bacteria. Let's calculate the growth rate of the population under these circumstances:

$$\frac{\Delta N}{\Delta t} = r_{\max} N \frac{(K-N)}{K}$$

$$\frac{\Delta N}{\Delta t} = (0.7)(100)\left[\frac{(2000-100)}{2000}\right]$$

$$\frac{\Delta N}{\Delta t} = (70)(0.95)$$

$$\frac{\Delta N}{\Delta t} = 66.5$$

The growth rate is slower under these circumstances due to the limited availability of resources.

If you need more information, the following tutorial can help to further explain these concepts:

Khan Academy: Exponential and logistic growth in populations

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