

Unit 1

Indicate the true sentence. A population will be in Hardy-Weinberg equilibrium if:

- A. There is random mating within the population
- B. There are no mutations occurring in the population
- C. The population is infinitely large
- D. All of the previous answers are correct

In a population of 1000 individuals, there are two alleles, A and a. The frequency of allele A is

0.6. Indicate the false option:

- A. The frequency of allele a is 0.4
- B. The expected frequency of heterozygotes (Aa) is 0.48
- C. The expected frequency of homozygous recessive individuals (aa) is 0.36
- D. The population is in Hardy-Weinberg equilibrium if the actual genotype frequencies match the expected frequencies

Which of the following is false regarding polymorphisms and divergence?

- A. Polymorphisms refer to genetic differences within a species
- B. Divergence refers to genetic differences between species
- C. All genetic differences that reach a frequency of >1% are considered polymorphisms
- D. Divergence can eventually lead to the formation of new species if populations become reproductively isolated

Indicate which of the following statements about mutation is false:

- A. Mutations are always harmful to the organism
- B. Mutations are the source of genetic variation within populations
- C. Mutations occur randomly during DNA replication
- D. Not all mutations become polymorphisms; some may disappear from the population

In a diploid organism, the genotype frequencies for a gene with two alleles (A and a) are given.

Indicate the false sentence:

- A. The frequency of allele A can be calculated as
- B. The frequency of allele a can be calculated as
- C. If the population is in Hardy-Weinberg equilibrium
The frequency of heterozygotes (Aa) is given by

$$\begin{array}{l} p^2 + \frac{1}{2}(2pq) \\ q^2 + \frac{1}{2}(2pq) \\ p^2 + 2pq + q^2 = 1 \\ 2pq \end{array}$$

A population has the following genotype frequencies: 0.16 for AA, 0.48 for Aa, and 0.36 for aa.

Indicate the false option:

- A. The allele frequency of A is 0.4
- B. The allele frequency of a is 0.6
- C. The population is in Hardy-Weinberg equilibrium
- D. The frequency of homozygous recessive individuals (aa) is 0.36

Lactase persistence in human populations is an example of:

- A. A mutation in the coding region of the LCT gene
- B. A regulatory change affecting the expression of the LCT gene
- C. A neutral polymorphism with no phenotypic effect
- D. An allele frequency change due to genetic drift

Indicate the false statement about the CCR5-Δ32 allele, which provides resistance to HIV-1:

- A. The mutation is a 32-bp deletion in the coding region of the CCR5 gene
- B. Individuals homozygous for the deletion are resistant to HIV-1 infection
- C. The allele frequency of CCR5-Δ32 is the same in all human populations
- D. The mutation disrupts the function of the CCR5 receptor

Indicate the true statement. Genetic drift can lead to:

- A. Increased genetic variation within a large population
- B. Fixation of alleles in small populations
- C. New mutations appearing at a constant rate
- D. Decreased divergence between populations

In a plant population with two codominant alleles for flower color, there are 100 individuals with red flowers (RR), 200 with pink flowers (Rr), and 100 with white flowers (rr). Indicate the false statement:

- A. The frequency of the R allele is 0.5
- B. The frequency of the r allele is 0.5
- C. The population is in Hardy-Weinberg equilibrium
- D. The expected genotype frequencies match the observed frequencies

Unit 2

Indicate the true sentence. Genetic drift will have a more pronounced effect in a population if:

- A. The population size is large
- B. The population size is small
- C. There is no migration
- D. There is high mutation rate

Answer: The population size is small

In a population of 20 individuals, there are two alleles, A and a. The frequency of allele A is 0.4.

Indicate the false option:

- A. The frequency of allele a is 0.6
- B. The expected frequency of homozygous recessive individuals (aa) is 0.36
- C. Genetic drift is likely to cause significant changes in allele frequencies
- D. The population will quickly reach Hardy-Weinberg equilibrium

Answer: The population will quickly reach Hardy-Weinberg equilibrium

Explanation: Small populations are more influenced by genetic drift and less likely to remain in Hardy-Weinberg equilibrium.

Which of the following is false regarding the Wright-Fisher model?

- A. It assumes an infinite population size
- B. It assumes no migration occurs
- C. It assumes all individuals contribute equally to the gene pool
- D. It predicts no change in allele frequencies over time

Answer: It predicts no change in allele frequencies over time

Explanation: The Wright-Fisher model allows for changes in allele frequencies due to genetic drift.

Indicate which of the following statements about mutation is false:

- A. Mutations introduce new alleles into a population
- B. All mutations are harmful to the organism
- C. Mutations can occur during DNA replication
- D. Mutations in the germ line can be passed to offspring

Answer: All mutations are harmful to the organism

Explanation: Not all mutations are harmful; some are neutral or beneficial.

The binomial distribution is used to model genetic drift because:

- A. There are only two possible outcomes for each allele
- B. The probability of each outcome changes with each trial
- C. Trials are dependent on each other
- D. Allele frequencies remain constant across generations

Answer: There are only two possible outcomes for each allele

Explanation: The binomial distribution applies when there are two possible outcomes, such as the presence of two alleles.

In a small population of 10 individuals, the initial frequency of allele A is 0.7. Indicate the false option:

- A. The probability of allele A becoming fixed is 0.7
- B. The probability of allele A being lost is 0.3
- C. Allele frequencies will not change due to genetic drift
- D. The population is likely to experience significant changes in allele frequencies

Answer: Allele frequencies will not change due to genetic drift

Explanation: In a small population, genetic drift can cause significant changes in allele frequencies.

Which of the following statements about the founder effect is true?

- A. It increases genetic diversity in the new population
- B. It results from a large population migrating to a new location
- C. It can cause rapid divergence between source and founder populations
- D. It does not affect allele frequencies

Answer: It can cause rapid divergence between source and founder populations

Explanation: The founder effect often leads to rapid changes in allele frequencies and divergence due to a small number of initial individuals.

Indicate the false statement about the effective population size (N_e):

- A. N_e is always equal to the census population size (N_c)
- B. N_e is influenced by the number of breeding individuals
- C. N_e can be affected by fluctuations in population size
- D. N_e is usually smaller than N_c

Answer: N_e is always equal to the census population size (N_c)

Explanation: N_e is usually smaller than N_c due to factors like unequal sex ratios and fluctuating population sizes.

Indicate the true sentence. The probability of fixation of a neutral allele in a population is:

- A. Equal to its initial frequency in the population
- B. Always 50%
- C. Dependent on the mutation rate
- D. Inversely proportional to the population size

Answer: Equal to its initial frequency in the population

In a population undergoing genetic drift, heterozygosity will:

- A. Increase over time
- B. Decrease over time
- C. Remain constant
- D. Fluctuate unpredictably

Answer: Decrease over time

Explanation: Genetic drift tends to reduce heterozygosity as alleles are fixed or lost.

Unit 3

Indicate the true sentence about natural selection:

- A. Natural selection does not depend on the environment
- B. Natural selection requires existing heritable variation in a population
- C. Natural selection acts on individual alleles rather than on phenotypes
- D. Natural selection results in random changes in allele frequencies

Answer: Natural selection requires existing heritable variation in a population

In a population of beach mice, light coat color is advantageous in sandy environments, while dark coat color is advantageous in wooded areas. The relative fitness values for light (AA), light-dark (Aa), and dark (aa) coat color genotypes are 1.0, 0.8, and 0.6 respectively. Indicate the false option:

- A. Light mice have the highest relative fitness in sandy environments
- B. Dark mice are at a disadvantage in sandy environments
- C. Heterozygotes (Aa) have a fitness advantage over homozygous light mice (AA) in sandy environments
- D. Natural selection will increase the frequency of the AA genotype in sandy environments

Answer: Heterozygotes (Aa) have a fitness advantage over homozygous light mice (AA) in sandy environments

Explanation: AA has the highest fitness in sandy environments.

Which of the following is false regarding the Hardy-Weinberg equilibrium?

- A. It assumes no selection is acting on the population
- B. It predicts allele frequencies will remain constant over generations in the absence of evolutionary forces
- C. It assumes the population is infinitely large
- D. It accounts for the effects of genetic drift and mutation

Answer: It accounts for the effects of genetic drift and mutation

Explanation: Hardy-Weinberg equilibrium assumes no genetic drift and no mutation.

Indicate which of the following statements about fitness is false:

- A. Absolute fitness measures the number of offspring an individual produces
- B. Relative fitness compares the survival and reproduction of different genotypes
- C. Fitness depends on the environment
- D. Fitness is a measure of an individual's strength and speed

Answer: Fitness is a measure of an individual's strength and speed

Explanation: Fitness is about reproductive success, not physical strength or speed.

The persistence of sickle-cell anemia in certain populations is an example of:

- A. Directional selection
- B. Stabilizing selection
- C. Disruptive selection
- D. Balancing selection

Answer: Balancing selection

Explanation: Heterozygotes have a fitness advantage in malaria-endemic regions.

In a population with an initial frequency of 0.2 for allele A and 0.8 for allele a, which of the following is true if allele A confers a fitness advantage and natural selection is acting on this population?

- A. The frequency of allele A will decrease over time
- B. The frequency of allele a will increase over time
- C. The frequency of allele A will increase over time
- D. The population will reach Hardy-Weinberg equilibrium

Answer: The frequency of allele A will increase over time

Explanation: Allele A is advantageous, so its frequency will increase.

Which of the following statements about the types of selection is true?

- A. Directional selection leads to the fixation of deleterious alleles
- B. Purifying selection removes advantageous alleles from the population
- C. Balancing selection maintains both alleles in the population
- D. Positive selection removes neutral alleles from the population

Answer: Balancing selection maintains both alleles in the population

Explanation: Balancing selection maintains genetic diversity by favoring heterozygotes.

Indicate the false statement about lactase persistence:

- A. It is an example of positive selection in human populations
- B. The trait is regulated by cis-acting elements in the MCM6 gene
- C. It provides a fitness advantage in societies that domesticate milk-producing animals
- D. Lactase persistence has no genetic basis and is purely environmental

Answer: Lactase persistence has no genetic basis and is purely environmental

Explanation: Lactase persistence is genetically regulated.

Which of the following statements about the selection coefficient (s) is false?

- A. It measures the reduction in fitness of a genotype compared to another
- B. A higher selection coefficient indicates stronger selection against a genotype
- C. It is always equal to 1
- D. It can range from 0 to 1

Answer: It is always equal to 1

Explanation: The selection coefficient ranges from 0 to 1 and indicates the strength of selection.

Indicate the true sentence. Overdominance or heterozygote superiority results in:

- A. Fixation of one allele and loss of the other
- B. Higher fitness of heterozygotes compared to both homozygotes
- C. Lower average fitness in the population
- D. Rapid decrease in genetic diversity

Answer: Higher fitness of heterozygotes compared to both homozygotes

Explanation: Overdominance maintains both alleles due to the advantage of the heterozygote.

Unit 4

Indicate the true statement about migration in populations:

- A. Migration increases the genetic divergence between populations
- B. Migration introduces new alleles into a population, causing gene flow
- C. Migration decreases the overall genetic diversity within a population
- D. Migration has no effect on allele frequencies

Answer: Migration introduces new alleles into a population, causing gene flow

In a continent-island model, if 20% of alleles in the island population come from the continent each generation, what is the value of the migration rate (m)?

- A. 0.1
- B. 0.2
- C. 0.5
- D. 0.8

Answer: 0.2

Explanation: The migration rate m represents the proportion of alleles coming from the continent each generation.

Which of the following is false regarding the Wahlund effect?

- A. It generates an excess of heterozygotes compared to Hardy-Weinberg expectations
- B. It indicates population subdivision
- C. It results in a deficit of heterozygotes in the pooled population
- D. It can be used to identify population structure

Answer: It generates an excess of heterozygotes compared to Hardy-Weinberg expectations

Explanation: The Wahlund effect causes a deficiency, not an excess, of heterozygotes.

Indicate which of the following statements about the fixation index (F_{ST}) is false:

- A. F_{ST} values range from 0 to 1
- B. An F_{ST} value of 0 indicates no differentiation between subpopulations
- C. F_{ST} is used to measure the genetic divergence among subpopulations
- D. An F_{ST} value of 1 indicates no genetic variation within subpopulations

Answer: An F_{ST} value of 1 indicates no genetic variation within subpopulations

Explanation: An F_{ST} value of 1 indicates complete differentiation between subpopulations.

In a population where genetic drift and migration are in equilibrium, the F_{ST} value for 61 genes in *Drosophila melanogaster* is stable. Which assumption must hold true?

- A. Natural selection is strongly operating
- B. Populations have not reached genetic drift-migration equilibrium
- C. Migration rate is very high
- D. Divergence between populations is exclusively caused by genetic drift

Answer: Divergence between populations is exclusively caused by genetic drift

Explanation: The assumption is that natural selection is not operating, and divergence is due to genetic drift alone.

Which of the following scenarios would result in high differentiation and low genetic flow between populations?

- A. High dispersal, low distance, weak barriers
- B. Low dispersal, high distance, strong barriers
- C. Short divergence time, large population size
- D. Frequent migration between populations

Answer: Low dispersal, high distance, strong barriers

Explanation: These factors reduce gene flow and increase genetic differentiation.

Which of the following is a consequence of migration limiting genetic divergence among subpopulations?

- A. Increased F_{ST} values over time
- B. Stabilization of allele frequencies across subpopulations
- C. Decreased genetic diversity within subpopulations
- D. Increased number of private alleles in subpopulations

Answer: Stabilization of allele frequencies across subpopulations

Explanation: Migration homogenizes allele frequencies among subpopulations.

Indicate the false statement about private alleles:

- A. Private alleles are present only in one population
- B. High migration rates increase the number of private alleles
- C. Low migration rates can maintain private alleles in a population
- D. Private alleles can indicate population isolation

Answer: High migration rates increase the number of private alleles

Explanation: High migration rates decrease the number of private alleles.

What is the effect of population subdivision on heterozygosity within subpopulations compared to the total population?

- A. It increases heterozygosity within subpopulations
- B. It decreases heterozygosity within subpopulations
- C. It has no effect on heterozygosity within subpopulations
- D. It increases heterozygosity in the total population

Answer: It decreases heterozygosity within subpopulations

Explanation: Subdivision typically results in lower heterozygosity within subpopulations compared to the total population.

Which factor does not contribute to the effective population size (N_e) being smaller than the census population size (N_c)?

- A. Different number of males and females
- B. Fluctuations in population size
- C. Equal offspring number among individuals
- D. Presence of overlapping generations

Answer: Equal offspring number among individuals

Explanation: Variations in offspring number among individuals contribute to N_e being smaller than N_c . Equal offspring number does not reduce N_e .

Unit 5

Which statement is true according to the neutral theory of molecular evolution?

- A. Most genetic variation is maintained by natural selection
- B. Most genetic variation is maintained by genetic drift of neutral mutations
- C. Harmful mutations are more likely to become fixed than neutral mutations
- D. Beneficial mutations are more common than neutral mutations

Answer: Most genetic variation is maintained by genetic drift of neutral mutations

In the context of the neutral theory, what is the primary evolutionary process affecting neutral mutations?

- A. Natural selection
- B. Genetic drift
- C. Mutation rate
- D. Gene flow

Answer: Genetic drift

Which of the following is false regarding polymorphism and divergence under the neutral theory?

- A. Polymorphism refers to the amount of genetic variation within a population
- B. Divergence refers to genetic differences between species
- C. Most new alleles will quickly become fixed or lost
- D. High levels of polymorphism are expected with low mutation rates

Answer: High levels of polymorphism are expected with low mutation rates

Explanation: High levels of polymorphism are expected with high mutation rates.

Indicate which of the following statements about measuring DNA polymorphism is false:

- A. Nucleotide diversity (π) measures the average number of nucleotide differences per site between two random DNA sequences in a population
- B. Watterson's theta (θ) is a measure of the proportion of segregating sites corrected by sample size
- C. Nucleotide diversity is typically higher in exons than introns
- D. The proportion of segregating sites can indicate the amount of genetic variation in a population

Answer: Nucleotide diversity is typically higher in exons than introns

Explanation: Nucleotide diversity is typically higher in introns than exons because introns are less constrained by functional constraints.

Which of the following statements about synonymous and non-synonymous positions within coding regions is true?

- A. Non-synonymous positions have higher substitution rates than synonymous positions
- B. Synonymous positions do not affect the amino acid sequence of proteins
- C. Non-synonymous positions do not affect the amino acid sequence of proteins
- D. Synonymous substitutions are less likely to be neutral than non-synonymous substitutions

Answer: Synonymous positions do not affect the amino acid sequence of proteins

In linkage disequilibrium (LD), which of the following is true?

- A. LD increases as the distance between variants increases
- B. LD decreases over time due to recombination
- C. LD is unaffected by the recombination rate
- D. LD is higher for variants on different chromosomes

Answer: LD decreases over time due to recombination

Indicate the false statement about the Ka/Ks ratio test:

- A. It compares the number of non-synonymous substitutions per non-synonymous site (Ka) to the number of synonymous substitutions per synonymous site (Ks)
- B. A Ka/Ks ratio greater than 1 suggests positive selection
- C. A Ka/Ks ratio less than 1 suggests purifying selection
- D. A Ka/Ks ratio equal to 1 indicates a high level of genetic drift

Answer: A Ka/Ks ratio equal to 1 indicates a high level of genetic drift

Explanation: A Ka/Ks ratio equal to 1 suggests neutral evolution, not necessarily high genetic drift.

Which of the following is a characteristic of a selective sweep?

- A. Increase in genetic diversity around a beneficial mutation
- B. Reduction of genetic diversity in the vicinity of a positively selected mutation
- C. No change in genetic diversity around the selected mutation
- D. Only affects neutral mutations

Answer: Reduction of genetic diversity in the vicinity of a positively selected mutation

What is genetic hitchhiking?

- A. The increase in frequency of an allele due to its own advantageous effects
- B. The increase in frequency of an allele due to its physical linkage to a beneficial mutation
- C. The decrease in frequency of an allele due to natural selection
- D. The process by which neutral mutations become fixed

Answer: The increase in frequency of an allele due to its physical linkage to a beneficial mutation

Which factor does not contribute to high levels of polymorphism according to the neutral theory?

- A. High mutation rates
- B. Large population size
- C. Low genetic drift
- D. High selection pressure

Answer: High selection pressure

Explanation: High selection pressure typically reduces polymorphism by favoring certain alleles over others.

Unit 6

Which of the following is a common neutrality test used to detect natural selection from sequence data?

- A. Hardy-Weinberg test
- B. Tajima's D test
- C. Fisher's exact test
- D. ANOVA

Answer: Tajima's D test

Indicate the false statement about the neutral theory of molecular evolution:

- A. Most polymorphisms are selectively neutral
- B. Genetic drift is the primary force acting on neutral mutations
- C. Neutral mutations have no effect on fitness
- D. All mutations are fixed or lost at the same rate regardless of selection

Answer: All mutations are fixed or lost at the same rate regardless of selection

Explanation: The rate at which mutations are fixed or lost depends on whether they are neutral, deleterious, or beneficial.

Which neutrality test compares the number of polymorphisms within a species to the number of fixed differences between species?

- A. HKA test
- B. Tajima's D test
- C. MK test
- D. Chi-square test

Answer: MK test

Indicate which of the following statements about Tajima's D test is false:

- A. It compares the number of segregating sites to the average number of nucleotide differences
- B. A significantly positive Tajima's D suggests balancing selection or population contraction
- C. A significantly negative Tajima's D suggests a recent population expansion or positive selection
- D. It requires knowledge of ancestral states to be calculated

Answer: It requires knowledge of ancestral states to be calculated

Explanation: Tajima's D test does not require knowledge of ancestral states.

In the context of neutrality tests, what does a significantly negative Tajima's D value indicate?

- A. Population bottleneck
- B. Positive selection or population expansion
- C. Balancing selection
- D. Genetic drift

Answer: Positive selection or population expansion

The HKA test compares which two aspects of genetic data?

- A. Polymorphism within species and divergence between species
- B. Synonymous and non-synonymous mutation rates
- C. Genotype and allele frequencies
- D. Recombination rates and mutation rates

Answer: Polymorphism within species and divergence between species

Which of the following is NOT an outcome when interpreting Tajima's D test results?

- A. Tajima's D = 0: Neutral evolution
- B. Tajima's D < 0: Excess of low-frequency polymorphisms
- C. Tajima's D > 0: Deficit of intermediate-frequency polymorphisms
- D. Tajima's D > 0: Excess of low-frequency polymorphisms

Answer: Tajima's D > 0: Excess of low-frequency polymorphisms

Explanation: A positive Tajima's D indicates a deficit of low-frequency polymorphisms and an excess of intermediate-frequency polymorphisms.

Which statement about the McDonald-Kreitman (MK) test is true?

- A. It uses data from multiple regions of the genome
- B. It compares synonymous and non-synonymous substitutions within a single gene
- C. It is used to detect genetic drift
- D. It requires a large sample size to be accurate

Answer: It compares synonymous and non-synonymous substitutions within a single gene

What does a neutrality index (NI) less than 1 indicate in the MK test?

- A. Positive selection
- B. Neutral evolution
- C. Negative selection
- D. Genetic drift

Answer: Positive selection

Explanation: An NI less than 1 indicates an excess of non-synonymous divergence, suggesting positive selection.

Indicate the true statement about the Site Frequency Spectrum (SFS):

- A. It only considers synonymous mutations
- B. It summarizes the distribution of allele frequencies in a sample of DNA sequences
- C. It is not useful for detecting natural selection
- D. It is only applicable to small populations

Answer: It summarizes the distribution of allele frequencies in a sample of DNA sequences

Which of the following is used to measure DNA polymorphism at the sequence level?

- A. Proportion of segregating sites
- B. Genotype frequency
- C. Allele frequency
- D. Recombination rate

Answer: Proportion of segregating sites

What is the significance of detecting an excess of low-frequency polymorphisms in a population?

- A. Indicates balancing selection
- B. Suggests recent population expansion or positive selection
- C. Reflects neutral evolution
- D. Points to a population bottleneck

Answer: Suggests recent population expansion or positive selection

Which test requires a contingency table to compare observed and expected values for polymorphisms and divergence?

- A. HKA test
- B. Tajima's D test
- C. MK test
- D. Chi-square test

Answer: HKA test

Indicate the false statement about the Hudson-Kreitman-Aguadé (HKA) test:

- A. It can detect evidence for positive selection
- B. It compares polymorphism and divergence between two or more regions
- C. It requires one region to be known to evolve under neutrality
- D. It only compares synonymous mutations

Answer: It only compares synonymous mutations

Explanation: The HKA test compares both polymorphism and divergence, not limited to synonymous mutations.

What does a significantly positive Tajima's D value suggest?

- A. Recent population expansion
- B. Population bottleneck or balancing selection
- C. Neutral evolution
- D. Genetic drift

Answer: Population bottleneck or balancing selection

These questions are crafted to align with the content in the provided document and cover key concepts such as neutrality tests, genetic variation, and measures of DNA polymorphism.

Unit 7

Which of the following statements is true about the molecular clock hypothesis?

- A. It suggests that all genes evolve at the same rate
- B. It proposes a constant rate of nucleotide substitutions over time
- C. It implies that evolutionary changes are driven solely by natural selection
- D. It cannot be used to estimate divergence times between species

Answer: It proposes a constant rate of nucleotide substitutions over time

According to the neutral theory of molecular evolution, most genetic variation is:

- A. Adaptive
- B. Deleterious
- C. Neutral
- D. Caused by gene flow

Answer: Neutral

Indicate the false statement about genetic divergence:

- A. It can be measured as the number of amino acid substitutions per site between two sequences
- B. Genetic divergence provides an estimate of evolutionary distance
- C. It is unaffected by the rate of mutation
- D. Higher genetic divergence indicates a longer time since two species diverged

Answer: It is unaffected by the rate of mutation

Explanation: Genetic divergence is directly influenced by the rate of mutation.

Which of the following methods can be used to correct observed genetic distances for multiple substitutions?

- A. Needleman-Wunsch algorithm
- B. Kimura's two-parameter model
- C. Tajima's D test
- D. BLAST algorithm

Answer: Kimura's two-parameter model

What does a linear relationship between the number of amino acid changes and time indicate in molecular evolution?

- A. Random genetic drift
- B. Constant rate of accumulation of mutations
- C. Variable mutation rates among different species
- D. High selection pressure

Answer: Constant rate of accumulation of mutations

Which of the following is a key concept of the neutral theory of molecular evolution?

- A. Positive selection is the primary force driving molecular evolution
- B. Most observed genetic variation is due to neutral mutations governed by genetic drift
- C. Deleterious mutations fix at a high rate
- D. Evolutionary changes occur episodically rather than at a constant rate

Answer: Most observed genetic variation is due to neutral mutations governed by genetic drift

The rate of amino acid substitution in histones is lower than in fibrinopeptides because:

- A. Histones are not subject to natural selection
- B. Fibrinopeptides have a higher mutation rate
- C. Histones are subject to strong purifying selection
- D. Fibrinopeptides evolve neutrally

Answer: Histones are subject to strong purifying selection

Which of the following best describes synonymous substitution rates?

- A. They are usually lower than non-synonymous rates
- B. They are higher because they do not affect protein function
- C. They occur at the same rate as non-synonymous substitutions
- D. They are unaffected by natural selection

Answer: They are higher because they do not affect protein function

What is the significance of the rate of substitution, r , in the context of the neutral theory?

- A. It measures the number of advantageous mutations per generation
- B. It equals the mutation rate for neutral mutations
- C. It indicates the frequency of deleterious mutations
- D. It varies significantly across different genes

Answer: It equals the mutation rate for neutral mutations

Which of the following factors does NOT contribute to the rate of molecular evolution according to the neutral theory?

- A. Mutation rate
- B. Population size
- C. Genetic drift
- D. Positive selection

Answer: Positive selection

Explanation: According to the neutral theory, the rate of molecular evolution is primarily determined by neutral mutations and genetic drift.

Indicate the true statement about the molecular clock:

- A. It is only applicable to coding regions of the genome
- B. It can be used to estimate divergence times between species
- C. It assumes all mutations are beneficial
- D. It suggests mutation rates are highly variable over time

Answer: It can be used to estimate divergence times between species

Which of the following observations supports the neutral theory of molecular evolution?

- A. High rate of adaptive substitutions in coding regions
- B. Constant rate of synonymous substitutions over time
- C. High variability in substitution rates among different proteins
- D. Predominance of deleterious mutations in the genome

Answer: Constant rate of synonymous substitutions over time

What does a dN/dS ratio greater than 1 indicate?

- A. Neutral evolution
- B. Purifying selection
- C. Positive selection
- D. Genetic drift

Answer: Positive selection

Explanation: A dN/dS ratio greater than 1 suggests that non-synonymous substitutions are favored, indicating positive selection.

Indicate the false statement about the neutral theory:

- A. It assumes most mutations are selectively neutral
- B. It predicts a constant rate of molecular evolution
- C. It explains the molecular clock as a result of neutral mutations
- D. It asserts that all genetic variations are adaptive

Answer: It asserts that all genetic variations are adaptive

Explanation: The neutral theory asserts that most genetic variations are neutral, not adaptive.

Which of the following is used to estimate the rate of nucleotide substitution?

- A. Mutation rate per generation
- B. Number of non-synonymous substitutions only
- C. Number of synonymous substitutions only
- D. Both synonymous and non-synonymous substitutions

Answer: Both synonymous and non-synonymous substitutions

These questions are crafted to align with the key concepts and information provided in the document, covering topics such as the molecular clock, the neutral theory of molecular evolution, genetic divergence, and substitution rates.

Unit 8

Which of the following models assumes that all nucleotide substitutions are equally likely?

- A. Jukes-Cantor model
- B. Kimura two-parameter model
- C. General Time Reversible model
- D. Hasegawa-Kishino-Yano model

Answer: Jukes-Cantor model

Explanation: The Jukes-Cantor model assumes equal probability for all nucleotide substitutions.

Indicate the false statement about multiple substitutions:

- A. They can be corrected using more sophisticated models like Kimura's two-parameter model
- B. They are less likely to be observed in closely related species
- C. They result in observed genetic distances being smaller than actual distances
- D. They do not affect the accuracy of phylogenetic analyses

Answer: They do not affect the accuracy of phylogenetic analyses

Explanation: Multiple substitutions can significantly affect the accuracy of phylogenetic analyses if not properly accounted for.

Which matrix is commonly used for scoring alignments of closely related proteins based on global alignments?

- A. BLOSUM
- B. PAM
- C. GTR
- D. HKY

Answer: PAM

Explanation: PAM (Point Accepted Mutations) matrices are based on global alignments of closely related proteins.

Indicate which of the following statements about the Kimura two-parameter model is false:

- A. It distinguishes between transitions and transversions
- B. It assumes equal base frequencies
- C. It is more accurate than the Jukes-Cantor model for highly divergent sequences
- D. It uses two different rates of substitution

Answer: It assumes equal base frequencies

Explanation: The Kimura two-parameter model allows for different substitution rates between transitions and transversions but does not assume equal base frequencies.

In the context of DNA sequence evolution models, what does the term 'transition' refer to?

- A. A change from a purine to a pyrimidine
- B. A change from a purine to another purine
- C. A change from a pyrimidine to a purine
- D. A change that involves insertion or deletion of bases

Answer: A change from a purine to another purine

Explanation: Transitions refer to changes between purines ($A \leftrightarrow G$) or between pyrimidines ($C \leftrightarrow T$).

Which substitution matrix is derived from real data rather than extrapolated from closely related proteins?

- A. PAM1
- B. PAM250
- C. BLOSUM62
- D. Dayhoff matrix

Answer: BLOSUM62

Explanation: BLOSUM matrices are based on observed alignments and not extrapolated.

What does a high score in the BLOSUM matrix indicate?

- A. The sequences are closely related
- B. The sequences are distantly related
- C. The sequences have no significant similarity
- D. The sequences have many gaps

Answer: The sequences are closely related

Explanation: A high BLOSUM score indicates that the sequences have high similarity.

Indicate the true statement about the General Time Reversible (GTR) model:

- A. It assumes all nucleotide substitutions have the same rate
- B. It considers different substitution rates and base frequencies
- C. It is less complex than the Jukes-Cantor model
- D. It is only applicable to protein sequences

Answer: It considers different substitution rates and base frequencies

Explanation: The GTR model is a complex model that accounts for different rates of substitution and base frequencies.

What is the primary purpose of substitution matrices like PAM and BLOSUM in sequence alignment?

- A. To estimate divergence times between species
- B. To correct for multiple substitutions
- C. To score and improve the accuracy of sequence alignments
- D. To calculate the rate of synonymous substitutions

Answer: To score and improve the accuracy of sequence alignments

Which of the following models is best suited for sequences with a high level of divergence?

- A. Jukes-Cantor model
- B. Kimura two-parameter model
- C. General Time Reversible model
- D. Hasegawa-Kishino-Yano model

Answer: General Time Reversible model

Explanation: The GTR model is suited for highly divergent sequences as it accounts for varying substitution rates and base frequencies.

What is the main advantage of the Kimura two-parameter model over the Jukes-Cantor model?

- A. It assumes equal substitution rates for all nucleotide changes
- B. It distinguishes between transition and transversion rates
- C. It is simpler to compute
- D. It does not require base frequency data

Answer: It distinguishes between transition and transversion rates

Which statement about the substitution rate r is false?

- A. It can be used to estimate the time since two species diverged
- B. It is influenced by the rate of mutation
- C. It remains constant across all genes and species
- D. It can be different for synonymous and non-synonymous changes

Answer: It remains constant across all genes and species

Explanation: The substitution rate varies among different genes and species.

Which substitution matrix is based on local alignments of distantly related proteins?

- A. PAM1
- B. PAM250
- C. BLOSUM
- D. Jukes-Cantor

Answer: BLOSUM

Explanation: BLOSUM matrices are based on local alignments of distantly related proteins.

Indicate the true statement about the twilight zone in sequence alignment:

- A. It refers to regions with extremely high sequence similarity
- B. It represents alignments where sequence identity is too low to be informative
- C. It occurs when sequences have identical amino acids
- D. It is a region of the matrix with the highest substitution scores

Answer: It represents alignments where sequence identity is too low to be informative

What does a log-odds score in a substitution matrix represent?

- A. The likelihood of a gap occurring in the alignment
- B. The probability of one amino acid mutating to another
- C. The overall quality of the sequence alignment
- D. The number of nucleotide substitutions per site per year

Answer: The probability of one amino acid mutating to another

These questions are crafted to align with the content in the provided document, covering key concepts such as models of DNA sequence evolution, substitution matrices, and genetic distance corrections.

Unit 9

Which of the following best describes a phylogenetic tree?

- A. A diagram that shows the physical characteristics of organisms
- B. A representation of evolutionary relationships among species based on molecular data
- C. A chart that depicts the distribution of species in different habitats
- D. A timeline of geological events

Answer: A representation of evolutionary relationships among species based on molecular data

Indicate the true statement about homologs in phylogenetics:

- A. Orthologs arise from gene duplication within the same species
- B. Paralogs result from speciation events
- C. Orthologs are genes in different species that evolved from a common ancestral gene by speciation
- D. Paralogs are genes in different species that perform the same function

Answer: Orthologs are genes in different species that evolved from a common ancestral gene by speciation

Which type of tree only shows the topology and not the branch lengths?

- A. Cladogram
- B. Additive tree
- C. Ultrametric tree
- D. Phylogram

Answer: Cladogram

Indicate the false statement about rooted and unrooted trees:

- A. Rooted trees have a root that denotes a common ancestor
- B. Unrooted trees specify the relationship among taxa without reference to direction of evolutionary time
- C. Rooted trees can show the direction of evolution
- D. Unrooted trees always represent evolutionary time

Answer: Unrooted trees always represent evolutionary time

Explanation: Unrooted trees do not specify evolutionary time or direction.

Which algorithm assumes a constant rate of molecular evolution when constructing phylogenetic trees?

- A. Neighbor-Joining (NJ)
- B. Maximum Likelihood (ML)
- C. Unweighted Pair Group Method with Arithmetic Mean (UPGMA)
- D. Bayesian Inference

Answer: Unweighted Pair Group Method with Arithmetic Mean (UPGMA)

Explanation: UPGMA assumes a constant rate of molecular evolution (molecular clock).

What is the purpose of bootstrapping in phylogenetic analysis?

- A. To create new species
- B. To measure the robustness of the tree topology
- C. To align DNA sequences
- D. To calculate genetic distances

Answer: To measure the robustness of the tree topology

Explanation: Bootstrapping assesses the reliability of the inferred phylogenetic tree by resampling data.

Which file format is commonly used to represent phylogenetic trees in a text format?

- A. FASTA
- B. Newick
- C. BED
- D. GFF

Answer: Newick

Explanation: The Newick format is widely used for representing phylogenetic trees.

Indicate the true statement about monophyletic groups:

- A. They include an ancestor and all its descendants
- B. They consist of organisms that do not share a common ancestor
- C. They exclude the most recent common ancestor
- D. They include only species with similar physical characteristics

Answer: They include an ancestor and all its descendants

What is the main difference between a phylogram and an ultrametric tree?

- A. Phylograms show branch lengths proportional to evolutionary time
- B. Ultrametric trees show branch lengths proportional to the number of nucleotide changes
- C. Phylograms depict evolutionary time, while ultrametric trees show genetic changes
- D. Ultrametric trees have branch lengths proportional to evolutionary time, while phylograms show genetic changes

Answer: Ultrametric trees have branch lengths proportional to evolutionary time, while phylograms show genetic changes

Which concept describes more than two descendant lineages emerging from a single node in a phylogenetic tree?

- A. Dichotomy
- B. Polytomy
- C. Monophyly
- D. Paraphyly

Answer: Polytomy

Explanation: Polytomy refers to a node in a phylogenetic tree that has more than two immediate descendants.

Indicate the false statement about Neighbor-Joining (NJ) method:

- A. It constructs phylogenetic trees without assuming a constant rate of evolution
- B. It is suitable for large datasets
- C. It always produces rooted trees
- D. It is based on a distance matrix

Answer: It always produces rooted trees

Explanation: Neighbor-Joining typically produces unrooted trees.

What is the primary goal of multiple sequence alignment (MSA) in phylogenetic analysis?

- A. To sequence DNA from different species
- B. To align homologous sequences to identify similarities and differences
- C. To extract DNA from organisms
- D. To calculate the mutation rate

Answer: To align homologous sequences to identify similarities and differences

Which of the following describes the method used to infer phylogenies by evaluating all possible tree topologies?

- A. Maximum Parsimony
- B. Maximum Likelihood
- C. Bayesian Inference
- D. Bootstrapping

Answer: Maximum Likelihood

Explanation: Maximum Likelihood evaluates all possible tree topologies to find the one that best explains the observed data.

What is the significance of using an outgroup in phylogenetic tree construction?

- A. To root the tree and provide a reference point for the ingroup
- B. To identify homologous sequences
- C. To perform multiple sequence alignment
- D. To increase the number of taxa in the analysis

Answer: To root the tree and provide a reference point for the ingroup

Indicate the true statement about paraphyletic groups:

- A. They include all descendants of a common ancestor
- B. They exclude some descendants of a common ancestor
- C. They include species from different evolutionary branches
- D. They are the same as monophyletic groups

Answer: They exclude some descendants of a common ancestor

These questions are crafted to align with the content in the provided document, covering key concepts such as phylogenetic tree construction, models of sequence evolution, and types of phylogenetic trees.

Unit 10

Which of the following statements about codon substitution models is true?

- A. They consider each nucleotide substitution independently
- B. They account for synonymous and non-synonymous substitutions separately
- C. They cannot be used to infer positive selection
- D. They are less accurate than nucleotide substitution models

Answer: They account for synonymous and non-synonymous substitutions separately

In the context of molecular adaptation, what does a dN/dS ratio (ω) greater than 1 indicate?

- A. Neutral evolution
- B. Purifying selection
- C. Positive selection
- D. Genetic drift

Answer: Positive selection

Indicate the false statement about selective forces acting on protein-coding genes:

- A. Deleterious mutations are rarely fixed due to negative selection
- B. Neutral mutations can be lost or fixed by genetic drift
- C. Beneficial mutations are quickly fixed by positive selection
- D. Synonymous mutations are always deleterious

Answer: Synonymous mutations are always deleterious

Explanation: Synonymous mutations are usually neutral as they do not alter the amino acid sequence of proteins.

Which of the following is a method to infer selective pressures in genomic studies by comparing sequences from different species?

- A. FST analysis
- B. Population-based approaches
- C. Fixed substitutions analysis
- D. Linkage disequilibrium patterns

Answer: Fixed substitutions analysis

What is the significance of a codon-based multiple sequence alignment (MSA) in evolutionary studies?

- A. It considers nucleotide substitutions independently
- B. It respects the structure of codons in coding regions
- C. It ignores synonymous substitutions
- D. It is used only for non-coding regions

Answer: It respects the structure of codons in coding regions

Which parameter is used in codon substitution models to estimate selection pressure?

- A. Alpha (α)
- B. Beta (β)
- C. Gamma (γ)
- D. Omega (ω)

Answer: Omega (ω)

Indicate the true statement about models for heterogeneous selection pressure:

- A. They use a single ω value for the entire alignment
- B. They cannot detect lineage-specific selection
- C. They estimate one ω value per lineage
- D. They ignore the evolutionary history of species

Answer: They estimate one ω value per lineage

What is a potential issue when using nucleotide correction models for codon-based analyses?

- A. Overestimation of non-synonymous sites
- B. Underestimation of synonymous sites
- C. Ignoring codon usage bias
- D. Inaccurate tree topology

Answer: Ignoring codon usage bias

Which of the following approaches is used to study the functional divergence of genes?

- A. Analyzing intraspecific genetic diversity
- B. Estimating the dN/dS ratio across lineages
- C. Comparing genetic drift rates
- D. Calculating nucleotide diversity

Answer: Estimating the dN/dS ratio across lineages

Indicate the false statement about natural selection and molecular adaptation:

- A. Positive selection leads to rapid fixation of beneficial mutations
- B. Purifying selection removes deleterious mutations from the population
- C. Balancing selection maintains genetic diversity within a population
- D. Neutral mutations are always subject to strong selection pressure

Answer: Neutral mutations are always subject to strong selection pressure

In codon substitution models, what does a dN/dS ratio (ω) less than 1 indicate?

- A. Positive selection
- B. Neutral evolution
- C. Purifying selection
- D. Balancing selection

Answer: Purifying selection

Which of the following is a challenge when performing multiple sequence alignment (MSA) for coding sequences?

- A. Aligning sequences with different lengths
- B. Accounting for codon structure in the alignment
- C. Ensuring uniform substitution rates across sites
- D. Ignoring insertion and deletion events

Answer: Accounting for codon structure in the alignment

What does the term 'relaxation of selection' refer to in the context of gene evolution?

- A. Increased purifying selection pressure
- B. Reduced selection pressure allowing more neutral mutations
- C. Increased rate of beneficial mutations
- D. Elimination of all genetic variation

Answer: Reduced selection pressure allowing more neutral mutations

Which of the following is an advantage of using codon substitution models over nucleotide substitution models?

- A. They simplify the analysis by ignoring synonymous substitutions
- B. They provide more accurate estimates of selection pressure
- C. They are easier to compute
- D. They do not require coding sequence alignment

Answer: They provide more accurate estimates of selection pressure

Indicate the true statement about the impact of codon usage bias on estimating selection pressure:

- A. Codon usage bias does not affect the estimation of selection pressure
- B. Ignoring codon usage bias can lead to overestimating the number of synonymous sites
- C. Codon usage bias is only relevant for non-coding regions
- D. Correcting for codon usage bias is unnecessary in codon-based models

Answer: Ignoring codon usage bias can lead to overestimating the number of synonymous sites

These questions are crafted to align with the content in the provided document, covering key concepts such as codon substitution models, selective pressures, and molecular adaptation.