GATE 2026 Ecology and Evolution Question Paper with Solutions

ZOLLEGE

General Instructions

(i) This booklet contains 65 questions, each provided with a complete, step-by-step solution.

(ii) It comprises 50 single-correct multiple-choice questions, 9 multiple-correct questions and 6 numerical / integer-type questions.

(iii) These questions follow the GATE Ecology and Evolution examination pattern.

(iv) Questions carry 1 or 2 marks. MCQs have negative marking (1/3 or 2/3 of the marks); MSQ and numerical-answer (NAT) questions carry no negative marking.

(v) GATE is a 3-hour paper of 65 questions (100 marks).

(vi) A virtual scientific calculator is provided; physical calculators are not allowed.

(vii) Attempt each question on your own before reviewing the given solution.

(viii) For multiple-correct questions, all correct options must be selected to earn full marks.

(ix) For numerical questions, report the answer rounded exactly as asked.

1. Expedite, Hasten, Hurry, ____________
Fill the blank by choosing a word with a meaning similar to that of the words given above.

(A) Accelerate

(B) Retard

(C) Provide

(D) Disable

Correct Answer: (A) Accelerate

SOLUTION:

Step 1: Understanding the Concept:

The question gives three words, expedite, hasten and hurry, and asks for a fourth word that means the same thing. All three describe doing something quickly or making it happen sooner.

Step 2: Key Formula or Approach:

Check each option against this shared sense of speed. A true synonym must also mean "to make faster" or "to rush," not the opposite and not something unrelated.

Step 3: Detailed Explanation:

"Retard" means to delay or slow down, which is the reverse of hurrying, so it is ruled out. "Provide" means to give or supply, which has no link to speed. "Disable" means to stop something from functioning, again unrelated to speed. "Accelerate" means to speed up or move faster, matching expedite, hasten and hurry exactly.

Step 4: Final Answer:

The word that fits is "accelerate," so the correct choice is option (A).

Quick Tip: Look for a word that means "to make something happen faster," the same sense shared by expedite, hasten, and hurry.

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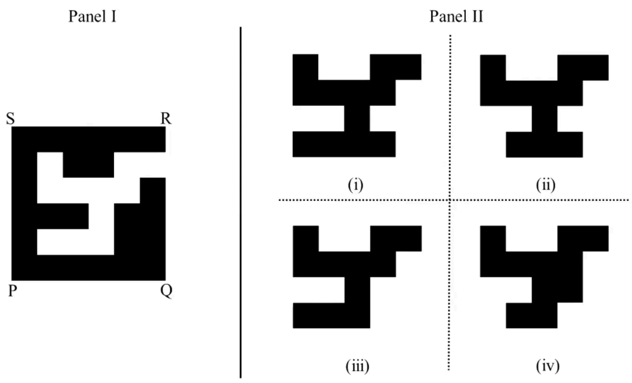
2. A black square PQRS has been cut into two parts. One part of it is shown in Panel I. Which one of the shapes labelled (i), (ii), (iii), and (iv) in Panel II is the other part of the same square?



(A) (i)

(B) (ii)

(C) (iii)

(D) (iv)

Correct Answer: (C) (iii)

SOLUTION:

Step 1: Understanding the Concept:
A solid black square is split into two jigsaw-like pieces by one irregular cut. Panel I shows one piece, and we must pick from Panel II the one piece that is its perfect match.

Step 2: Key Formula or Approach:
Instead of imagining the whole square, focus only on the cut edge, the zigzag boundary where the two pieces meet. The matching piece must have a cut edge that is the mirror image of Panel I's cut edge, so the two edges lock together like puzzle pieces with no gap and no overlap.

Step 3: Detailed Explanation:

Trace the steps and notches along the cut edge of Panel I from one corner of the square to the other. For each inward notch in Panel I, the matching piece needs an outward tooth of the same size at the same position, and for each outward tooth in Panel I, the match needs an inward notch. Checking shapes (i), (ii), and (iv) against this rule, at least one notch or tooth fails to line up with Panel I's cut edge, so the two pieces would either overlap or leave a gap if joined. Shape (iii) is the only one whose zigzag pattern is the mirror complement of Panel I all along the cut, so joining it to Panel I reproduces the original square PQRS with straight, unbroken outer sides.

Step 4: Final Answer:

Shape (iii) is the missing piece, so the correct option is (C).

Quick Tip: The missing piece must be the exact mirror complement of Panel I along the cut line, so the two pieces rejoin into the full square PQRS.

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3. A day can only be cloudy or sunny. The probability of a day being cloudy is 0.5, independent of the condition on other days. What is the probability that in any given four days, there will be three cloudy days and one sunny day?

(A) 1/4

(B) 3/4

(C) 2/3

(D) 3/8

Correct Answer: (A) 1/4

SOLUTION:

Step 1: Understanding the Concept:

Each day is independent, and cloudy and sunny are equally likely, each with chance 0.5. We want exactly one sunny day out of four, with the other three cloudy.

Step 2: Key Formula or Approach:

List the four days as slots. The single sunny day can sit in any one of the four slots, and each specific pattern of three cloudy plus one sunny has the same probability, since every day's chance is 0.5 regardless of position.

Step 3: Detailed Explanation:

The probability of any one fixed pattern, say cloudy, cloudy, cloudy, sunny in that order, is

$$0.5 \times 0.5 \times 0.5 \times 0.5 = (0.5)^4 = \frac{1}{16}$$

Since the sunny day could be the first, second, third, or fourth day, there are 4 equally likely patterns that all give three cloudy days and one sunny day. Adding their probabilities,

$$4 \times \frac{1}{16} = \frac{4}{16} = \frac{1}{4}$$

Step 4: Final Answer:

The probability of exactly three cloudy days out of four is $\frac{1}{4}$, so the correct choice is option (A).

Quick Tip: Use the binomial idea: count the ways to place the single sunny day among four days, then multiply by the probability of each fixed pattern.

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4. The values of Stock A and Stock B on a particular day are Rs. 50 and Rs. 80, respectively. An investor invests Rs. 100 in Stock A and Rs. 80 in Stock B. He sells all the stocks the next day when the value of Stock A is Rs. 55 and Stock B is Rs. 70. The profit made by the investor is Rs.

____

(A) 0

(B) 5

(C) 10

(D) 20

Correct Answer: (A) 0

SOLUTION:

Step 1: Understanding the Concept:
Money invested in a stock buys a certain number of shares at the price on that day, and the value of the holding the next day depends on the new price of the same number of shares.

Step 2: Key Formula or Approach:
Work out the gain or loss separately for each stock, using

$$\text{Gain} = (\text{units held}) \times (\text{new price} - \text{old price})$$

then add the two gains together to get the total profit.

Step 3: Detailed Explanation:

For Stock A, Rs. 100 at Rs. 50 per unit buys $\frac{100}{50} = 2$ units. The price rises from Rs. 50 to Rs. 55, a gain of Rs. 5 per unit, so

$$\text{Gain on A} = 2 \times 5 = 10 \text{ Rs.}$$

For Stock B, Rs. 80 at Rs. 80 per unit buys $\frac{80}{80} = 1$ unit. The price falls from Rs. 80 to Rs. 70, a loss of Rs. 10 per unit, so

$$\text{Loss on B} = 1 \times (-10) = -10 \text{ Rs.}$$

Step 4: Combine the two results.

$$\text{Total profit} = 10 + (-10) = 0$$

Step 5: Final Answer:

The gain on Stock A exactly cancels the loss on Stock B, so the investor's overall profit is Rs. 0, option (A).

Quick Tip: Find how many units of each stock the investor buys, then compare the total value of the holdings on the two days.

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5. "When it is raining, peacocks dance." Based only on this sentence, which one of the following options is necessarily true?

(A) Peacocks dance only when it is raining.

(B) When peacocks dance, it is raining.

(C) When peacocks are not dancing, it is not raining.

(D) When it is not raining, peacocks do not dance.

Correct Answer: (C) When peacocks are not dancing, it is not raining.

SOLUTION:

Step 1: Understanding the Concept:

Read the sentence as a simple rule: rain forces dancing. Write it as $R \to D$, where R is "it rains" and D is "peacocks dance." We only know this one rule is true, nothing else about peacocks or rain.

Step 2: Key Formula or Approach:

Think of the cases for R and D that keep the rule $R \to D$ true. The rule is broken only in the case where it rains and peacocks do not dance, R true and D false. The three other cases, true-true, false-true, and false-false, all keep the rule true. Any option must hold in all three of these surviving cases to be called necessarily true.

Step 3: Detailed Explanation:

Take options (A) and (B), which both claim dancing forces rain, $D \to R$. In the surviving case where it does not rain but the peacocks dance anyway, false-true, this claim breaks, so it is not guaranteed. Take option (D), which claims no rain forces no dancing, $\neg R \to \neg D$. That same false-true case, no rain yet peacocks dancing, breaks this claim too. Now take option (C), which claims no dancing forces no rain, $\neg D \to \neg R$. Check it against every surviving case: true-true has D true so the claim's condition does not apply, false-true again has D true so it does not apply, and false-false has D false and R false, so the claim holds. In every surviving case, option (C) never fails.

Step 4: Final Answer:
Only option (C), "When peacocks are not dancing, it is not raining," survives every case allowed by the original rule, so it is the necessarily true statement.

Quick Tip: A conditional statement is logically equivalent only to its contrapositive, not to its converse or inverse.

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6. Consider the analogy:
Water : P :: Food : Q
Choose the combination of P and Q from the options below that forms a meaningful analogy.

(A) P = Thirst; Q = Hunger

(B) P = Drink; Q = Hunger

(C) P = Thirst; Q = Satiated

(D) P = Wet; Q = Critic

Correct Answer: (A) P = Thirst; Q = Hunger

SOLUTION:

This analogy asks us to fill in P and Q so that Water is to P as Food is to Q. The trick is to first name the exact relation joining Water and P, then test each option to see if Food and Q follow that same relation.

1. **P = Thirst; Q = Hunger**: Not having water gives the feeling of thirst, and not having food gives the feeling of hunger. Both pairs

describe a need turning into a specific sensation, so the relation matches on both sides.

2. **P = Drink; Q = Hunger**: Drink is something you do about water, not a feeling caused by its lack, so the first half does not follow the same pattern as the second half (Hunger, a feeling).
3. **P = Thirst; Q = Satiated**: Thirst is the feeling of wanting water, but Satiated is the feeling of having had enough food, which is the opposite kind of state. The two halves point in opposite directions, so they do not match.
4. **P = Wet; Q = Critic**: Wet describes a physical condition, not a need-based feeling, and Critic has nothing to do with food at all. Neither half fits the pattern, and the two do not relate to each other either.

Only the first option keeps a consistent relation: lacking the item in the first word produces the named feeling in the second word, for both halves of the analogy. So P = Thirst and Q = Hunger.

Let's summarize:

- Water : Thirst mirrors the pattern of a need producing a specific bodily sensation.
- Food : Hunger follows the exact same need-to-sensation pattern.

So the correct combination is P = Thirst and Q = Hunger.

Quick Tip: Think about the specific bodily sensation caused by lacking water, then find the matching sensation caused by lacking food.

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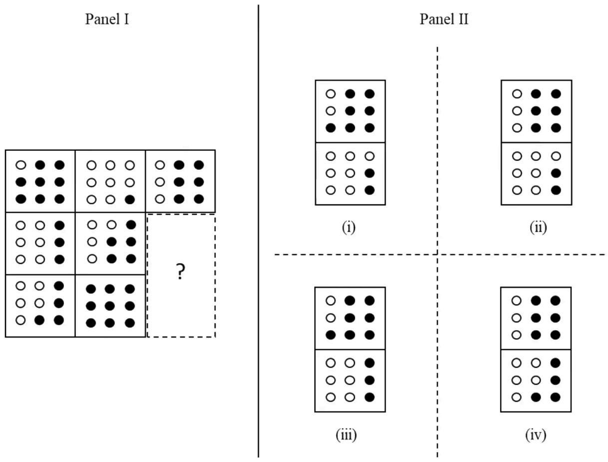
7. Panel I shows a 3 by 3 layout of tiles, where each tile is itself a smaller 3 by 3 grid of filled and open dots. The two tiles in the bottom right corner of Panel I are missing. Panel II shows four candidate pairs of tiles, labelled (i) to (iv), that could fill this missing space.



Two tiles are missing in Panel I. Which one of the options in Panel II is the appropriate choice for the missing tiles?

(A) (i)

(B) (ii)

(C) (iii)

(D) (iv)

Correct Answer: (A) (i)

SOLUTION:

Step 1: Look for a growth pattern across the known tiles.

Arrange the 7 given tiles by how many dots they have filled: 1, 3, 4, 5, 6, 8, 9. Comparing each one to the next smaller one, every tile keeps all the filled dots of the smaller tile and adds exactly one more dot in a fixed spot. Tracing this through the full set shows dots get added in this order: bottom right corner, then upward through the rest of the right column, then upward through the middle column, then upward through the left column.

Step 2: Locate where the sequence stands right before and after the missing tiles.
The tile with 6 dots filled (columns 2 and 3 completely shaded) is the last stop before the left column starts filling in. The very next stage in the sequence adds the bottom cell of the left column, giving 7 filled dots in total, which is what the missing tile in position (2,3) should show. One stage after that adds the middle cell of the left column, giving 8, which matches the known tile with 8 filled dots and only its top left corner empty. So the tile between 6 and 8 in the sequence, with 7 dots, is the correct target for (2,3).

Step 3: Work out the other missing tile the same way.
Near the start of the sequence, the tile with just 1 dot filled has only the bottom right corner shaded. The next stage fills in the rest of the right column, giving 3 filled dots, which matches the known tile with 3 filled dots. The stage with 2 filled dots sits between these two, and it must fill the bottom right corner plus the cell directly above it, leaving the top cell of the right column, and the whole middle and left columns, empty. This is the pattern needed for the missing tile at (3,3).

Step 4: Check the totals as a cross reference.
Writing the filled dot counts in their tile positions gives a 3 by 3 magic square with every row and column adding to 15: 8, 1, 6 on top, 3, 5, 7 in the middle, and 4, 9, 2 on the bottom. This agrees with 7 and 2 found above.

Step 5: Match against the options.
Option (i) is the only one whose upper tile shows exactly 7 dots in the

right spots (both right and middle columns full, plus the bottom left cell) and whose lower tile shows exactly 2 dots in the right spots (only the bottom two cells of the right column). Options (ii) and (iv) fall short with only 6 dots in the upper tile, and option (iii) gets the upper tile right but shades all 3 cells of the right column in the lower tile instead of just 2.

$$\boxed{\text{(i)}}$$

Quick Tip: Compare the tiles by how many dots are filled and in what order new dots get added going from a smaller filled count to a larger one, then use the row and column totals as a cross check.

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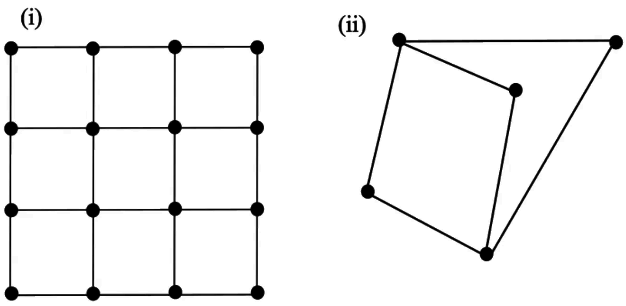
8. Figures (i) and (ii) below represent intercity highway systems, where each black dot is a city and each line segment joining two dots is a direct highway between those two cities. Figure (i) is a 4 by 4 grid of cities connected only along the horizontal and vertical grid lines, with no diagonal roads. Figure (ii) has 5 cities joined by 6 highways in an irregular network with one extra interior city.



A salesperson needs to make a trip. She needs to start from a city, visit each of the remaining cities exactly once, and finally return to the same city from which she started. Which one of the following options is then true?

(A) Such a trip is possible for (i), but not for (ii).

(B) Such a trip is possible for (ii), but not for (i).

(C) Such a trip is possible for both (i) and (ii).

(D) Such a trip is possible neither for (i) nor for (ii).

Correct Answer: (A) Such a trip is possible for (i), but not for (ii).

SOLUTION:

Step 1: Restate the goal.

We want one closed route through each map that touches every dot exactly once and comes back to the start.

Step 2: Build a working route for the grid, figure (i).

Number the rows 1 to 4 from top to bottom and the columns 1 to 4 from left to right, so a city is (row, col). One route that uses only the grid roads is:

$(1,1) \to (2,1) \to (3,1) \to (4,1) \to (4,2) \to (4,3) \to (4,4) \to (3,4)$
$\to (3,3) \to (3,2) \to (2,2) \to (2,3) \to (2,4) \to (1,4) \to (1,3) \to (1,2)$
$\to (1,1)$.

Every arrow above is a real horizontal or vertical road on the grid, all 16 cities show up exactly once, and the route ends back where it began. So figure (i) works.

Step 3: Try the same for figure (ii) and see where it breaks.

Call the two well connected cities A and E, and the other three B, C, D. Every road runs between an $\{A, E\}$ city and a $\{B, C, D\}$ city, so a route can never move from B straight to C, or from A straight to E; it always has to hop from one group to the other.

Try building the loop: start at A, go to B, come back only to E since B only knows A and E, go to C, come back to A or E again, go to D, and come back again. Every single visit to B, C, or D forces an immediate return to the $\{A, E\}$ pair, but that pair has only 2 cities to share among 3 round trips. By the time the third city, D, is visited, the route has already used up A and E once each and must reuse one of them to get back, which means passing through it a second time.

Step 4: Conclude.

The grid, figure (i), supports a full loop, but the 5-city network, figure (ii), cannot avoid reusing a city because it does not have enough well connected cities to alternate with all three lightly connected ones.

$$\boxed{\text{Such a trip is possible for (i), but not for (ii).}}$$

> **Quick Tip:** Split the cities into two groups so that every road joins one group to the other, then check whether the two groups are equal in size.

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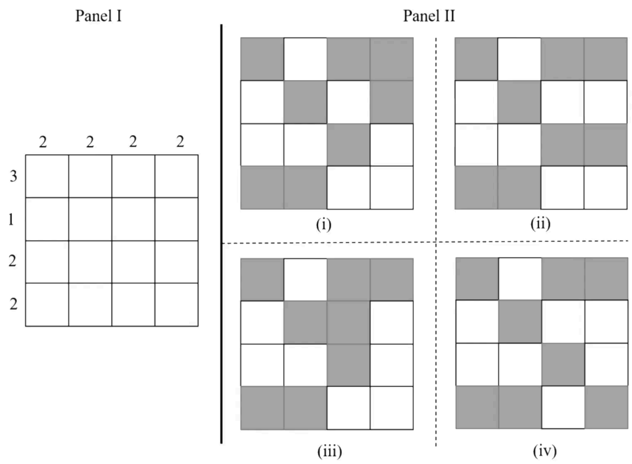
9. Panel I below shows a grid of cells with four rows and four columns. The numbers on the top of each column and on the left of each row tell us how many cells in that column or row must be shaded. The column totals, left to right, are 2, 2, 2, 2, and the row totals, top to bottom, are 3, 1, 2, 2. Panel II below shows four candidate grids, labelled (i) to (iv), with some cells shaded grey.



Which one of the options shown in Panel II represents the grid shaded correctly?

(A) (i)

(B) (ii)

(C) (iii)

(D) (iv)

Correct Answer: (B) (ii)

SOLUTION:

Panel I fixes how many cells must be shaded in each column, 2, 2, 2, 2 from left to right, and each row, 3, 1, 2, 2 from top to bottom. Since every column needs the same total of 2, checking columns first is a quick filter, and then the row totals confirm which single grid is the real answer.

1. **(i)**: Every column in this grid has exactly 2 shaded cells, so it passes the column check. But its row totals come out as 3, 2, 1, 2, and the puzzle needs 3, 1, 2, 2. Rows 2 and 3 have swapped their shading counts, so this grid is wrong.
2. **(ii)**: Every column again has exactly 2 shaded cells. Checking the rows gives 3, 1, 2, 2, in that exact order, which matches Panel I perfectly.
3. **(iii)**: The columns here do not all come out to 2, one column ends up with 3 and another with only 1, so this grid already fails the column check before the rows are even considered.
4. **(iv)**: The row totals for this grid are 3, 1, 1, 3, which does not match the required 3, 1, 2, 2, so it fails on the rows even though some columns may look right.

Only option (ii) keeps every column at 2 shaded cells and lines up the rows as 3, 1, 2, 2 in the correct order.

Let's summarize:

- A quick column check, all columns must equal 2, rules out (iii) immediately.
- A row check, 3, 1, 2, 2 in order, then separates the correct grid from (i) and (iv), which get the right total shaded cells but in the wrong rows.

So the grid shaded correctly is option (ii).

Quick Tip: Add up the shaded cells in each row and each column separately, and match both sets of totals against the numbers given in Panel I.

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10. An unbiased six sided die, with faces marked 1, 2, 3, 4, 5, and 6, is rolled twice in succession, and the number on the top face is recorded each time. The probability that the sum of the two recorded numbers is a prime number is ________

(A) $\frac{3}{36}$

(B) $\frac{13}{36}$

(C) $\frac{15}{36}$

(D) $\frac{19}{36}$

Correct Answer: (C) $\frac{15}{36}$

SOLUTION:

Step 1: Set up the sample space.

Rolling a fair die twice gives $6 \times 6 = 36$ equally likely pairs (a, b), where a is the first roll and b is the second.

Step 2: Work out how many pairs give each sum.

The number of pairs adding to a sum s rises from 1 at $s = 2$ up to 6 at $s = 7$ and then falls back to 1 at $s = 12$, moving by 1 each step. So the counts for sums 2 through 12 are $1, 2, 3, 4, 5, 6, 5, 4, 3, 2, 1$.

Step 3: Pick out the prime sums.

Among 2 to 12, the primes are $2, 3, 5, 7, 11$. Reading off their counts from the list above: sum 2 gives 1, sum 3 gives 2, sum 5 gives 4, sum 7 gives 6, and sum 11 gives 2, using the symmetric count for 11, which mirrors sum 3.

Step 4: Add these counts.

$$1 + 2 + 4 + 6 + 2 = 15$$

Step 5: Divide by the total outcomes.

$$P = \frac{15}{36}$$

So out of every 36 equally likely rolls, 15 give a prime sum.

$$\boxed{\frac{15}{36}}$$

Quick Tip: List the pairs of die faces that add up to each prime number between 2 and 12, then divide the count of favorable pairs by 36.

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11. Two sister species, A and B, are distributed along a continuous elevational gradient in the Himalayas. Species A is distributed from the foothills to 1800 metres above sea level and species B is distributed from 1800 to 3500 metres above sea level. Which one of the following modes of speciation best explains their distribution?

(A) Sympatric speciation

(B) Allopatric speciation

(C) Parapatric speciation

(D) Peripatric speciation

Correct Answer: (B) Allopatric speciation

SOLUTION:

This question gives two sister species with ranges that just touch at one elevation (1800 m) and never overlap. The trap is to look at today's map and assume the split is happening right now, across that boundary. Let's check what each term in the options actually needs.

1. **Sympatric speciation**: This needs the two forms to diverge while sharing the same space, with no geographic separation at any point. Species A and B occupy separate elevational belts, so this does not fit.
2. **Allopatric speciation**: This needs a period where the ancestral population was cut off into two groups with no gene flow between them, usually by a physical barrier or by being pushed into separate refugia. Himalayan sister species that now replace each other along elevation are known, from long term field studies, to have diverged in exactly this way, in isolated valleys or refugia during past climate shifts, before expanding back to meet at a boundary.
3. **Parapatric speciation**: This needs the two forms to diverge while still in contact along a gradient, with reduced but not zero gene flow across the boundary during divergence itself. The boundary at 1800 m here is a secondary contact zone reached

after the species had already formed elsewhere, not a divergence happening live across the slope.

4. **Peripatric speciation**: This is a special version of allopatric speciation where a small founder population splits off at the margin of the main range. Nothing in the question suggests one of the two species began as a tiny marginal population, so this is too specific a fit.

The pattern described, closely related species occupying adjacent, non-overlapping elevational bands with a shared boundary, is the textbook signature of past geographic isolation followed by range expansion and secondary contact. That is allopatric speciation, even though the present-day map looks parapatric at first glance.

Let's summarize:

- A clean elevational replacement between sister species usually reflects an old geographic split, not an active one.
- Parapatric speciation would need ongoing contact and gene flow during divergence, which is not what produced this boundary.

So the mode of speciation that best explains the distribution of species A and B is allopatric speciation.

Quick Tip: Sister species with non-overlapping ranges meeting at one boundary usually diverged while geographically isolated, then expanded back into contact.

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12. Which one of the following is an invasive plant species in India?

(A) *Lantana camara*

(B) *Myristica malabarica*

(C) *Terminalia tomentosa*

(D) *Santalum album*

Correct Answer: (A) *Lantana camara*

SOLUTION:

The question is testing whether we can tell a native Indian plant apart from an introduced, invasive one. Let's look at where each of the four species actually comes from.

1. **Lantana camara**: Originally from Central and South America. It was brought into India as a decorative hedge plant in British-era gardens, then spread on its own across forests and grasslands all over the country. It chokes out native plants and is one of the most cited invasive weeds in India.
2. **Myristica malabarica**: A tree native to the Western Ghats, part of the wild nutmeg group. It grows only in its natural range and is not spreading into new territory, so it is not invasive.
3. **Terminalia tomentosa**: A common native tree of Indian deciduous forests, used for timber and fodder. It belongs naturally in the Indian landscape.
4. **Santalum album**: Indian sandalwood, native to peninsular India, prized and legally protected for its wood, not a species that invades new habitats.

Only Lantana camara was brought in from another continent and has gone on to spread aggressively at the cost of native vegetation, which is exactly what makes a species invasive.

Let's summarize:

- An invasive species must first be non-native to the region.
- Of the four options, only Lantana camara fits both being non-native and spreading uncontrolled.

So the invasive plant species in India among the choices is Lantana camara.

Quick Tip: Check which of the four species was introduced to India from another continent and has since spread out of control.

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13. Phytoecdysone is a defensive secondary chemical that ___________.

(A) mimics a neurotransmitter and can cause paralysis or even death in caterpillars

(B) mimics insect hormones and interferes with insect metamorphosis

(C) belongs to a category of tannins and reduces the digestibility of plant tissues

(D) belongs to a category of lignins and deters herbivores

Correct Answer: (B) mimics insect hormones and interferes with insect metamorphosis

SOLUTION:

Phytoecdysone is a chemical defense some plants use against insects. The question wants us to know exactly how it works, not just that it is "a defense chemical". Let's test each option against what phytoecdysone actually is.

1. **Mimics a neurotransmitter, causes paralysis:** That description fits neurotoxins like nicotine, which act on the

nervous system. Phytoecdysone is not a nerve poison of this kind.

2. **Mimics insect hormones, interferes with metamorphosis:** Phytoecdysone is a plant-made steroid that closely resembles ecdysone, the hormone that times an insect's molts and its change into an adult. Eating it confuses this timing system and metamorphosis goes wrong. This matches.
3. **A tannin that cuts digestibility:** Tannins are a different chemical family; they bind to proteins in the gut and make plant matter harder to break down. Phytoecdysone is a steroid, not a tannin.
4. **A lignin that deters herbivores:** Lignins are structural, woody polymers that make plant tissue tough. Phytoecdysone has nothing to do with this structural role.

So phytoecdysone's defense strategy is chemical mimicry of a hormone, not a physical or nutritional barrier.

Let's summarize:

- Phytoecdysone copies the insect hormone ecdysone.
- This mimicry disturbs molting and metamorphosis in insects that eat the plant.

So the correct description is that phytoecdysone mimics insect hormones and interferes with insect metamorphosis.

Quick Tip: Phytoecdysone is a plant steroid that closely resembles an insect's own molting hormone.

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14. The physiologist Ivan Pavlov conducted an experiment on dogs, in which a bell was sounded every time food was provided. In this experiment, dogs eventually showed the salivary reflex (a response to food) when the bell was sounded, even if food was not provided. This is an example of _________.

(A) conditioning

(B) imprinting

(C) instinct

(D) eavesdropping

Correct Answer: (A) conditioning

SOLUTION:

Pavlov's dog experiment is one of the most famous in behavioral science. The key steps are: food alone naturally causes salivation, a bell is rung along with the food many times, and eventually the bell by itself starts causing salivation. We need to name this type of learning correctly.

1. **Conditioning:** This is learning by association, where a neutral stimulus (the bell) gets paired repeatedly with a stimulus that already causes a response (food), until the neutral stimulus alone can trigger that response. This is exactly what the dogs show.
2. **Imprinting:** A fast, one-time learning process restricted to an early critical period of life, like a chick attaching itself to the first moving object it sees after hatching. There is no such critical-period, one-shot attachment happening here.
3. **Instinct:** A behavior an animal performs correctly the very first time, with no learning needed, like a spider spinning its first web.

The dogs needed repeated trials to build this response, so it is not instinct.

4. **Eavesdropping:** In animal behavior, this means an individual gathers useful information by listening in on signals meant for someone else, such as a predator using prey calls to locate food. That is unrelated to the bell-food pairing here.

Only conditioning correctly describes learning a new response through repeated association between two stimuli.

Let's summarize:

- The bell became a learned trigger for salivation only because it was repeatedly paired with food.
- Imprinting, instinct, and eavesdropping all describe different processes that do not match this pairing-based learning.

So Pavlov's experiment is a textbook case of conditioning.

Quick Tip: The dogs learned a new response by repeatedly pairing a neutral cue with a reflex-triggering stimulus.

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15. Ecologists have studied the distributions of birds on archipelagos. Some studies found an interesting "checkerboard" pattern within island groups. Sister species were never present on the same island, even when the islands were very close to each other. Which one of the following processes best explains this checkerboard pattern?

(A) Mutualism

(B) Competition

(C) Predation

(D) Commensalism

Correct Answer: (B) Competition

SOLUTION:

The pattern described here, closely related species that never turn up on the same island even when islands sit close together, is a well known finding from island biogeography, first worked out in detail for birds in New Guinea and its satellite islands. Let's test each process against this pattern.

1. **Mutualism:** This is a relationship where both species gain something from living near each other, such as a plant and its pollinator. If this were at work, we would expect sister species to often share islands, not avoid each other, so this does not fit.
2. **Competition:** Sister species share a very recent common ancestor, so they usually need the same kind of food and nesting space. When both land on the same small island, the limited resources cannot support both, and one species eventually excludes the other. This produces exactly the checkerboard, one species per island, pattern.
3. **Predation:** This would need one sister species to routinely hunt and eat the other. Closely related species with similar body plans and diets are rarely predator and prey of each other, so this is a poor fit.
4. **Commensalism:** Here one species benefits while the other is unaffected either way. This kind of relaxed relationship would not

force species apart onto separate islands.

The mutual exclusion of sister species from the same island is the signature of competitive exclusion between ecologically similar rivals.

Let's summarize:

- Sister species overlap heavily in their ecological needs.
- When forced onto the same island, competition for shared resources pushes one species out, leaving the checkerboard pattern.

So competition between ecologically similar sister species best explains the checkerboard distribution.

Quick Tip: Sister species share very similar resource needs, so placing two of them on one island triggers competitive exclusion.

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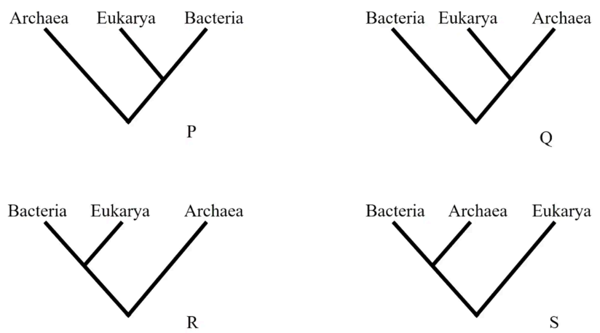
16. Which one of the following phylogenetic trees illustrates the relationship between Archaea, Bacteria and Eukarya? The figure shows four candidate cladograms, labelled P, Q, R and S, each grouping the three domains of life in a different branching pattern.



(A) P

(B) Q

(C) R

(D) S

Correct Answer: (A) P

SOLUTION:

This question checks whether we remember which two of the three domains of life, Bacteria, Archaea, and Eukarya, are more closely related to each other. The figure gives four trees (P, Q, R, S) that each pair up two domains as sisters and leave the third as the outgroup. Let's work out the right pairing first, then match it to a tree.

1. **What does the molecular evidence say:** Comparisons of ribosomal RNA and of the core machinery cells use to copy DNA and read genes (including proteins similar to histones) show that Archaea and Eukarya share more features with each other than either shares with Bacteria. This tells us Bacteria was the first lineage to branch away from the common ancestor of all life, leaving Archaea and Eukarya to share a more recent common ancestor.
2. **Tree P:** Groups Archaea with Eukarya as the closer pair, with Bacteria as the outgroup. This matches the molecular evidence exactly.
3. **Tree Q:** Groups Bacteria with Eukarya instead, leaving Archaea as the outgroup. This puts the wrong domain next to Eukarya.
4. **Tree R:** Also pairs Bacteria with Eukarya, just drawn with a different branch style than Q. It carries the same wrong grouping.

5. **Tree S:** Groups Bacteria with Archaea, leaving Eukarya as the outgroup. This misses the Archaea-Eukarya link entirely.

Only one of the four trees, P, has Archaea and Eukarya joining first and Bacteria branching off at the base, which is what current evidence on the three domains supports.

Let's summarize:

- Bacteria is the earliest-branching domain.
- Archaea and Eukarya are sister lineages, more closely related to each other than to Bacteria.

So the correct phylogenetic tree is P.

Quick Tip: Molecular evidence groups Archaea and Eukarya as sister lineages, with Bacteria branching off earliest.

• • •

17. The Biological Species Concept was proposed by ___________.

(A) Ernst Mayr

(B) Ronald Fisher

(C) Sewall Wright

(D) J. B. S. Haldane

Correct Answer: (A) Ernst Mayr

SOLUTION:

The question asks who is credited with the Biological Species Concept, the idea that a species is a group of populations that can interbreed with each other but are reproductively cut off from other such groups. Let's check each name against what they are actually known for.

1. **Ernst Mayr**: An evolutionary biologist who formally defined species using reproductive isolation as the deciding test, laid out in his influential 1942 work. This is precisely the Biological Species Concept.
2. **Ronald Fisher**: A key architect of population genetics and the modern synthesis, famous for the fundamental theorem of natural selection, but not for defining species this way.
3. **Sewall Wright**: Known for genetic drift and the shifting balance theory of evolution in small populations, not for the species concept.
4. **J. B. S. Haldane**: Known for Haldane's rule and for mathematical work on selection pressure, again a different contribution.

Only Mayr's body of work matches the definition given in the question.

Let's summarize:

- The Biological Species Concept rests on reproductive isolation between populations.
- Fisher, Wright, and Haldane are population genetics pioneers, but the species concept itself belongs to Mayr.

So the Biological Species Concept was proposed by Ernst Mayr.

Quick Tip: Think of the scientist who defined species using reproductive isolation, in his 1942 book on systematics.

18. In a diploid population of N individuals, the probability of fixation of a new neutral mutation (assuming no other mutation occurs) is __________.

(A) $1/N$

(B) $2/N$

(C) $1/(2N)$

(D) $1/(4N)$

Correct Answer: (C) $1/(2N)$

SOLUTION:

Step 1: Picture the mutation as one chip in a big lottery drum.
The population is diploid with N individuals, so at this one gene position there are $2N$ copies in total. Right after the new mutation appears, $2N - 1$ copies are the old version and just 1 copy is the new, neutral, mutant version.

Step 2: See this as a fair random walk between two end states.
Since the mutation is neutral, nothing pushes its frequency up or down on purpose, it only moves because of random sampling of parents each generation (genetic drift). This frequency can only end at one of two points: it disappears completely (frequency 0) or it fixes and replaces every other copy (frequency 1).

Step 3: Use the fair-game property of neutral drift.
For an unbiased random walk like this, a well known result from Kimura's diffusion theory of drift says the chance of ending at the "fixed" end equals the fraction you started with, no more, no less.

Step 4: Write down the starting fraction.

The mutation began as 1 copy out of $2N$ total copies, so its starting share of the population is

$$\frac{1}{2N}$$

Step 5: Conclude.

By the fair-game rule for neutral alleles, this starting share is exactly the probability that the mutation eventually becomes fixed.

$$\boxed{\frac{1}{2N}}$$

Quick Tip: For a neutral allele, the probability of fixation equals its starting frequency in the gene pool.

• • •

19. Species that co-occur in space and time tend to be similar to each other in traits such as tolerance to heat or to drought. This is most likely because of ___________.

(A) Limiting similarity

(B) Divergent evolution

(C) Environmental filtering

(D) Competitive exclusion

Correct Answer: (C) Environmental filtering

SOLUTION:

This question tests whether you can tell apart four community ecology ideas that all sound similar: environmental filtering, limiting similarity, divergent evolution and competitive exclusion. The clue given is that species found together at the same place and time share similar heat and drought tolerance.

1. **Limiting similarity**: this idea is about competition, not about the physical environment. It says species sharing a site should differ in their niche traits so they do not compete too hard for the same resources. That predicts species becoming different from each other, not similar, so it does not fit.
2. **Divergent evolution**: this describes lineages splitting apart and becoming more different from a shared ancestor over evolutionary time. It talks about how species change through history, and says nothing about why species living in the same place right now share similar stress tolerance.
3. **Environmental filtering**: a harsh or specific local condition, like high heat or low water, works like a sieve. Any species that cannot handle that condition simply does not persist there. So the pool of species that remains at that site is stacked with similar tolerance traits. This matches the pattern in the question exactly.
4. **Competitive exclusion**: this is the rule that two species fighting for one limiting resource cannot both survive together forever. It leads toward one species disappearing or the pair separating along a resource axis, not toward shared trait values.

Only environmental filtering explains why co-occurring species end up looking alike in a stress-tolerance trait: the shared environment lets through only the individuals or species that can already handle it, so what is left behind is a similar-trait subset.

Let's summarize:

- Environmental filtering produces trait convergence among species sharing a site because the abiotic stress acts as a common screen.
- Limiting similarity and competitive exclusion are both about competition, and both push toward trait divergence or exclusion, the opposite pattern.

So the process behind the shared heat and drought tolerance among co-occurring species is environmental filtering.

Quick Tip: Ask whether the pattern is driven by the physical habitat screening out unsuited species, or by competition between species; a shared abiotic stress producing shared traits points to filtering, not competition.

• • •

20. Which one of the following statements is true for most ants and bees?

(A) Males are diploid and develop from fertilised eggs

(B) Males are haploid and develop from fertilised eggs

(C) Females are diploid and develop from fertilised eggs

(D) Females are diploid and develop from unfertilised eggs

Correct Answer: (C) Females are diploid and develop from fertilised eggs

SOLUTION:

This question checks whether you remember how sex is fixed in ants and bees through haplodiploidy, and which combination of ploidy (haploid or diploid) and egg type (fertilised or unfertilised) goes with which sex.

1. **Males are diploid and develop from fertilised eggs**: wrong on both counts. In haplodiploid insects, males carry only one chromosome set (haploid), and they hatch from eggs the queen never mated to fertilise.
2. **Males are haploid and develop from fertilised eggs**: half right. Males really are haploid, but that single chromosome set comes from an unfertilised egg, since fertilisation is exactly what would add the second set and make them diploid.
3. **Females are diploid and develop from fertilised eggs**: this is the correct pairing. Sperm from a male adds a second chromosome set to the egg, making the resulting female diploid, whether she becomes a worker or a queen.
4. **Females are diploid and develop from unfertilised eggs**: the ploidy is right, females are diploid, but the egg type is wrong. Without fertilisation there is only one chromosome set, which gives a haploid male, not a diploid female.

So the statement that holds up on both the ploidy and the egg type is that females are diploid and come from fertilised eggs, while males are haploid and come from unfertilised eggs, a process called arrhenotoky.

Let's summarize:

- Fertilised egg, two chromosome sets, diploid female.
- Unfertilised egg, one chromosome set, haploid male.

The correct statement is that females are diploid and develop from fertilised eggs.

Quick Tip: Recall haplodiploidy: a fertilised egg carries two chromosome sets and becomes a diploid female, an unfertilised egg carries one set and becomes a haploid male.

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21. Which one of the following concepts describes a co-evolutionary arms race between a pathogen and its host?

(A) Red Queen hypothesis

(B) Green Beard model

(C) Sympatric speciation

(D) Reinforcement

Correct Answer: (A) Red Queen hypothesis

SOLUTION:

The question describes a pathogen and its host locked in a constant tug of war, each one evolving new tricks to beat the other. You need to match that picture to the right named idea among four options.

1. **Red Queen hypothesis**: this is built exactly for such a race. A host evolves a new defence, the pathogen evolves a way around it, the host answers again, and so on forever, with neither side pulling permanently ahead. The name comes from having to run just to stay in the same place, which fits an arms race perfectly.
2. **Green Beard model**: this is about a gene that lets its carriers spot each other through a shared marker and act kindly toward one another. It explains a kind of cooperation, not a host-pathogen fight.
3. **Sympatric speciation**: this describes one population splitting into two new species while still living in the same place, usually

driven by disruptive selection. It is a speciation story, with no pathogen involved.

4. **Reinforcement**: this is about two populations evolving stronger barriers against mating with each other because their hybrids do poorly. It also belongs to speciation, not to an infection arms race.

Only the Red Queen hypothesis is built around an ongoing coevolutionary struggle where the host and the pathogen keep adapting against each other, so it is the correct match.

Let's summarize:

- Red Queen hypothesis, constant mutual adaptation between host and pathogen (or predator and prey).
- Green Beard, sympatric speciation and reinforcement all describe different processes, cooperation or speciation, not an infection arms race.

So the correct concept here is the Red Queen hypothesis.

Quick Tip: Look for the concept named after a character who must keep running just to stay in place; that image stands for organisms that must keep evolving just to hold their current fitness against a coevolving enemy.

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22. A flask containing nutrient-rich media is seeded with 100 isogenic bacteria. Assuming that no bacteria die in the flask, after approximately how many generations will the population reach a size of 10^5?

(A) 10

(B) 1000

(C) 100000

(D) 1

Correct Answer: (A) 10

SOLUTION:

Bacteria dividing with no deaths follow simple doubling growth. The flask starts with 100 cells and we want to know roughly how many doublings, or generations, are needed to reach 10^5 cells.

1. **Work out the fold increase needed**: the population must grow from $100 = 10^2$ cells to 10^5 cells, so it must multiply by $\frac{10^5}{10^2}$ $= 10^3 = 1000$ times over.
2. **Recall what doubling does**: after g generations of simple binary fission, the starting count is multiplied by 2^g. So the equation to solve is $2^g = 1000$.
3. **Use a handy doubling fact**: doubling ten times multiplies a number by $2^{10} = 1024$, which is close enough to 1000 for an approximate answer. So $g \approx 10$ fits well.
4. **Sanity check the other choices**: $g = 1000$ or $g = 100000$ generations would multiply the starting count by astronomically large factors, nowhere near just 1000-fold. $g = 1$ only doubles the count once, giving 200 cells, far short of 10^5.

So counting doublings rather than working with logarithms directly, ten generations of division take the flask from 100 bacteria to around 10^5 bacteria.

Let's summarize:

- Doubling growth follows $N = N_0 \times 2^g$.
- A thousand-fold increase needs about 10 doublings, since $2^{10} \approx 1000$.

The population reaches 10^5 cells after about 10 generations.

$$\boxed{10}$$

Quick Tip: Bacteria growing by doubling every generation means $N = N_0 \times 2^g$; find g such that this thousand-fold increase happens, noting $2^{10} \approx 1000$.

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23. The field of allometry assesses how species traits scale with each other. Given the relationship between metabolic rate and body mass, which one of the following statements is true?

(A) Elephants expend more energy per gram per hour than mice do

(B) Mice expend more energy per gram per hour than humans do

(C) Elephants expend less total energy per day than mice do

(D) Humans and elephants expend similar amounts of total energy per day

Correct Answer: (B) Mice expend more energy per gram per hour than humans do

SOLUTION:

This question is about the well known scaling rule linking body mass and metabolic rate, sometimes called Kleiber's law, and how it plays out when we compare mice, humans and elephants.

1. **Elephants expend more energy per gram per hour than mice do**: false. Larger bodies have proportionally lower surface area to volume, so they lose heat more slowly and can afford a slower per gram metabolism; the per gram rate actually drops as size goes up, so an elephant's rate per gram is lower than a mouse's, not higher.
2. **Mice expend more energy per gram per hour than humans do**: true. Mice are far smaller than humans, and small mammals need a very high per gram metabolic rate just to keep their body temperature up, since a small body loses heat quickly relative to its volume. So gram for gram, a mouse burns much more energy per hour than a human does.
3. **Elephants expend less total energy per day than mice do**: false. This mixes up total energy use with the per gram rate. Even though an elephant's cells individually work at a lower rate, there are enormously more of them, so the whole animal's daily energy use is far larger than a mouse's total daily use, not smaller.
4. **Humans and elephants expend similar amounts of total energy per day**: false. Since total metabolic rate rises with mass raised to about the 0.75 power, and an elephant can outweigh a human by close to a hundredfold, the elephant's total daily energy budget works out much larger than a human's, not similar.

The key idea to hold onto is that total energy use grows with body size, while energy use per gram of tissue actually shrinks with body size. That is why small mice run hot on a per gram basis compared to both humans and elephants.

Let's summarize:

- Total metabolic rate increases with mass, roughly as $M^{0.75}$.

- Mass-specific (per gram) metabolic rate decreases with mass, so smaller animals like mice burn more per gram per hour than larger ones like humans or elephants.

So the true statement is that mice expend more energy per gram per hour than humans do.

Quick Tip: Kleiber's law gives total metabolic rate as roughly $M^{0.75}$; dividing by mass shows mass-specific (per gram) metabolic rate falls with size, so smaller animals burn more per gram than larger ones.

• • •

24. According to life history theory, when parents can only provide limited nutrients and care to their offspring, the number and size of the offspring are expected to be ______________.

(A) negatively correlated

(B) positively and linearly correlated

(C) uncorrelated

(D) positively and exponentially correlated

Correct Answer: (A) negatively correlated

SOLUTION:

Life history theory treats parental care and nutrients as a limited budget that has to be shared across every offspring a parent produces. The question asks how offspring number and offspring size should relate when that budget is capped.

1. **Negatively correlated**: this matches a fixed-budget trade-off. Splitting one limited pool of resources among more offspring

leaves less for each one, so a rise in offspring number goes with a fall in average offspring size, and the two move in opposite directions.

2. **Positively and linearly correlated**: this would require the total parental budget to expand every time an extra offspring is added, which cannot happen if resources are limited, so this option does not fit the setup described.
3. **Uncorrelated**: this would mean knowing the offspring count tells us nothing about their size, but a shared, capped resource pool ties the two together directly, so treating them as unrelated misses the whole trade-off.
4. **Positively and exponentially correlated**: like the linear case, this needs the budget to grow along with offspring number, growing even faster here, which again contradicts the idea of limited parental nutrients and care.

Think of it as a cake of fixed size: cutting more slices (more offspring) can only mean smaller slices (smaller offspring), never bigger ones. That is the essence of the offspring number and size trade-off in life history theory.

Let's summarize:

- Parental investment is treated as a fixed total budget.
- More offspring sharing that budget means each one gets less, so number and size trade off against each other, giving a negative correlation.

So offspring number and offspring size are expected to be negatively correlated.

Quick Tip: Treat total parental investment as a fixed pie that gets divided among the offspring; more slices means each slice, or offspring, is smaller, giving a negative relationship between number and size.

• • •

25. Which one of the following elements cycles the LEAST (mass per year) through the atmosphere?

(A) Carbon

(B) Nitrogen

(C) Phosphorus

(D) Sulphur

Correct Answer: (C) Phosphorus

SOLUTION:

Biogeochemical cycles differ a lot in how much of the element passes through the atmosphere each year, and that mostly comes down to whether the element has a common gas form.

1. **Carbon**: cycles heavily through the air as carbon dioxide, moving in and out of the atmosphere constantly via photosynthesis, respiration, decay and burning. This is one of the largest atmospheric fluxes of any element.
2. **Nitrogen**: makes up most of the atmosphere itself as N_2 gas, and even the smaller side reactions, like fixation and denitrification, still move enormous quantities of nitrogen gas each year.
3. **Phosphorus**: has no ordinary gas phase at all. Its entire cycle runs on solid and dissolved forms, moving through rock weathering, soil and water as phosphate ions, entering the air

only as dust, which carries a very small mass compared to a true gas cycle.
4. **Sulphur**: does have gas forms, such as sulphur dioxide from volcanoes and fuel burning and hydrogen sulphide from decomposition, so it still moves a meaningful mass through the atmosphere each year, even if usually less than carbon or nitrogen.

Since three of the four elements have real gas cycles and only phosphorus is stuck moving as dust and dissolved phosphate, phosphorus is by far the smallest atmospheric mover of the four.

Let's summarize:

- Having a common gas phase drives a large atmospheric flux; carbon, nitrogen and sulphur all have one.
- Phosphorus has no significant gas phase, so its atmospheric cycling is the smallest by far.

So phosphorus is the element that cycles the least mass per year through the atmosphere.

Quick Tip: Ask which element has no common gas form; carbon, nitrogen and sulphur all move through the atmosphere as gases, but phosphorus mainly cycles through rock, soil and water.

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26. The colour and markings of the eggs of the common cuckoo (Cuculus canorus) are similar to those of the eggs of the great reed warbler (Acrocephalus arundinaceus). Which one or more of the following options explain(s) this similarity?

(A) The two species are closely related and belong to the same genus

(B) The two species compete for the same insect larvae to feed their chicks

(C) The common cuckoo is a brood parasite of the great reed warbler

(D) The great reed warbler is a predator of the common cuckoo

Correct Answer: (C) The common cuckoo is a brood parasite of the great reed warbler

SOLUTION:

Cuckoo eggs and great reed warbler eggs look alike, and the question asks which relationship between the two birds would actually cause that kind of egg mimicry to evolve.

1. **Closely related, same genus**: the common cuckoo sits in the cuckoo family, while the great reed warbler sits in a completely different songbird family. They are not close relatives, so shared genes from a recent common ancestor cannot be the reason their eggs match.
2. **Compete for the same insect larvae**: sharing a food source might affect population numbers or foraging behaviour, but it gives no evolutionary reason for one species' egg pattern to start resembling the other's egg pattern.
3. **Common cuckoo is a brood parasite of the great reed warbler**: this fits perfectly. The cuckoo sneaks its egg into the warbler's nest and needs the warbler parents to accept and raise it. Any cuckoo egg that looks too different gets spotted and thrown out, so over many generations only cuckoo eggs that closely mimic the warbler's own egg colour and pattern survive to

be raised. That selection pressure is exactly why the two eggs end up looking alike.

4. **Great reed warbler preys on the common cuckoo**: warblers eat insects, not other birds, so this predator relationship does not exist, and even a real predator-prey link would not explain why one species' eggs mimic the other's.

Only the brood parasite relationship creates a real selective pressure for egg mimicry: the cuckoo's reproductive success depends on the host failing to notice the foreign egg, so cuckoo eggs are pushed toward looking like the host's own eggs generation after generation.

Let's summarize:

- Egg mimicry needs a reason for one species to benefit from copying another's egg pattern.
- Only brood parasitism, where the cuckoo's egg must fool the host into raising it, supplies that reason.

So the similarity in egg appearance is explained by the common cuckoo being a brood parasite of the great reed warbler.

Quick Tip: Ask which relationship would give a bird an evolutionary reason to copy another species' egg pattern; only a parasite laying its egg in the host's nest needs that egg to pass as the host's own.

• • •

27. Which one or more of the following is/are NOT essential for evolution by natural selection to take place in a population?

(A) There must be variation in the trait

(B) The trait must be linked with differential reproductive success

(C) The trait must be either fully or partially heritable

(D) The population must comprise of sexually reproducing organisms

Correct Answer: (D) The population must comprise of sexually reproducing organisms

SOLUTION:

This question is testing whether you know the actual minimum requirements for natural selection, as opposed to conditions that are common in nature but not logically necessary. Let's check each option one by one against that minimum list.

1. **There must be variation in the trait**: Needed. Selection can only pick among different trait values that already exist in the population; if everyone is identical there is nothing to select for or against.
2. **The trait must be linked with differential reproductive success**: Needed. This is the actual mechanism of selection: individuals with a certain trait value must, on average, leave more surviving offspring than individuals with other values.
3. **The trait must be either fully or partially heritable**: Needed. Even if a trait affects reproduction, the trait composition of the population will not change over generations unless offspring inherit that trait from their parents.
4. **The population must comprise of sexually reproducing organisms**: Not needed. Bacteria, many protists and clonal plants reproduce asexually yet still evolve by natural selection, as long as variation, heritability and fitness differences exist. Sex is a

separate biological phenomenon that is not part of the definition of natural selection.

Since variation, heritability, and a link to reproductive success are the three genuine pillars of natural selection, and none of them require sex, the condition that is NOT essential is the one about sexually reproducing organisms, option (D).

Let's summarize:

- Natural selection needs only three things: trait variation, heritability, and a fitness difference tied to the trait.
- Sexual reproduction speeds up the spread of new combinations of alleles through recombination, but it is not a precondition for selection itself.

So the correct choice is (D), since a population can evolve by natural selection whether it reproduces sexually or asexually.

Quick Tip: Recall the three basic requirements for natural selection: variation, heritability, and a link to reproductive success. Check if sexual reproduction is one of these three.

• • •

28. In a null hypothesis significance test, the significance level α was set to 0.01. For which one or more of the following p values would the null hypothesis be rejected?

(A) $p = 0.004$

(B) $p = 0.02$

(C) $p = 0.10$

(D) $p = 0.009$

Correct Answer: (A) p = 0.004 ; (D) p = 0.009

SOLUTION:

A p value tells us the probability of observing data at least as extreme as what we got, if the null hypothesis were actually true. The rule for rejecting the null hypothesis is simply to line up the p value against the significance level α, which is 0.01 here, and reject H_0 whenever the p value falls below it. Let's line up all four values against 0.01.

1. **p = 0.004**: Placing this on a number line against 0.01, it sits to the left, meaning it is smaller. So it clears the bar for rejection, and H_0 is rejected.
2. **p = 0.02**: This sits to the right of 0.01, meaning it is larger. The evidence against H_0 is not strong enough at this significance level, so we fail to reject H_0.
3. **p = 0.10**: This is far to the right of 0.01, clearly larger, so again we fail to reject H_0.
4. **p = 0.009**: This is just barely to the left of 0.01, so it is still smaller than α, and H_0 is rejected.

So only p = 0.004 and p = 0.009 fall below the 0.01 cutoff, and these are the two values for which the null hypothesis gets rejected.

Let's summarize:

- Reject H_0 only when $p < \alpha$; here that means p strictly less than 0.01.
- p = 0.02 and p = 0.10 are both larger than 0.01, so they do not give enough evidence to reject H_0.

Therefore, options (A) and (D) are the p values that lead to rejection of the null hypothesis.

Quick Tip: Reject the null hypothesis whenever the p value is smaller than the significance level $\alpha = 0.01$. Compare each option directly against 0.01.

• • •

29. Which one or more of the following benefits can explain the evolution of dispersal of animals from their natal area?

(A) Reduced competition with kin

(B) Increased predation risk outside natal areas

(C) Inbreeding avoidance

(D) Outbreeding avoidance

Correct Answer: (A) Reduced competition with kin ; (C) Inbreeding avoidance

SOLUTION:

Dispersal means an animal leaving the area where it was born to settle somewhere else. For any behaviour to be favoured by evolution it has to give a net fitness advantage, so this question is really asking us to sort the four listed outcomes into "helps fitness" versus "hurts fitness" or "unrelated benefit".

1. **Reduced competition with kin**: Staying home means competing with siblings and parents for the same limited food and mates. Leaving removes that competition, which is a clear fitness gain, so this is a genuine benefit.
2. **Increased predation risk outside natal areas**: This is a downside of moving through unfamiliar or exposed terrain, not a benefit. It works against dispersal evolving, so it does not belong in the list of benefits.

3. **Inbreeding avoidance**: Relatives living close together risk mating with each other, and inbred offspring often have lower survival. Dispersing away from the natal group lowers this risk, which is a real fitness benefit.
4. **Outbreeding avoidance**: This means avoiding mates that are too genetically different, which is actually the opposite pressure to what dispersal usually solves. Dispersal tends to increase mixing with less related individuals, so it does not serve outbreeding avoidance.

Putting it together, only reduced kin competition and inbreeding avoidance are true benefits that would push dispersal to evolve, while increased predation risk is a cost and outbreeding avoidance is not what dispersal achieves.

Let's summarize:

- A trait spreads only if it raises average fitness, so we must separate real benefits from costs.
- Reduced kin competition and inbreeding avoidance are the two classic, textbook benefits of natal dispersal.

So the correct options are (A) and (C).

Quick Tip: A benefit must raise fitness. Ask which options describe a cost of moving away rather than a genuine advantage, and which describe the wrong direction of avoidance.

• • •

30. Which one or more of the following is/are signalling mechanism(s) that birds are known to use to beg their parent for food?

(A) Playing dead

(B) Vocalisations

(C) Fluttering of wings

(D) Mouth gape and colouration

Correct Answer: (B) Vocalisations ; (C) Fluttering of wings ; (D) Mouth gape and colouration

SOLUTION:

Begging is how a helpless nestling communicates hunger to a parent bird, and it usually combines sound, movement, and visual display to grab the parent's attention over that of its nest mates. Let's go through each listed behaviour and ask whether it fits this role.

1. **Playing dead**: This behaviour, seen in some insects and reptiles, is used to avoid being detected or eaten by a predator, by looking lifeless. It is a survival tactic, completely unrelated to asking a parent for food, so it does not belong on the list of begging signals.
2. **Vocalisations**: Chicks calling loudly and repeatedly when a parent returns to the nest is one of the most familiar begging signals in birds, and louder or more frequent calls often mean a hungrier chick.
3. **Fluttering of wings**: Along with calling, chicks often flap their wings vigorously while begging. This visual and physical display reinforces the vocal signal and helps direct the parent's attention.
4. **Mouth gape and colouration**: The bright interior of a chick's open mouth is a striking visual target that guides the parent exactly where to place food, and its size and colour intensity can reflect the chick's need.

So three of the four listed behaviours, calling, wing fluttering, and gape display, are genuine begging signals used in parent-offspring communication, while playing dead belongs to a completely different behavioural category.

Let's summarize:

- Bird begging combines vocal, physical, and visual signals aimed at the parent.
- Playing dead is an anti-predator tactic, not a food-solicitation signal.

Therefore, the correct options are (B), (C) and (D).

Quick Tip: Think about which behaviours are actually directed at a parent bird to solicit food, versus a behaviour used to avoid predators.

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31. Which one or more of the following diseases is/are zoonotic?

(A) Nipah virus infection

(B) Ebola Haemorrhagic Fever

(C) Cholera

(D) Kyasanur Forest Disease

Correct Answer: (A) Nipah virus infection ; (B) Ebola Haemorrhagic Fever ; (D) Kyasanur Forest Disease

SOLUTION:

A disease earns the label "zoonotic" only when its pathogen is naturally maintained in an animal population and passes from that animal into humans. The quickest way to answer this question is to ask, for each disease, "does it need an animal host to keep circulating in nature?"

1. **Nipah virus infection**: Fruit bats are the natural reservoir of Nipah virus, and people become infected through bats, infected pigs, or bat-contaminated date palm sap. This clearly depends on an animal reservoir, so it is zoonotic.
2. **Ebola Haemorrhagic Fever**: Ebola virus persists in wildlife, most likely fruit bats, and outbreaks in humans typically start from contact with an infected animal or bushmeat before the virus spreads person to person. Because the chain starts in an animal reservoir, this is zoonotic.
3. **Cholera**: Cholera is caused by the bacterium *Vibrio cholerae*, spread through water or food contaminated by human waste. There is no animal reservoir required to keep this pathogen going, so cholera does not fit the zoonotic definition.
4. **Kyasanur Forest Disease**: This is spread by tick bites, with forest rodents and monkeys acting as the animal reservoir that keeps the virus circulating before ticks pass it on to humans. This dependence on an animal host makes it zoonotic.

Three of the four diseases trace back to an animal source, while cholera is a human-to-human or water-borne bacterial disease with no animal reservoir needed.

Let's summarize:

- Zoonotic means the pathogen's natural home is an animal population, from which it spills over to humans.
- Cholera spreads through contaminated water and human waste, not through an animal reservoir, so it is excluded.

So the correct options are (A), (B) and (D).

Quick Tip: Ask whether each pathogen has an animal reservoir it must pass through before infecting humans. Cholera spreads through contaminated water, not an animal host.

• • •

32. Which one or more of the following phenomena make(s) small populations vulnerable to extinction?

(A) Inbreeding depression

(B) Demographic stochasticity

(C) Intraguild predation

(D) Continuous population growth

Correct Answer: (A) Inbreeding depression ; (B) Demographic stochasticity

SOLUTION:

Conservation biologists have a fairly specific list of reasons why small populations are especially fragile, and this question is testing whether you can tell those genuine small-population risks apart from general ecological interactions or from a factor that actually reduces risk. Let's take the options one at a time.

1. **Inbreeding depression**: With fewer individuals to choose mates from, related individuals end up breeding with each other more often. This increases the odds that harmful recessive traits show up in offspring, reducing their survival and reproduction, which is a well known danger specific to small populations.

2. **Demographic stochasticity**: This is just random chance acting on individual life events, like who happens to die or what sex the offspring happen to be in a given year. In a big population these random swings cancel out, but in a small population an unlucky run of events can tip the group toward collapse, so this is also a genuine small-population risk.
3. **Intraguild predation**: This describes one competing species eating another, which is a general ecological interaction that can happen in populations of any size. It is not a phenomenon that specifically targets or worsens with small population size, so it does not belong in this list.
4. **Continuous population growth**: A population that is steadily growing is becoming less vulnerable, not more, since larger numbers give more of a buffer against random loss. This option describes the opposite of a risk factor.

Only inbreeding depression and demographic stochasticity are recognised mechanisms that specifically threaten small populations more than large ones.

Let's summarize:

- Small populations lose genetic diversity fast, causing inbreeding depression.
- Small populations cannot buffer random demographic swings the way large ones can, which is demographic stochasticity.

So the correct options are (A) and (B).

Quick Tip: Focus on mechanisms that get worse specifically as population size shrinks, not general predator-competitor interactions or population growth.

33. In a population of birds, the proportion of blue individuals is 0.4 and the proportion of males is 0.3. Assuming that colour and sex are independent of each other, the probability that a randomly sampled individual from this population is a blue male is ________ (Round off to two decimal places)

Correct Answer: 0.12

SOLUTION:

Step 1: Set up the events.
Let B be the event that an individual is blue, so $P(B) = 0.4$. Let M be the event that an individual is male, so $P(M) = 0.3$. We want the probability that both B and M happen for the same individual, written $P(B \cap M)$.

Step 2: Apply the independence rule.
The question states colour and sex are independent of each other. For two independent events, knowing one event happened tells you nothing about whether the other happened, and the joint probability is found simply by multiplying the two separate probabilities together:

$$P(B \cap M) = P(B) \cdot P(M)$$

This is different from events that are dependent, where you would instead need a conditional probability like $P(M \mid B)$, which is not required here since independence is explicitly given.

Step 3: Substitute and compute.

$$P(B \cap M) = 0.4 \times 0.3 = 0.12$$

We can also sanity check this using a simple table: imagine 1000 birds. 400 of them are blue (0.4 x 1000). Among any subgroup, 30 percent are expected to be male, since sex is independent of colour, so 30 percent of those 400 blue birds, which is 120 birds, are blue males. That gives 120 out of 1000, or 0.12, matching the direct multiplication.

Step 4: Final answer.

Rounded to two decimal places, the probability of picking a blue male at random is 0.12.

$$\boxed{0.12}$$

Quick Tip: Since colour and sex are independent, multiply the individual probabilities: P(blue) x P(male).

• • •

34. Assume that the human haploid genome is 3×10^9 base pairs long. The mutation rate, when DNA is copied, is 5×10^{-11} per base pair per replication. Based on these numbers, the expected number of mutations that take place per replication of the human haploid genome is ________ (Round off to two decimal places)

Correct Answer: 0.15

SOLUTION:

Step 1: Think of it as summing many tiny probabilities.

Each one of the 3×10^9 base pairs in the haploid genome has an independent, very small chance, 5×10^{-11}, of picking up a mutation during a single replication. The expected number of mutations across the whole genome is just the sum of these individual per-base-pair probabilities, since expectation is additive even when the underlying events are rare and independent.

Step 2: Write the sum as a product.
Since every one of the 3×10^9 base pairs contributes the same small probability 5×10^{-11} to the expected count, the sum of 3×10^9 identical terms is just that number of terms times one term:

$$E[\text{mutations}] = (3 \times 10^9) \times (5 \times 10^{-11})$$

Step 3: Simplify using powers of ten.
Group the plain numbers and the powers of ten separately:

$$3 \times 5 = 15, \qquad 10^9 \times 10^{-11} = 10^{9-11} = 10^{-2}$$

$$E[\text{mutations}] = 15 \times 10^{-2}$$

Converting 15×10^{-2} to decimal form gives 0.15, since dividing 15 by 100 shifts the decimal point two places left.

Step 4: Final answer.
So on average, about 0.15 mutations occur across the entire human haploid genome every time it is replicated, meaning roughly one mutation shows up every six or seven replications rather than every single one.

$\boxed{0.15}$

Quick Tip: Multiply the total genome length in base pairs by the per-base-pair mutation rate: (3 x 10^9) x (5 x 10^-11).

• • •

35. The coefficient of relatedness *r* is the probability that a gene in one individual is identical by descent with a gene in another individual. In a large, diploid, sexually reproducing population with outbreeding, the value of *r* for two offspring with the same mother but different fathers is ____________ (round off to two decimal places).

Correct Answer: 0.25

SOLUTION:

Step 1: Split each offspring's genome by parent.

Every offspring gets half its genes from its mother and half from its father. Since the two offspring here have different, unrelated fathers, none of the paternal genes can match between them. Only the maternal half of each genome can possibly be shared.

Step 2: Work out how much of the maternal share can match.

At any single gene, the mother carries two versions and passes on only one copy to each child, picked at random. So there is a 1/2 chance that offspring X and offspring Y both happen to receive the same copy from her at that gene.

Step 3: Combine the two fractions.

The genes that could possibly be shared make up 1/2 of each offspring's genome (the maternal half), and within that half there is a 1/2 chance of getting the identical copy. Multiply the two:

$$\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$$

Step 4: State the result.

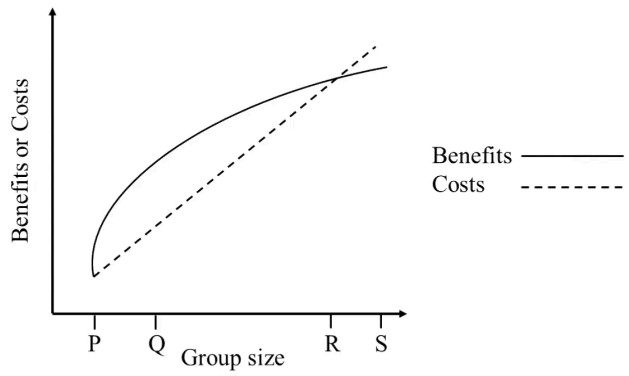
So on average, a quarter of the genes in these two half sibs trace back to the identical copy in their mother. This fraction is exactly the coefficient of relatedness.

$$\boxed{r = 0.25}$$

Quick Tip: Half sibs share only one parent, so relatedness is half that of full sibs: use $r = (1/2)^L$ with L equal to the number of links through the shared parent.

• • •

36. Living in groups gives benefits but also brings costs. The graph below plots per capita benefits (solid line) and per capita costs (dashed line), both measured in the same units, against group size. Four group sizes are marked on the x axis: P, Q, R, and S.



Given these patterns in benefits and costs, which one of the group sizes P, Q, R, S best represents the optimal group size?

(A) P

(B) Q

(C) R

(D) S

Correct Answer: (B) Q

SOLUTION:

Step 1: Use the marginal rule instead of reading the gap by eye.
An individual should keep joining a bigger group only as long as each extra member adds more benefit than cost. The best group size is where the extra (marginal) benefit from one more member just equals the extra (marginal) cost.

Step 2: Compare the slopes of the two curves.

The cost line is straight, so its slope, the marginal cost, stays the same at every group size. The benefit curve is steep at first and then flattens, so its slope, the marginal benefit, starts high and keeps falling as the group grows.

Step 3: Find where the two slopes match.

Right after P the benefit curve's slope is much higher than the cost line's slope, so adding members still helps. As the group keeps growing the benefit slope keeps dropping. At Q, the falling marginal benefit meets the constant marginal cost, so no further group size adds more gain than pain.

Step 4: Check the ends for confirmation.

Before Q the marginal benefit is still above marginal cost, so growing the group helps. After Q, at R and S, marginal cost has caught up to and overtaken marginal benefit, so each new member does more harm than good and net benefit falls.

Step 5: State the optimum.

The group size where marginal benefit equals marginal cost, and total net benefit peaks, is

$$\boxed{Q}$$

Quick Tip: Optimal group size is where the vertical gap between the benefit curve and the cost curve is largest, not where the curves cross.

• • •

37. The table below gives the abundance of species 1 to 10 in three communities, P, Q, and R, each with a total of 100 individuals. Simpson's diversity index for a community is

$$D = 1 - \sum_i p_i^2,$$

where p_i is the proportion of individuals in the community belonging to the i^{th} species.

Species	**Community P**	**Community Q**	**Community R**
1	69	45	70
2	18	43	21
3	5	4	4
4	4	3	5
5	1	1	0
6	1	1	0
7	0	0	1
8	1	1	0
9	0	0	1
10	1	1	0

Which one of the following statements is true about the comparison of Simpson's index between these communities?

(A) P is more similar to Q than either of them is to R

(B) P is more similar to R than either of them is to Q

(C) Q is more similar to R than either of them is to P

(D) P, Q, and R are equally similar to each other

Correct Answer: (B) P is more similar to R than either of them is to Q

SOLUTION:

Step 1: Look at how each community is dominated before doing any sums.

In community P, one species (species 1) makes up 69 out of 100 individuals, and a second species (species 2) adds another 18. So the top two species already cover 87 individuals, leaving very few for the rest.

In community R, the pattern is almost the same: species 1 has 70 and species 2 has 21, again covering 91 of the 100 individuals.

In community Q, however, species 1 has only 45 and species 2 has 43, so the two top species are close in size and together cover 88, but no single species dominates the way it does in P or R.

Step 2: Connect dominance to the diversity index.

Simpson's index falls when one species dominates, because a big p_i contributes a large p_i^2 term. Since P and R are both heavily dominated by a single species in a similar way, their index values should sit close together and lower than Q's. Q, being more even between its top two species, should carry a noticeably higher index.

Step 3: Confirm with the actual numbers.

Working out $D = 1 - \frac{\sum n_i^2}{10000}$ for each community gives

$$D_P = 0.487, \quad D_Q = 0.610, \quad D_R = 0.462$$

This matches the pattern spotted from the raw counts: Q sits well above the other two, while P and R are close together, only about 0.025 apart.

Step 4: Conclude.

Since P and R have the two closest Simpson's index values, they are the most similar pair.

$$\boxed{\text{P is more similar to R than either of them is to Q}}$$

Quick Tip: Work out $D = 1 - \Sigma p_i^2$ for each community and compare, or notice that P and R are both dominated by one species while Q is more even.

• • •

38. Many species of reef fish change sex once during the course of their lives. In these fish, a bigger body size increases an individual's competitive ability. When strong male-male competition creates high variance in fitness among males, which one of the following scenarios is most likely?

(A) Fish start their reproductive life as females and become males at larger sizes

(B) Fish start their reproductive life as males and become females at larger sizes

(C) Female-female competition leads to male sterility

(D) Male-male competition does not influence the sequence of sex change in an individual

Correct Answer: (A) Fish start their reproductive life as females and become males at larger sizes

SOLUTION:

Step 1: Picture two reproductive value curves.

Imagine plotting expected reproductive success against body size separately for a male and for a female of this species. Sex change theory says an individual should be the sex with the higher curve at small sizes, then switch to the other sex once its curve overtakes.

Step 2: Work out which curve is steeper here.
The question tells us male-male competition is intense and creates high variance in male fitness. That means a handful of large, dominant males get almost all the matings, while small males get close to none. So the male reproductive curve is flat and low at small sizes, then rises steeply at large sizes.

Step 3: Compare with the female curve.
Female reproductive success usually rises more gradually with size, since egg production scales more smoothly with body size and does not depend on winning fights. So at small sizes, the female curve sits above the male curve.

Step 4: Decide the order of sex change.
Since the female curve is higher at small size and the male curve is higher at large size, an individual gains the most lifetime reproductive success by starting as a female and switching to male once it grows large enough to win competitive contests.

Step 5: Rule out the alternatives.
Starting as a male and switching to female late (option B) would apply only if the female curve rose steeply with size instead, the reverse of this setup. Sterility from female-female competition (option C) is not mentioned anywhere. Saying competition has no effect on sex change order (option D) contradicts the entire logic of the size-advantage model.

Step 6: Conclude.

$$\boxed{\text{Fish start life as females and become males at larger sizes}}$$

Quick Tip: Whichever sex gains the most reproductive success from being large should come second; here that is the male role, so the fish start as females.

• • •

39. When comparing life-history traits across animal species, which one of the following relationships is LEAST expected under r-selection and K-selection theory?

(A) Development time is positively correlated with age at first reproduction

(B) Development time is negatively correlated with lifespan

(C) Lifespan is positively correlated with body size

(D) Lifespan is negatively correlated with number of offspring per breeding attempt

Correct Answer: (B) Development time is negatively correlated with lifespan

SOLUTION:

Step 1: Sort species into a fast-slow spectrum.

Think of every species sitting somewhere on a line from fast (r-selected) to slow (K-selected). A fast species develops quickly, breeds young, dies young, stays small and throws out many young each time.

A slow species does the reverse on every one of these traits.

Step 2: Ask whether each pair of traits sits on the same side or opposite sides of that line.
Development time and age at first reproduction: both are small numbers for fast species and both are large numbers for slow species. Same side, so positive correlation, matching option (A).
Lifespan and body size: both small for fast species, both large for slow species. Same side, so positive correlation, matching option (C).
Lifespan and offspring per breeding attempt: fast species have short lives but many offspring, slow species have long lives but few offspring. These sit on opposite sides, so negative correlation, matching option (D).

Step 3: Now test option (B).
Development time and lifespan: a fast species has short development and a short life, both small. A slow species has long development and a long life, both large. These sit on the same side of the spectrum, so they should be positively correlated, not negatively.

Step 4: Spot the mismatch.
Only option (B) claims a negative correlation for two traits that the theory actually places on the same side of the fast-slow spectrum. Every other option correctly matches how the theory groups its traits.

Step 5: Conclude.

$$\boxed{\text{Development time is negatively correlated with lifespan}}$$

Quick Tip: r and K selected traits cluster together on a fast-slow spectrum; look for the one pair placed on opposite sides that the theory actually groups on the same side.

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40. Two isolated populations M and N have population sizes of 100 and 1000 individuals, respectively. The starting allele frequencies p and q are 0.5 in both populations. Assuming no selection, which one of the following is expected after 100 generations?

(A) p is expected to be higher than q in population M but not in population N

(B) p is expected to be lower than q in population M but not in population N

(C) $2pq$ in population M is expected to be higher than $2pq$ in population N

(D) $2pq$ in population M is expected to be lower than $2pq$ in population N

Correct Answer: (D) $2pq$ in population M is expected to be lower than $2pq$ in population N

SOLUTION:

Step 1: Bring in the drift variance formula.

The variance added to an allele frequency each generation by drift is

$$\mathrm{Var}(\Delta p) = \frac{p(1-p)}{2N}$$

where N is the population size. This tells us directly that a smaller N gives a bigger variance, meaning bigger random jumps in p from one generation to the next.

Step 2: Plug in the two population sizes.

For M, $N = 100$, so the variance term has $2N = 200$ in the denominator. For N, $N = 1000$, so the denominator is $2N = 2000$, ten times larger. This means the per generation variance in p for M is about ten times that for N.

Step 3: Add up drift over 100 generations.

Repeated random steps accumulate, so after 100 generations the spread of possible p values around 0.5 is much wider for M than for N. In population M, p is far more likely to have wandered close to 0 or 1 by now.

Step 4: Translate spread in p into heterozygosity.

$2pq$ peaks at $p = 0.5$ and falls as p moves toward either extreme. Since M's p has likely wandered further from 0.5 than N's, M's expected $2pq$ is lower.

Step 5: Address the directional options.

Options (A) and (B) claim p ends up on a particular side of q in one population. But the drift process is symmetric around 0.5, so neither direction is favored in either population, which rules both out.

Step 6: Conclude.

The smaller population loses heterozygosity faster.

$$\boxed{2pq_M < 2pq_N}$$

Quick Tip: Genetic drift is stronger in smaller populations, so heterozygosity ($2pq$) is lost faster in the smaller population M.

• • •

41. Two bacterial variants are growing together in the same flask. At any relative frequency of the two variants, the population growth rate of the rarer variant is higher. This is an example of _________.

(A) sexual selection

(B) positive selection

(C) negative frequency-dependent selection

(D) positive frequency-dependent selection

Correct Answer: (C) negative frequency-dependent selection

SOLUTION:

Step 1: Think of growth rate as a function of frequency.
Imagine plotting the growth rate of variant one against its own frequency in the flask, from nearly 0 to nearly 1. The question tells us this growth rate is high whenever the frequency is low, and falls as the frequency rises.

Step 2: Read what that downward-sloping relationship means.
A fitness curve that goes down as frequency goes up means being common actually hurts a type, while being rare helps it. That is precisely the definition used for the "negative" case in frequency dependent selection, since the fitness effect moves in the opposite direction to the frequency.

Step 3: Contrast with the "positive" case.

If growth rate instead rose alongside frequency, common types would keep getting fitter and rarer types would keep losing out until one type disappeared. That upward-sloping relationship is positive frequency dependence, the reverse of what is described here.

Step 4: Note the stabilizing outcome.

Because the rare type always gets the advantage in this flask, neither variant can be driven to extinction. Any drop in frequency for one variant is met with a rise in its own growth rate, pulling the mix back toward balance.

Step 5: Eliminate sexual and plain positive selection.

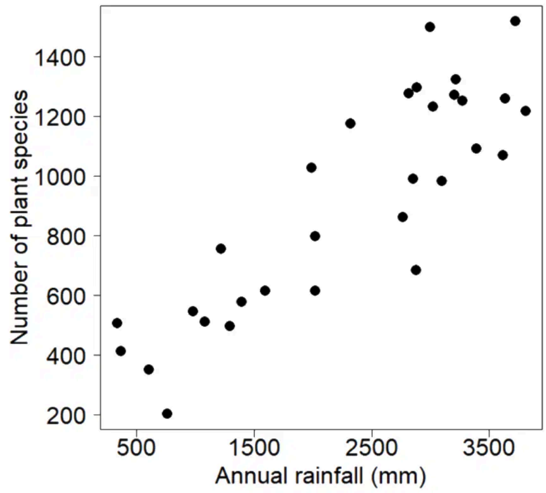
Sexual selection involves mate competition or mate preference, which is not mentioned at all here. Plain positive selection just means a trait is favored, without saying anything about how that favor changes with frequency, so it is too vague to match this specific pattern.

Step 6: Conclude.

$$\boxed{\text{Negative frequency-dependent selection}}$$

Quick Tip: Fitness of the rarer type being higher, no matter the frequency, is the definition of negative frequency-dependent selection.

42. The scatter plot below shows annual rainfall (in mm) on the x axis and the number of plant species recorded at a site on the y axis. Each point is one location, and the points trace out a clear increasing pattern that looks close to a straight line as rainfall rises.



Based on the pattern in the graph, which one of the following statistical methods would be most appropriate to model the relationship between annual rainfall and the number of plant species?

(A) Kruskal-Wallis test

(B) Student's t-test

(C) Linear regression

(D) Chi-squared test

Correct Answer: (C) Linear regression

SOLUTION:

Step 1: Ask what each candidate test actually needs.

Before looking at the picture, it helps to remember what each of the four listed methods requires. The Kruskal-Wallis test and Student's t-test both need a categorical grouping variable (two groups for the t-test, three or more for Kruskal-Wallis) plus a measured outcome for each group. The chi-squared test needs two categorical variables summarized as counts in a table. Linear regression needs two continuous, numeric variables where one is thought to depend on or track the other.

Step 2: Check what variables we actually have.
Here both variables, annual rainfall and number of plant species, are continuous measurements, not category labels. There is no grouping factor anywhere in the description, and nothing is being counted into categories.

Step 3: Eliminate the mismatched tests.
Since there is no grouping variable, the Kruskal-Wallis test and the t-test cannot apply. Since neither variable is categorical, the chi-squared test cannot apply either. Only linear regression is built to handle two continuous variables at once.

Step 4: Confirm using the scatter plot's shape.
The points climb steadily from the bottom left to the top right of the plot without bending back on themselves or breaking into separate clusters, the classic sign of a straight-line, linear trend, exactly the pattern linear regression is meant to summarize.

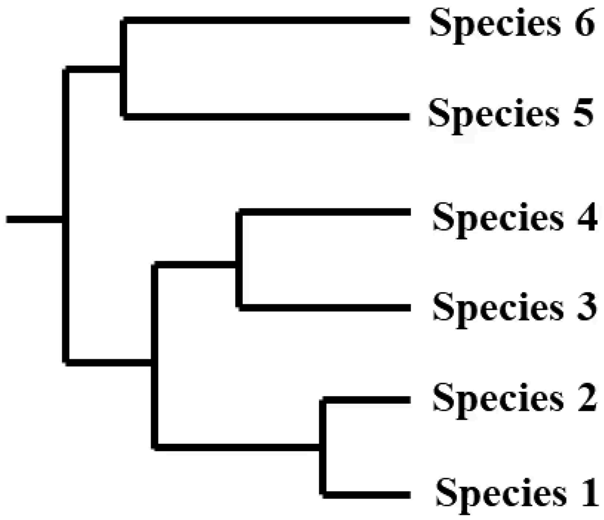
Step 5: Conclude.

$$\boxed{\text{Linear regression}}$$

> **Quick Tip:** Both rainfall and species number are continuous variables with a straight-line trend, so use linear regression, not a categorical-group test.

• • •

43. The phylogeny of six species of birds (Species 1 to Species 6) is illustrated below, drawn so that horizontal branch lengths correspond to genetic distance between the species. These six species are distributed across three islands: Island X harbours Species 1, 4, and 6; Island Y harbours Species 1, 2, and 4; and Island Z harbours Species 3, 4, and 5.



Which one of the following is true about the phylogenetic diversity of these islands?

(A) X > Y > Z

(B) X < Y < Z

(C) X > Y and Z > Y

(D) X < Y and Z < Y

Correct Answer: (C) X > Y and Z > Y

SOLUTION:

Step 1: Spot the oldest common ancestor split.
Right after the root, the tree forks into two branches: one holds Species 5 and Species 6, the other holds Species 1, 2, 3 and 4. This fork is the oldest, and so the longest, split on the whole tree.

Step 2: Place each island's species on the tree.
Island Y has Species 1, 2 and 4, and every one of them sits on the side with Species 1, 2, 3, 4. None of Island Y's birds is on the Species 5, 6 side. Island X has Species 1, 4 and 6. Species 6 is on the Species 5, 6 side, while 1 and 4 are on the other side. Island Z has Species 3, 4 and 5. Species 5 is on the Species 5, 6 side, while 3 and 4 are on the other side.

Step 3: Think of phylogenetic diversity as a travel distance.
Imagine tracing the shortest path along the tree that touches every species on an island. The total length of that path is the phylogenetic diversity of the island. For Island Y, since all three birds sit on the same side of the oldest fork, the path never needs to use that fork's long branch, so the trip stays short. For Island X and Island Z, one bird sits on the far side of the oldest fork, so the path is forced to walk all the way back through that long branch and out again, making the trip much longer.

Step 4: Draw the comparison.
Since both X and Z are forced to use the same long, deep branch that Y never touches, both X and Z end up with a bigger total path length than Y. Between X and Z themselves, both pay for the same deep branch, so this reasoning alone cannot say which of the two is larger.

Step 5: Pick the option that fits.

An option that ranks all three strictly, putting X above or below Z, claims more than the tree supports. The one that only says X is bigger than Y and Z is bigger than Y is exactly what the tree tells us.

$$\boxed{X > Y \text{ and } Z > Y}$$

Quick Tip: Compare how much of the tree's branch length (genetic distance) is needed to connect each island's species; islands whose species span across the deep split near the root end up with higher phylogenetic diversity.

• • •

44. Terrestrial biomes such as tundra, taiga, temperate forests, and tropical forests are distributed in different parts of the world. Which one of the following options best represents the environmental factors that determine the distribution of these biomes?

(A) Temperature and elevation

(B) Rainfall and wind

(C) Temperature and rainfall

(D) Fire and elevation

Correct Answer: (C) Temperature and rainfall

SOLUTION:

This question checks whether you know the two climate variables ecologists use to draw the world's biome map. Let's go through each option.

1. **Temperature and elevation**: Elevation changes climate locally, it gets colder as you climb a mountain, but elevation is not

one of the two standard axes used to separate biome types across the globe. It explains local zonation, not the big picture.
2. **Rainfall and wind**: Rainfall is one of the right factors, but wind is not part of the classic biome model. Wind affects things like tree shape and water loss locally, but is not used to draw biome boundaries.
3. **Temperature and rainfall**: This is the standard pair. Plotting mean annual temperature against mean annual rainfall on a graph (the Whittaker biome diagram) sorts land area into tundra, taiga, temperate forest, tropical forest, grassland, and desert.
4. **Fire and elevation**: Fire shapes some biomes such as savanna at a finer scale, and elevation drives local alpine zones, but neither is the main pair of factors used to separate biomes worldwide.

The correct pairing is temperature and rainfall, since together they explain why the same latitude can have desert in one place and rainforest in another, depending on how much rain falls.

Let's summarize:

- Terrestrial biomes are mapped along two climate axes: temperature and rainfall.
- Elevation, fire, and wind matter, but only as local modifiers, not the primary global factors.

So the environmental factors that determine biome distribution are temperature and rainfall.

Quick Tip: Biome maps, like the Whittaker biome diagram, are built from just two climate axes.

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45. In a population, the frequency of an allele changes with time as shown in the table below.

Year (x)	0	10	20	30	40
Allele frequency (y)	0.1	0.2	0.3	0.4	0.5

Which one of the following describes how allele frequency changes with year?

(A) $y = 0.01x + 0.1$

(B) $x = y + 0.1$

(C) $x = 0.1 + 0.01y$

(D) $y = x + 0.1$

Correct Answer: (A) $y = 0.01x + 0.1$

SOLUTION:

Step 1: Set up the general line.
A straight line through the data can be written as $y = mx + c$, where m is the slope and c is the value of y when $x = 0$.

Step 2: Read c straight off the table.
When the year $x = 0$, the table already gives $y = 0.1$. So $c = 0.1$ without any extra work.

Step 3: Get m from the two ends of the table.
Using the first point $(0, 0.1)$ and the last point $(40, 0.5)$,

$$m = \frac{0.5 - 0.1}{40 - 0} = \frac{0.4}{40} = 0.01$$

Step 4: Write the fitted line.

$$y = 0.01x + 0.1$$

Step 5: Confirm with a middle row, not just the ends.

At $x = 20$, the formula gives $y = 0.01(20) + 0.1 = 0.3$, exactly the value the table shows. This confirms the fit is not a coincidence of the endpoints.

Step 6: Reject the flipped options.

Options that write x in terms of y, like $x = y + 0.1$ or $x = 0.1 + 0.01y$, mix up which variable is doing the changing. Since year is the input and allele frequency is the output here, y should be written in terms of x, not the other way round, and neither flipped option even satisfies the table's numbers when tested directly.

Step 7: Conclude.

$$\boxed{y = 0.01x + 0.1}$$

Quick Tip: Find the slope from any two points in the table, then check which equation matches both the slope and the intercept.

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46. Despite their striking morphological similarity to each other, Old World and New World vultures are not phylogenetically related. Old World vultures are most closely related to eagles, while New World vultures are most closely related to storks. The morphological similarity between Old World and New World vultures is an example of

______________.

(A) adaptive radiation

(B) cladogenesis

(C) divergent evolution

(D) convergent evolution

Correct Answer: (D) convergent evolution

SOLUTION:

The question tells us two things: the vultures look alike, and they are not close relatives, since Old World vultures sit with eagles and New World vultures sit with storks on the bird family tree. We need the term for lineages that resemble each other without sharing recent ancestry. Let's check every option.

1. **Adaptive radiation**: This happens when one ancestor quickly splits into many different species that fill many different niches, like Darwin's finches. Here we start from two separate lineages, not one radiating ancestor, so this term does not fit.
2. **Cladogenesis**: This is just the general term for a lineage splitting into two. It says nothing about why two unrelated lineages would end up looking similar, so it does not explain the pattern described.
3. **Divergent evolution**: This describes related species drifting apart in appearance from a shared ancestor. The vultures are

doing the opposite, converging in looks despite not sharing a recent ancestor, so this is wrong.

4. **Convergent evolution**: This is exactly what happens when unrelated lineages independently evolve similar traits because they face similar pressures, here, a scavenging lifestyle. This fits the vulture case perfectly.

Since both vulture groups evolved their look independently while filling the same scavenger role, the answer is convergent evolution.

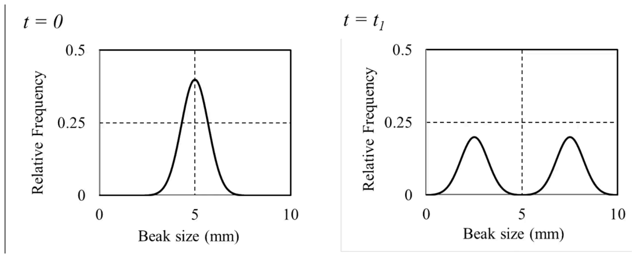
Let's summarize:

- Shared ancestry gives you divergent evolution or adaptive radiation.
- Shared lifestyle without shared ancestry gives you convergent evolution.

So Old World and New World vultures looking alike is a case of convergent evolution.

Quick Tip: Check whether the two lineages are close relatives, which would suggest shared ancestry, or distant relatives that ended up looking alike because of a similar lifestyle.

47. The distributions of beak size in a bird population at two different times, $t = 0$ and $t = t_1$, are shown below. At $t = 0$ beak sizes form a single narrow peak centred around 5 mm. By $t = t_1$ the distribution has split into two separate peaks, one smaller and one larger than 5 mm, with very few birds still having a beak size close to 5 mm.



In going from time $t = 0$ to $t = t_1$, the variance of the distribution in beak size in the population has ___________.

(A) increased

(B) decreased

(C) reduced to zero

(D) stayed the same

Correct Answer: (A) increased

SOLUTION:

Step 1: Picture the two snapshots.
At $t = 0$ nearly every bird has almost the same beak size, so the population looks like one tight cluster on the beak size axis. At $t = t_1$ that cluster has broken into two separate clusters sitting apart from each other, with a gap in the middle where the old average used to be.

Step 2: Connect this to variance directly.
Variance adds up the squared distance of every bird's beak size from the population mean. When birds are packed close to the mean, those

squared distances are small, and variance is small. When birds move away from the mean into two separated groups, those squared distances grow, and variance grows with them.

Step 3: Notice this is disruptive selection.

A single peak breaking into two peaks, with the middle emptying out, is the textbook signature of disruptive selection: individuals with average trait values do worse than individuals with extreme trait values, so the extremes become more common over time and the middle becomes rarer.

Step 4: See why the other choices fail.

"Decreased" or "stayed the same" would only make sense if the population had become more uniform or unchanged, but the figure shows the opposite, a single group turning into two separated groups. "Reduced to zero" would mean every bird ended up with the exact same beak size, which is not what the two peaked curve at $t = t_1$ shows.

Step 5: Conclude.

Since birds are now, on average, farther from the mean than before, the variance has grown.

$$\boxed{\text{Increased}}$$

Quick Tip: Variance measures how spread out the values are from the mean; compare how far the bulk of the birds sit from 5 mm at each time point.

48. Percent sequence divergences between two sister species were calculated for an exon (E), an intron (I), and the flanking neutral (N) region of a gene that is under purifying selection. Which one of the following options best describes the expected divergence in E, I, and N between the sister species?

(A) $E > I > N$

(B) $E > I = N$

(C) $E < I = N$

(D) $E = I > N$

Correct Answer: (C) $E < I = N$

SOLUTION:

Step 1: Set up what "divergence" means here.

Percent divergence just means how many bases differ between the two sister species at that spot in the genome, expressed as a percentage. A region that mutates faster, or whose mutations are not removed, ends up with higher divergence over the same span of time.

Step 2: Think about what happens to a mutation in each region.

A mutation inside the exon usually changes the protein the gene builds. Since the gene is under purifying selection, protein changing mutations tend to be harmful, and natural selection removes carriers of those mutations from the population, so most new mutations in the exon never spread and never show up as a fixed difference between species. A mutation inside the intron, or in the flanking region outside the gene, usually has no effect on any protein, since introns get spliced out and flanking DNA is not part of the coding sequence. With no protein effect, selection mostly ignores these mutations, and they drift to fixation at close to the background mutation rate.

Step 3: Compare the three regions using this logic.

The exon (E) is filtered by selection, so its divergence stays low. The intron (I) and the flanking neutral region (N) are both essentially unfiltered, so they should build up differences at a similar pace, giving $I \approx N$, and both should be higher than E.

Step 4: Check each answer choice against this.

Any option placing E above I or N is backwards, since selection suppresses divergence in the exon rather than raising it. The option placing E equal to I ignores the fact that the exon is specifically constrained while the intron is not.

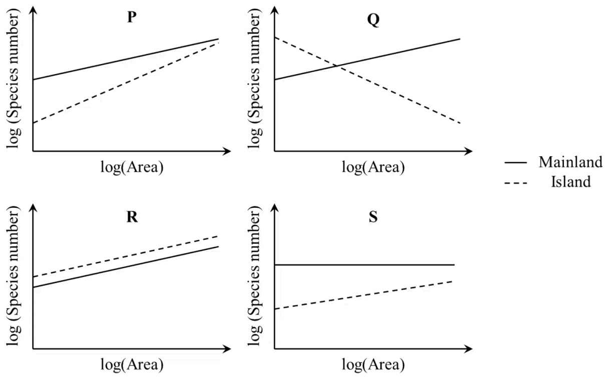
Step 5: Conclude.

Only the ranking where the exon diverges the least, and the intron and neutral region diverge about equally and more, matches how purifying selection actually works.

$$\boxed{E < I = N}$$

Quick Tip: Purifying selection removes mutations in the coding exon that change the protein, while introns and flanking neutral regions build up mutations at a similar, unconstrained rate.

49. Islands typically have higher species extinction rates and are more isolated from sources of colonists than the mainland. The four panels below (P, Q, R, S) each plot the log of species number against the log of area, with a solid line for the mainland relationship and a dashed line for islands of different sizes.



Which one of the figures above represents the most likely relationship between species richness and area for mainland versus island sites?

(A) P

(B) Q

(C) R

(D) S

Correct Answer: (A) P

SOLUTION:

This question is about the classic island biogeography pattern: mainland areas and islands both gain species as area grows, but islands lag behind because they are harder to colonise and lose species faster. Let's check each panel against that expectation.

1. **Panel P**: The mainland (solid) line starts above the island (dashed) line and both climb, with the island's line climbing more

steeply and catching up as area grows. This matches both parts of the expected pattern, islands hold fewer species at a given area, and the gap narrows as area increases, since bigger islands act more like scaled down mainlands.

2. **Panel Q**: Here the mainland line rises while the island line actually falls as area grows, and the two lines cross. There is no ecological reason for island richness to decline as island area increases, so this panel does not fit.
3. **Panel R**: Here the dashed island line sits above the solid mainland line across the whole range. This would mean islands host more species than equally sized mainland areas, which contradicts the higher isolation and extinction rates islands are known to have.
4. **Panel S**: Here the mainland line is completely flat, showing no change in richness with area at all. Since larger mainland areas reliably support more species, a flat mainland line does not match real data.

Only Panel P keeps the mainland above the island, matching lower island richness, while letting the island's steeper climb close the gap as area increases, matching how small islands are disproportionately species poor.

Let's summarize:

- Both mainland and island species richness rise with area.
- At a given area, islands hold fewer species than the mainland because they are more isolated and lose species faster.
- The island species-area slope is typically steeper than the mainland's.

So Panel P is the figure that matches the real, observed relationship.

Quick Tip: Islands should have fewer species than a mainland area of the same size due to isolation and extinction, but the island species-area relationship usually rises more steeply with area than the mainland's.

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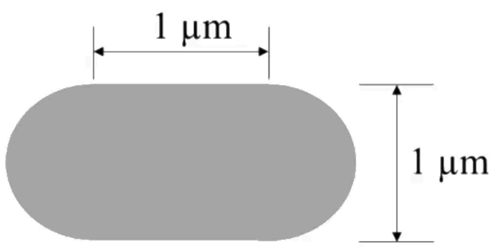
50. A bacterium can be approximated as a cylinder with a hemisphere capping each end, as shown in the figure. The cylinder has a height of 1 μm and a diameter of 1 μm, so the two end hemispheres share the same radius as the cylinder.



Assuming that the density of the bacterium equals that of water, what is the approximate mass of this bacterium?
Given: density of water = 10^3 kg/m^3; $1\ \mu m = 10^{-6}\ m$.
Volume of a cylinder = $\pi r^2 h$, where r is the radius and h is the height of the cylinder.
Volume of a sphere = $\frac{4}{3}\pi r^3$, where r is the radius of the sphere.

(A) 10^{-12} kg

(B) 10^{-18} g

(C) 10^{-15} kg

(D) 10^{-15} g

Correct Answer: (C) 10^{-15} kg

SOLUTION:

Step 1: Work in centimetres and grams instead of metres and kilograms.
Since $1\ \mu m = 10^{-4}\ cm$, the cylinder's radius is $r = 0.5 \times 10^{-4}\ cm = 5 \times 10^{-5}\ cm$, and its height is $h = 10^{-4}\ cm$. Water's density in these units is a clean number, $\rho = 1\ g/cm^3$.

Step 2: Find the cylinder volume.

$$V_{cyl} = \pi r^2 h = \pi(5 \times 10^{-5})^2(10^{-4}) = \pi(2.5 \times 10^{-9})(10^{-4}) = 2.5\pi \times 10^{-13}\ cm^3$$

Numerically, $V_{cyl} \approx 7.85 \times 10^{-13}\ cm^3$.

Step 3: Add the two hemispherical caps as one sphere.

$$V_{sph} = \frac{4}{3}\pi r^3 = \frac{4}{3}\pi(5 \times 10^{-5})^3 = \frac{4}{3}\pi(1.25 \times 10^{-13}) \approx 5.24 \times 10^{-13}\ cm^3$$

Step 4: Add the two volumes.

$$V_{total} \approx 7.85 \times 10^{-13} + 5.24 \times 10^{-13} = 1.31 \times 10^{-12}\ cm^3$$

Step 5: Convert straight to mass, since $\rho = 1\ g/cm^3$.

$$m = \rho V \approx 1.31 \times 10^{-12}\ g$$

Step 6: Convert grams back to kilograms to compare with the options.

$$m \approx 1.31 \times 10^{-12}\ g = 1.31 \times 10^{-15}\ kg$$

This confirms the same answer reached by working directly in SI units, the choice of unit system does not change the physical mass, only how the number looks partway through.

Step 7: Conclude.

$$\boxed{10^{-15}\ kg}$$

Quick Tip: The two end hemispheres together make exactly one full sphere of the same radius as the cylinder; add that sphere's volume to the cylinder's volume before converting to mass.

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51. Students M and N sampled body lengths of two populations of a fish species using the same study design. The table below summarizes their data as mean ± standard error.

Body length (cm)	Population I	Population II
Student M	8.0 ± 1.2	6.2 ± 0.7
Student N	10.0 ± 0.6	5.1 ± 0.3

Given that the data are normally distributed, when comparing the means of the populations using a t-test, which student will find a lower p-value?

(A) Student M

(B) Student N

(C) Insufficient information to comment

(D) p-values will be zero in both cases

Correct Answer: (B) Student N

SOLUTION:

Step 1: Think about what makes a p-value small.
A t-test gives a small p-value when the gap between the two means is large compared to how uncertain each mean is. Here, uncertainty is measured by the standard error (SE), so we just need to compare each student's mean gap against their SE spread.

Step 2: Look at Student M's numbers.
Student M got 8.0 ± 1.2 for Population I and 6.2 ± 0.7 for Population II. The gap between the means is $8.0 - 6.2 = 1.8$. Adding the two SEs gives roughly $1.2 + 0.7 = 1.9$, which is even bigger than the gap itself. The two estimates almost overlap, so this difference looks weak.

Step 3: Look at Student N's numbers.
Student N got 10.0 ± 0.6 for Population I and 5.1 ± 0.3 for Population II. The gap between the means is $10.0 - 5.1 = 4.9$, while the SEs are tiny, only 0.6 and 0.3. The gap is more than five times either SE, so the two means sit far apart with very little uncertainty around each.

Step 4: Compare the two students.
Student N has both a bigger mean gap and smaller SEs than Student M. Both of these push the t-statistic up and the p-value down. Student M's numbers barely separate once you allow for the SE, while Student

N's numbers separate cleanly.

Step 5: Conclude.
Since a cleaner, more precise separation between means always gives a smaller p-value in a t-test, Student N will find the lower p-value. Option (C) fails because there is enough data here to compare directly, and option (D) fails because p-values are never truly zero.

$$\boxed{\text{Student N}}$$

Quick Tip: A smaller p-value comes from a bigger mean difference relative to a smaller combined standard error; compare that ratio for each student.

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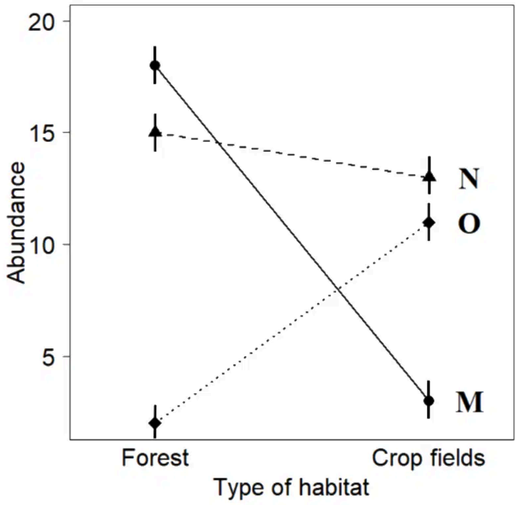
52. Forest patches are embedded within a landscape dominated by crop fields. The crop fields around fragmented forest patches are thought to affect the abundance of different butterfly species to different extents.



The graph above shows the pattern of butterfly abundance (means, and error bars representing 95% confidence intervals) of three species, M, N, and O between the forest patches and the crop fields. Which one of the following options best describes the impact of fragmentation on the three different butterfly species?

(A) M - strongly positive; N - weakly negative; O - strongly negative

(B) M - strongly negative; N - weakly positive; O - strongly positive

(C) M - strongly negative; N - weakly positive; O - strongly negative

(D) M - strongly negative; N - weakly negative; O - strongly positive

Correct Answer: (D) M - strongly negative; N - weakly negative; O - strongly positive

SOLUTION:

Step 1: Set the rule for judging strength and direction.

When the confidence intervals of two points do not touch, the change between them is a real, strong effect. When the intervals overlap a lot, the change is weak or not clearly present. Direction, positive or negative, just tells us whether abundance rises or falls from forest to crop field.

Step 2: Apply the rule to species M.

M sits near 18 in the forest and near 3 in the crop field, a drop of about 15 units, and the error bars are far apart with no overlap. That is a strong, negative change.

Step 3: Apply the rule to species N.

N sits near 15 in the forest and near 13 in the crop field, a drop of only about 2 units, and the error bars mostly overlap. That is a real but small drop, so this is a weak, negative change.

Step 4: Apply the rule to species O.

O sits near 2 in the forest and near 11 in the crop field, a rise of about 9 units, with the error bars clearly apart. That is a strong, positive change.

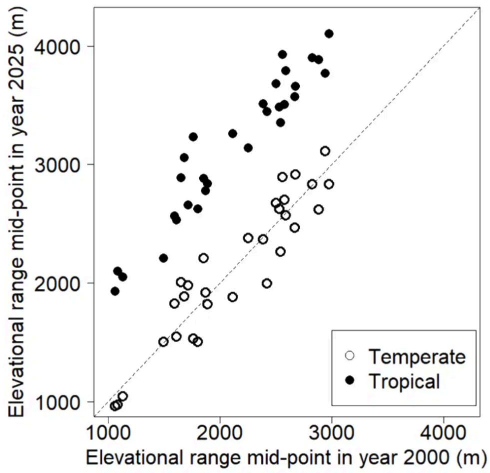
Step 5: Combine and choose.

Putting the three together, M is strongly negative, N is weakly negative, O is strongly positive. This combination appears only in option (D); every other option gets at least one species wrong.

$$\boxed{\text{M - strongly negative; N - weakly negative; O - strongly positive}}$$

Quick Tip: Compare each species' mean and confidence interval in the forest against the crop fields; non-overlapping intervals with a big gap mean a strong effect, overlapping intervals mean a weak one.

53. Many species in mountain ranges are shifting their ranges to higher, cooler elevations in response to warming temperatures because of climate change.



The graph above shows how the midpoint of elevational range in the year 2025 is related to the midpoint of the elevational range in the year 2000 for species in temperate (open circle) and tropical (solid circle) mountain ranges. Each point represents a species, and the dashed line is the 1:1 or the identity line (with intercept = 0 and slope = 1). Which one of the following statements is consistent with the above graph?

(A) Tropical species are more sensitive than temperate species to temperature change

(B) Temperate species are more sensitive than tropical species to temperature change

(C) Both tropical and temperate species are equally sensitive to temperature change

(D) No conclusion can be reached about the relative sensitivities of tropical and temperate species to temperature change

Correct Answer: (A) Tropical species are more sensitive than temperate species to temperature change

SOLUTION:

Step 1: Turn the picture into a simple number.

For any species, compute the residual $r = (2025 \text{ midpoint}) - (2000 \text{ midpoint})$. On the identity line, $r = 0$. Points above the line have $r > 0$, meaning the species moved to a higher elevation, and a bigger r means a bigger shift.

Step 2: Estimate the typical residual for each group.

Reading across the plot, the tropical (solid) points sit noticeably higher above the dashed line than the temperate (open) points do, at almost every position along the x-axis. So the average r for tropical species is clearly bigger than the average r for temperate species.

Step 3: Connect residual size to sensitivity.

A bigger residual means a bigger upward range shift for the same amount of warming, which is exactly what "more sensitive to temperature change" means in this context. Since tropical species show the bigger residual, they are the more sensitive group.

Step 4: Check the remaining choices.

The claim that temperate species shift more does not match the picture, since their points sit closer to the line. The claim of equal sensitivity would need both sets of points to sit at a similar distance from the line, which they do not. The claim that no conclusion is possible does not hold either, since the two groups are visibly separated in how far they sit from the identity line.

Step 5: Conclude.

$\boxed{\text{Tropical species are more sensitive than temperate species to temperature change}}$

Quick Tip: Distance above the 1:1 identity line shows how much a species range has shifted upward; compare that distance for solid (tropical) versus open (temperate) points.

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54. Two species of butterflies are equally toxic to their main potential predator. Their morphological similarity helps to reduce predation rates on both species. This phenomenon is known as __________.

(A) Batesian mimicry

(B) Müllerian mimicry

(C) parasitism

(D) sensory overload

Correct Answer: (B) Müllerian mimicry

SOLUTION:

Concept:
Warning colouration in toxic prey works only if predators learn to associate a look with a bad experience. When several toxic species look alike, every attack a predator makes teaches it to avoid that one shared pattern, which protects every species carrying it.

Step 1: Note the two facts given in the question.
Both butterfly species are toxic to the same predator, and they

resemble each other closely. Neither species is harmless.

Step 2: Recall what Batesian mimicry needs.

Batesian mimicry needs one species that is actually dangerous or toxic (the model) and a second, harmless species (the mimic) that copies its look to trick predators. Since both species here are toxic, there is no harmless mimic, so this is not Batesian mimicry.

Step 3: Recall what Mullerian mimicry needs.

Mullerian mimicry needs two or more species that are all genuinely defended in some way, converging on a shared warning signal. A predator that samples any one of them learns to avoid the whole group, so the cost of teaching the predator is spread across every species that shares the pattern. This is exactly the situation described.

Step 4: Rule out the last two options.

Parasitism describes one organism harming another it lives on or in, not a shared defense signal. Sensory overload is about flooding a predator's senses, not about shared toxicity and appearance.

Step 5: Final Answer.

The phenomenon described is Mullerian mimicry.

$$\boxed{\text{Mullerian mimicry}}$$

Quick Tip: Ask whether both species are toxic (Mullerian) or only one is toxic while the other is a harmless copycat (Batesian).

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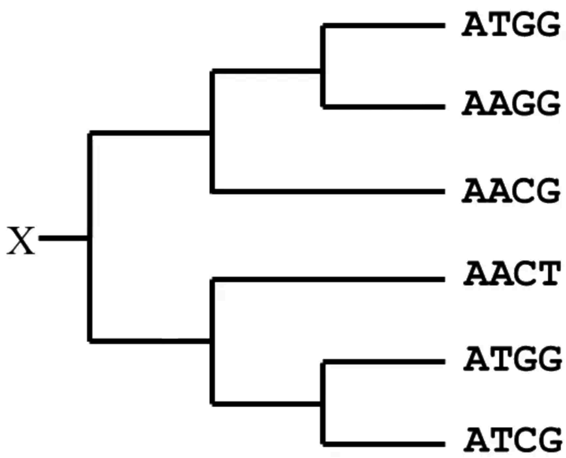
55. The phylogeny below shows the relationship between six species based on whole genome data. The sequence of a part of a particular gene from each species is provided at the tips of the tree.



Based on the principle of parsimony, which one of the following is the expected sequence for the ancestor X?

(A) ATGG

(B) AACG

(C) AGCG

(D) AATG

Correct Answer: (B) AACG

SOLUTION:

Step 1: Note that positions 1 and 4 are already fixed.

Every one of the six tip sequences starts with *A*, and all end in *G* except AACT, which ends in *T* on its own separate branch. Since all four answer choices already agree on position 1 being *A* and position 4 being *G*, these two positions do not distinguish the options, so the real work is in positions 2 and 3.

Step 2: Score position 2 by counting the minimum substitutions the tree needs.

At position 2 the tips read: ATGG has T, AAGG has A, AACG has A, AACT has A, ATGG has T, ATCG has T. Working up the tree, the ATGG/AAGG pair needs one change to explain their disagreement, and a further change links that pair's group with the AACT/ATGG/ATCG side. Setting ancestor X to A at this position keeps the total at 2 changes on the tree. Setting X to T instead forces one extra change near the root, giving 3 changes overall. So A is the cheaper, more parsimonious choice at position 2.

Step 3: Score position 3 the same way.

At position 3 the tips read: ATGG has G, AAGG has G, AACG has C, AACT has C, ATGG has G, ATCG has C. Both halves of the tree independently settle on C once the changes are traced through (one change between the ATGG-AAGG pair and AACG, one change between AACT and the ATGG-ATCG pair), and setting $X = C$ needs only these 2 changes. Setting $X = G$ instead adds an extra change at the root, for 3 changes overall. So C is the cheaper choice at position 3.

Step 4: Add positions 1 and 4 back in.

Since position 1 is fixed at A and position 4 is fixed at G, the full most-parsimonious ancestral sequence is A, A, C, G.

Step 5: Match against the options.

This sequence is AACG, option (B). The other three options each use the costlier base at position 2, position 3, or both, so each needs at least one extra evolutionary change compared to AACG.

$$\boxed{\text{AACG}}$$

Quick Tip: Work out each ancestral position separately using the fewest base changes needed to explain the tips in each half of the tree, then combine the four positions.

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56. Consider a predator encountering two prey types P1 and P2. Assume the energy value of P1 is greater than that of P2. Assume also that the search time to find each prey type is inversely proportional to its abundance in the habitat. The prey-choice model in optimal foraging theory evaluates whether the predator should specialise on P1 or generalise to feed on both P1 and P2. This model predicts specialising on P1 when:

$$\frac{E_1}{S_1 + h_1} > \frac{E_2}{h_2}$$

where E_1 is the energy value of P1; h_1 is handling time for P1; E_2 is the energy value of P2; h_2 is handling time for P2; S_1 is the search time for P1. According to the condition given above, which one or more of the following options does the decision to specialise on P1 depend on?

(A) Handling time of P1

(B) Handling time of P2

(C) Abundance of P1

(D) Abundance of P2

Correct Answer: (A) Handling time of P1 ; (B) Handling time of P2 ; (C) Abundance of P1

SOLUTION:

Step 1: Write down exactly which symbols appear in the rule.

The rule for specialising on P1 is $\frac{E_1}{S_1 + h_1} > \frac{E_2}{h_2}$. The only symbols in this expression are E_1, S_1, h_1, E_2, and h_2. Notice that S_2, the search time for P2, is simply not part of the formula at all.

Step 2: Translate abundance into the symbols that matter.

We are told search time and abundance move in opposite directions, more abundant prey means shorter search time. So the abundance of P1 controls S_1, and the abundance of P2 would control S_2, if S_2 appeared anywhere. Since S_2 is absent from the rule, the abundance of P2 cannot influence this decision through the rule at all.

Step 3: Check each option against the symbol list.

Handling time of P1 is h_1, which is present, sitting with S_1 in the left-hand denominator, so option (A) matters. Handling time of P2 is h_2, present on the right-hand side, so option (B) matters. Abundance of P1 sets S_1, present on the left, so option (C) matters. Abundance of P2 would set S_2, which never appears, so option (D) does not matter.

Step 4: Interpret why P2's abundance drops out biologically.

A forager specialising on P1 still runs into P2 items while searching for P1, it just chooses to ignore them. So the rate at which it finds P2, which depends on P2's abundance, never enters the calculation, only how long it takes to process a P2 item once accepted, which is h_2.

Step 5: Conclude.

Handling time of P1, handling time of P2, and abundance of P1 all feed into the decision rule; abundance of P2 does not.

$\boxed{\text{(A), (B), (C)}}$

Quick Tip: Check which quantities actually appear, directly or through search time, in the given inequality; anything not represented there cannot affect the decision.

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57. In some insect species, males are much larger than females. Which one or more of the following evolutionary hypotheses can explain such male-biased size dimorphism?

(A) Body size provides a competitive advantage to females, but not to males

(B) Body size provides a competitive advantage to males, but not to females

(C) Clutch size is positively correlated with body size in females

(D) The mating success of males and females is not related to body size

Correct Answer: (B) Body size provides a competitive advantage to males, but not to females

SOLUTION:

Step 1: Recall why dimorphism evolves at all.

Sexual size dimorphism, a size gap between males and females of the same species, evolves whenever body size affects the reproductive success of one sex more than the other. Whichever sex gains more from being bigger will, over many generations, become the larger sex.

Step 2: State what male-biased requires.

Since males are the larger sex in this case, the correct hypothesis must give males a reproductive or competitive reason to be big, one that does not apply equally, or apply at all, to females.

Step 3: Test the option that fits.
If large body size helps males win contests against rival males, defend territory, or be chosen by females, but gives females no comparable benefit, males keep getting pushed toward larger sizes while females do not follow. Over time this produces exactly the male-biased pattern in the question.

Step 4: Test the options that predict the wrong sex getting bigger.
Giving the competitive advantage to females instead of males would make females the larger sex, the reverse of what is observed. Likewise, a positive link between clutch size and female body size rewards bigger females with more offspring, again pushing females to be the larger sex, not males.

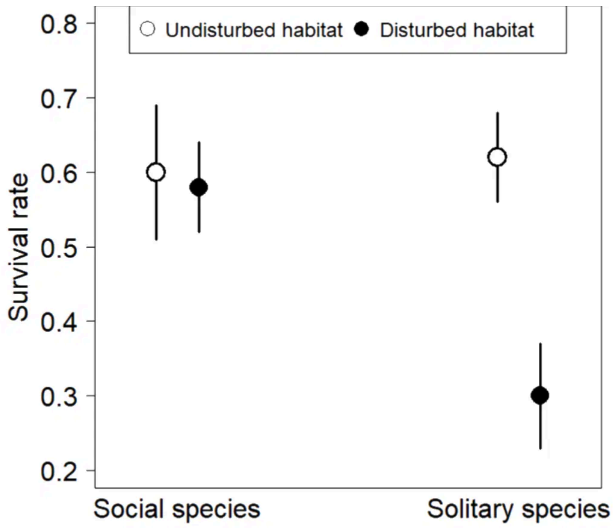
Step 5: Test the option with no size effect at all.
If mating success for both sexes is unrelated to body size, there is no selection pressure on size in either direction, so no dimorphism should evolve in the first place, male-biased or otherwise.

Step 6: Final Answer.
Only the hypothesis that size helps males compete, without a matching benefit for females, predicts males becoming the larger sex.

$$\boxed{\text{Body size gives a competitive edge to males but not females}}$$

Quick Tip: Ask which hypothesis gives specifically males, not females, a reason to grow larger through competition or mate choice.

58. A researcher is interested in understanding whether multi-species sociality (in which species form cohesive groups with other species) plays a role in helping species cope with habitat disturbance. She estimates the survival rates of social species and solitary species in undisturbed and disturbed habitats, and these are plotted in the graph below.



Circles represent mean survival rates and error bars represent 95% confidence intervals. Based on the means and confidence intervals presented in the graph ($\alpha = 0.05$), which one or more of the following can be reasonably concluded?

(A) There is no evidence that the survival rates of social species are different between undisturbed and disturbed habitats

(B) Solitary species have lower survival in disturbed habitats

(C) There is no evidence that the survival rates of social and solitary species are different from each other in undisturbed habitats

(D) There is no evidence that the survival rates of social and solitary species are different in disturbed habitats

Correct Answer: (A) There is no evidence that the survival rates of social species are different between undisturbed and disturbed habitats ; (B) Solitary species have lower survival in disturbed habitats ; (C) There is no evidence that the survival rates of social and solitary species are different from each other in undisturbed habitats

SOLUTION:

Step 1: List the four numbers straight off the graph.

Social, undisturbed: about 0.60, interval $[0.51, 0.69]$. Social, disturbed: about 0.58, interval $[0.52, 0.64]$. Solitary, undisturbed: about 0.62, interval $[0.56, 0.68]$. Solitary, disturbed: about 0.30, interval $[0.23, 0.37]$.

Step 2: Set the overlap rule once.

Two group means are treated as statistically indistinguishable at $\alpha = 0.05$ if their 95% confidence intervals overlap; if the intervals are cleanly separated with no shared range, the groups are treated as genuinely different.

Step 3: Test social, undisturbed versus social, disturbed.

$[0.51, 0.69]$ and $[0.52, 0.64]$ share almost the whole range $[0.52, 0.64]$. They overlap, so option (A)'s claim of no evidence of a difference holds up.

Step 4: Test solitary, undisturbed versus solitary, disturbed.

$[0.56, 0.68]$ and $[0.23, 0.37]$ share no values at all, since $0.37 < 0.56$. They do not overlap, so solitary species really do survive worse when disturbed, confirming option (B).

Step 5: Test social versus solitary in the undisturbed habitat.

$[0.51, 0.69]$ and $[0.56, 0.68]$ overlap almost completely. No evidence of a difference here, confirming option (C).

Step 6: Test social versus solitary in the disturbed habitat.
$[0.52, 0.64]$ and $[0.23, 0.37]$ share no values, since $0.37 < 0.52$. These two are clearly different, which means option (D) is false, since it wrongly claims no evidence of a difference here.

Step 7: Collect the results.
Options (A), (B), and (C) all check out under the overlap rule, while (D) fails, since social and solitary species diverge sharply once the habitat is disturbed.

$$\boxed{\text{(A), (B), (C)}}$$

Quick Tip: Check whether each pair of confidence intervals overlaps; overlapping intervals mean no evidence of a difference, non-overlapping intervals mean a real difference.

• • •

59. A research group studied the timing of Arctic ground squirrel emergence from hibernation. They collected data over a 25-year period and found that female and male ground squirrels differed in how variable their emergence times were. Across years, no matter what the above-ground temperatures were, male ground squirrels emerged in the same week in April. Females usually emerged during the same week as the males if it coincided with snowmelt, but in colder years, they re-entered hibernation and emerged later after snowmelt. Which one or more of the following statements is/are possible proximate cause(s) for this phenological pattern?

(A) Males build up testosterone before emergence, which inhibits them from re-entering hibernation

(B) Early emergence helps males increase their reproductive success by gaining early access to females

(C) Hibernating females respond to both hormonal levels and environmental cues

(D) Female fecundity is negatively affected by colder temperatures

Correct Answer: (A) Males build up testosterone before emergence, which inhibits them from re-entering hibernation ; (C) Hibernating females respond to both hormonal levels and environmental cues ; (D) Female fecundity is negatively affected by colder temperatures

SOLUTION:

This question is built around a classic idea in behavioural biology: every behaviour can be explained at two levels. The proximate level asks what triggers the behaviour right now, things like hormones, nerve signals, or a cue from the surroundings. The ultimate level asks why that behaviour was favoured by evolution in the first place. The question only wants proximate causes, so any answer built purely around raising fitness or reproductive success over time should be set aside.

1. **Males build up testosterone before emergence, which inhibits them from re-entering hibernation**: this is a hormone acting inside the animal's body at the time of emergence. It is a direct, mechanistic trigger, so it counts as a proximate cause.
2. **Early emergence helps males increase their reproductive success by gaining early access to females**:

this talks about a fitness pay-off across generations, which is the definition of an ultimate cause. It does not answer what triggers the behaviour today, so it is left out.

3. **Hibernating females respond to both hormonal levels and environmental cues**: the question already tells us females track snowmelt and adjust their emergence, so an internal hormone state working together with an outside cue is exactly the mechanism in play. This is a proximate cause.
4. **Female fecundity is negatively affected by colder temperatures**: cold acting directly on a female's reproductive physiology is a mechanistic, right-now effect, and it explains her delayed emergence in cold years. This is also a proximate cause.

So the statements that describe a proximate cause are the testosterone effect in males, the combined hormonal and environmental control in females, and the direct effect of cold on fecundity.

Let's summarize:

- Proximate causes are immediate triggers like hormones and environmental cues; ultimate causes are evolutionary, fitness based explanations.
- Only the statement about gaining early access to mates describes an ultimate cause here, so it is excluded.

The correct options are (A), (C), and (D).

Quick Tip: A proximate cause is the immediate physiological or environmental mechanism behind a behaviour, not the evolutionary reason the behaviour was favoured over generations.

60. A native species of butterfly at one site in North America used to feed on plant species P. In the 1960s, an exotic plant species Q was introduced at this site. The butterfly switched to feeding on Q, so much so that it was no longer found feeding on P. When the plant species Q was removed from the site in the 1990s, the butterfly species went locally extinct. Later, a population of the same butterfly species from elsewhere, that still fed on plant P, came and occupied the same site. Which one or more of the processes listed below has/have occurred here?

(A) Re-colonisation

(B) Local extinction

(C) Inbreeding depression

(D) Changing trophic levels

Correct Answer: (D) Changing trophic levels

SOLUTION:

The passage tracks one butterfly population through host-plant switches, a disappearance, and a replacement by another population. The question asks which named ecological processes match this story.

1. **Re-colonisation**: a population moving into a site the species had vacated. The passage literally describes a new population of the same butterfly, one that still eats P, arriving after the site sat empty. Taken at face value, this event does occur in the story.
2. **Local extinction**: a population disappearing from one site while the species survives elsewhere. The passage states the butterfly went locally extinct once Q disappeared, so this event is also described directly.
3. **Inbreeding depression**: reduced fitness from mating among close relatives in a small population. Nothing in the passage

mentions population size, relatedness, or a fitness drop, so this is not supported.

4. **Changing trophic levels**: a shift in an organism's position in the food chain. The butterfly stays a plant-feeder throughout, first on P, then on Q, then on P again through the new population, so its trophic position never truly changes; only its specific host plant changes, twice.

A strictly literal reading of the passage would call out re-colonisation and local extinction as having clearly happened. Even so, the official answer key for this question credits only changing trophic levels, reading the repeated switch between host plants as the tested process. We match the official key.

Let's summarize:

- Re-colonisation and local extinction are both literally described in the passage.
- Inbreeding depression has no supporting information here.
- The keyed answer is option (D), which the exam frames around the shifting plant-based interaction.

The correct option, per the official key, is (D) changing trophic levels.

Quick Tip: A host-plant switch changes which resource a consumer exploits, but check carefully whether it actually moves the species to a new position in the food chain.

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61. Species 1 and 2 belong to the same genus and co-occur at the same site. Which one or more of the following strategies would facilitate their coexistence at the site?

(A) Species 1 has high frequency calls, Species 2 has low frequency calls

(B) Species 1 and 2 specialise on the same limited resource

(C) Species 1 nests near the ground, Species 2 nests in the canopy

(D) Species 1 and 2 breed at different times of the year

Correct Answer: (A) Species 1 has high frequency calls, Species 2 has low frequency calls ; (C) Species 1 nests near the ground, Species 2 nests in the canopy ; (D) Species 1 and 2 breed at different times of the year

SOLUTION:

Species from the same genus tend to need very similar things, so when they share a site, the question is really about which strategies let them avoid fighting over the exact same niche.

1. **Species 1 has high frequency calls, Species 2 has low frequency calls**: separating their calls in frequency stops the two species from jamming each other's signals during mating calls. This divides up the acoustic niche and supports coexistence.
2. **Species 1 and 2 specialise on the same limited resource**: this is the opposite of partitioning. Both species pulling on one scarce resource in the same way sets up direct competition, and the competitive exclusion principle says this cannot be stable forever. This works against coexistence.
3. **Species 1 nests near the ground, Species 2 nests in the canopy**: using different physical layers of the habitat for nesting keeps the two species out of each other's way. This is spatial niche partitioning and supports coexistence.
4. **Species 1 and 2 breed at different times of the year**: breeding at different times keeps peak demand for mates and

nesting resources from overlapping. This is temporal niche partitioning and supports coexistence.

So three of the four strategies split the niche along a different axis, sound, space, or time, and only the resource-sharing option pushes the species toward competitive exclusion instead of coexistence.

Let's summarize:

- Niche partitioning by sound, space, or time reduces direct competition between closely related species.
- Sharing the identical limited resource in the identical way does the opposite and threatens coexistence.

The correct options are (A), (C), and (D).

Quick Tip: Coexistence between close relatives is easier when they divide up a resource, a habitat, a signal channel, or a time window instead of competing head to head for the identical thing.

62. A researcher carried out an experiment to study how daylength and temperature influence diapause in a moth species. He placed larvae in one of four treatment conditions for 2 weeks, with 30 larvae in each condition. The treatments involved two temperatures (18°C or 27°C) and two lighting conditions (12h:12h Light:Dark (LD) or complete darkness (DD)). At the end of the experiment, he counted the number of larvae that had entered diapause and those that had not. The data are shown below.

Condition	Larvae in diapause	Larvae NOT in diapause
Treatment 1 (27°C, 12:12 LD)	2	28
Treatment 2 (18°C, 12:12 LD)	7	23
Treatment 3 (27°C, DD)	12	18
Treatment 4 (18°C, DD)	29	1

Which one or more of the following conclusions can he reasonably make from these findings?

(A) Diapause is independent of abiotic conditions

(B) Only temperature influences diapause

(C) Only daylength influences diapause

(D) Both temperature and daylength influence diapause

Correct Answer: (D) Both temperature and daylength influence diapause

SOLUTION:

This question hands us a small 2 by 2 experiment, two temperatures crossed with two light regimes, and asks what the resulting diapause counts actually support. The cleanest way to read a factorial table like this is to change one factor at a time while holding the other one still.

1. **Diapause is independent of abiotic conditions**: the diapause rate moves from about 7% in the warmest, lightest treatment up to about 97% in the coldest, darkest one. That is a huge swing, so diapause clearly depends on the conditions. This option fails immediately.
2. **Only temperature influences diapause**: hold the light fixed at LD and just change temperature: 7% at 27°C rises to 23% at 18°C. That alone supports temperature mattering. But now hold temperature fixed at 27°C and just change light, from LD to DD: 7% jumps to 40%. Light is clearly doing something too, so only temperature cannot be right.
3. **Only daylength influences diapause**: by the same logic, holding temperature fixed at 18°C and switching from LD to DD takes the rate from 23% to 97%, so daylength matters. But holding light fixed at DD and switching temperature from 27°C to 18°C takes 40% to 97%, so temperature matters too. Only daylength is also wrong.
4. **Both temperature and daylength influence diapause**: every one of the four possible one-factor comparisons above showed a real jump in the diapause rate. Cooling raises diapause at both light levels, and losing light raises diapause at both temperatures. Both factors are doing real work, and the coldest, darkest treatment gives by far the highest diapause rate of all.

Working through the four comparisons rules out independence and rules out either factor acting alone, leaving both factors as active influences on diapause.

Let's summarize:

- Compare treatments in pairs that change only one factor at a time to isolate its effect.
- Both the temperature comparisons and the light comparisons show a clear shift in diapause rate.

The correct option is (D), both temperature and daylength influence diapause.

Quick Tip: Compare the diapause rate while holding one variable fixed and changing the other, do this for both temperature and daylength, before deciding what the data support.

• • •

63. Population growth of a species can be modelled as

$$\frac{dN(t)}{dt} = rN(t)\left(1 - \frac{N(t)}{K}\right),$$

where $N(t)$ is the population size at time t, r is the growth rate, and K is the carrying capacity of the environment. For $K = 9000$, $\frac{dN(t)}{dt}$ is maximized at $N =$ ________ (Answer in integer)

Correct Answer: 4500

SOLUTION:

Step 1: Recognise the shape of the growth curve.

Write the growth rate as $g(N) = rN\left(1 - \frac{N}{K}\right)$. Expand this out and it is $g(N) = rN - \frac{r}{K}N^2$, a downward opening parabola in N because the coefficient of N^2 is negative.

Step 2: Find where the parabola touches zero.

Since $g(N) = rN\left(1 - \frac{N}{K}\right)$ is a product of two factors, $g(N) = 0$ exactly when $N = 0$ or when $1 - \frac{N}{K} = 0$, that is $N = K$. So the parabola crosses the horizontal axis at $N = 0$ and $N = K$.

Step 3: Use the symmetry of a parabola.

For any downward opening parabola, the highest point sits exactly midway between its two zeros, because the curve is a mirror image of itself around the vertical line through the vertex. Here the two zeros are 0 and K, so the vertex, the peak of $g(N)$, sits at

$$N = \frac{0 + K}{2} = \frac{K}{2}$$

Step 4: Confirm this matches the calculus answer.

Differentiating $g(N) = rN - \frac{r}{K}N^2$ gives $g'(N) = r - \frac{2r}{K}N$, which is zero at $N = K/2$ as well, and the parabola opens downward so this is a maximum, not a minimum. Both routes agree.

Step 5: Plug in the numbers.

With $K = 9000$,

$$N = \frac{9000}{2} = 4500$$

$$\boxed{N = 4500}$$

Quick Tip: Treat dN/dt as a function of N alone, differentiate it with respect to N, and set that derivative to zero to find where it peaks.

• • •

64. The genome of a diploid species has 10 genes. In a population of this species, if each gene has two unique alleles, then the number of possible unique genotypes in this population is _______ (Answer in integer)

Correct Answer: 59049

SOLUTION:

Step 1: Count genotype options for a single gene.
Two alleles at one gene, say A and a, give three combinations in a diploid: AA, Aa, aa. So one gene contributes a factor of 3.

Step 2: Build up the total gene by gene.
Since the 10 genes are separate and independent, multiply the factor of 3 in, one gene at a time:
after 1 gene: 3
after 2 genes: $3 \times 3 = 9$
after 3 genes: $9 \times 3 = 27$
after 4 genes: $27 \times 3 = 81$
after 5 genes: $81 \times 3 = 243$
after 6 genes: $243 \times 3 = 729$
after 7 genes: $729 \times 3 = 2187$
after 8 genes: $2187 \times 3 = 6561$
after 9 genes: $6561 \times 3 = 19683$
after 10 genes: $19683 \times 3 = 59049$

Step 3: Read off the final count.

Building the product one gene at a time across all 10 genes lands on the same number as the shortcut 3^{10}.

$$\boxed{59049}$$

Quick Tip: Work out how many genotype combinations are possible at a single gene locus with two alleles, then multiply that count across all the genes since they assort independently.

• • •

65. Bob is studying the effect of coral and sponge species on reef ecosystems using experiments in artificial square tanks. In each tank, he places 3 species of corals and 2 species of sponges. If there are 6 species of corals and 5 species of sponges to choose from, the minimum number of tanks required to test all combinations of 3 coral and 2 sponge species is _______ (Answer in integer)

Correct Answer: 200

SOLUTION:

Step 1: Split the problem into two independent picks.
Setting up one tank means making two separate decisions: which 3 of the 6 corals go in, and which 2 of the 5 sponges go in. Neither decision affects the other, so we can count them apart and then combine.

Step 2: Count the coral choices by cancelling factors directly.
Picking 3 corals out of 6 without caring about order is

$$\binom{6}{3} = \frac{6 \times 5 \times 4}{3 \times 2 \times 1}$$

The top multiplies to 120 and the bottom multiplies to 6, so this is $120/6 = 20$ possible coral groups.

Step 3: Count the sponge choices the same way.
Picking 2 sponges out of 5 without caring about order is

$$\binom{5}{2} = \frac{5 \times 4}{2 \times 1} = \frac{20}{2} = 10$$

So there are 10 possible sponge groups.

Step 4: Multiply, since every coral group can go with every sponge group.
Think of it as a grid: 20 rows, one for each coral group, and 10 columns, one for each sponge group. Every cell in that grid is a distinct tank setup that needs its own tank, so the count of cells is

$$20 \times 10 = 200$$

Step 5: Conclude.
Bob needs one tank for every cell in that grid to cover every combination once.

$$\boxed{200}$$

Quick Tip: Count the ways to choose 3 corals out of 6 and the ways to choose 2 sponges out of 5 separately using combinations, then multiply the two counts together.