GAT B Biology

Sample Paper – 7

Duration: 23 Minutes **Maximum Marks: 15**

Instructions

- This paper contains **15** Multiple Choice Questions (Single Correct Answer), modelled on the Biology portion of **GAT B** entrance (Section A).
- Each correct answer carries **+1 mark**. There is **a deduction of 0.5 marks for each incorrect answer**.
- Only **one** option is correct. Choose carefully.
- Syllabus level: **NCERT Class 11 & 12 Biology — Cell Biology, Genetics, Plant & Human Physiology, Ecology, Evolution, and Biotechnology.**
- Use of mobile phones, calculators, or electronic gadgets is strictly prohibited.

Section A — Biology (15 Questions)

Q1. Which cytoskeletal element is responsible for forming the spindle fibres that pull chromosomes towards opposite poles of the cell during mitosis?

(A) Intermediate filaments (e.g., keratin, vimentin)

(B) Actin microfilaments (F-actin)

(C) Centrioles alone

(D) Microtubules (polymerised α/β-tubulin dimers)

Q2. Which of the following human traits is the best example of polygenic inheritance, showing a continuous, bell-shaped (normal) distribution in a population?

(A) ABO blood groups

(B) Tongue rolling ability

(C) Skin colour

(D) Albinism

Q3. The normal resting heart rate (pulse rate) in a healthy adult human is approximately:

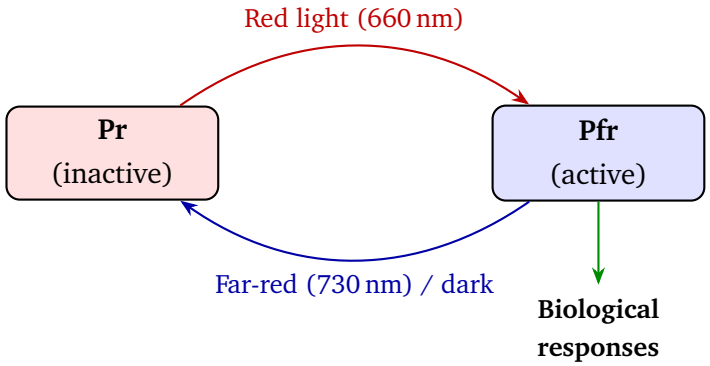
(A) 40 beats per minute

(B) 72 beats per minute

(C) 100 beats per minute

(D) 120 beats per minute

Q4. Phytochrome is a photoreversible pigment-protein photoreceptor in plants. The diagram below shows its two interconvertible forms. Which form, generated by absorption of red light (660 nm), promotes seed germination and other photo-morphogenic responses?



(A) Pfr (the far-red-absorbing, physiologically active form)

(B) Pr (the red-absorbing, inactive ground-state form)

(C) Both Pr and Pfr are equally active in promoting germination

(D) Phytochrome has no role in seed germination

Q5. Phylum Chordata is characterised by four fundamental features present at some stage of the life cycle. Which of the following is the defining character shared by *all* chordates, including tunicates and lancelets?

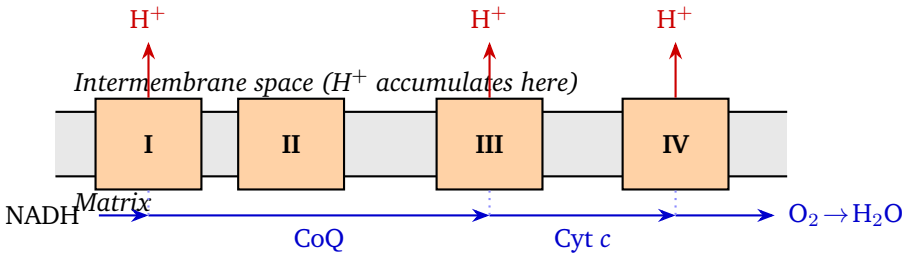
(A) Presence of a vertebral column (backbone) throughout life

(B) Bilateral symmetry and a true coelom

(C) An endoskeleton composed entirely of bone

(D) Presence of a notochord at some stage of the life cycle

Q6. In the mitochondrial electron transport chain (ETC) shown below, which complex directly accepts electrons from cytochrome c and reduces molecular oxygen (O_2) to water?



(A) Complex I (NADH dehydrogenase / NADH-ubiquinone oxidoreductase)

(B) Complex II (succinate dehydrogenase / succinate-ubiquinone oxidoreductase)

(C) Complex IV (cytochrome c oxidase)

(D) Complex III (ubiquinol-cytochrome c oxidoreductase / bc_1 complex)

Q7. Epigenetics involves heritable changes in gene expression without alterations in the DNA nucleotide sequence. Which of the following epigenetic modifications is most strongly associated with stable, long-term gene silencing (transcriptional repression)?

(A) Histone acetylation at lysine residues in histone tails

(B) DNA methylation at CpG dinucleotide sites in gene promoters

(C) Histone H3 phosphorylation at serine 10 during mitosis

(D) Chromatin remodelling by the SWI/SNF ATP-dependent complex

Q8. In the ABO and Rh blood group classification, which blood group individual is referred to as the "universal donor" for red blood cell (RBC) transfusions, because their RBCs can be given to recipients of any ABO and Rh type without triggering an immediate haemolytic reaction?

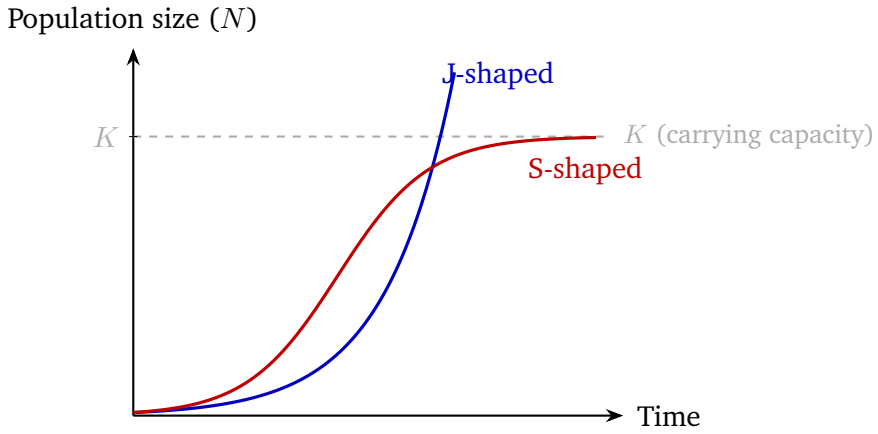
(A) O negative (O^-)

(B) O positive (O^+)

(C) AB positive (AB^+)

(D) AB negative (AB^-)

Q9. Which model of population growth produces the S-shaped (sigmoidal) growth curve shown below and incorporates a carrying capacity (K) at which growth approaches zero?



(A) Exponential (Malthusian) growth model

(B) Arithmetic (linear) growth model

(C) Hyperbolic growth model

(D) Logistic growth model (Verhulst model)

Q10. The coconut palm (*Cocos nucifera*) produces large fruits with a thick, spongy fibrous mesocarp (husk) filled with air-containing fibres that make the fruit highly buoyant. This structural adaptation is suited for which specific mode of seed dispersal?

(A) Anemochory (dispersal by wind)

(B) Hydrochory (dispersal by water)

(C) Zoochory (dispersal by animals)

(D) Autochory (self-dispersal via explosive dehiscence)

Q11. The "molecular clock" concept, proposed by Zuckerkandl and Pauling (1965), allows scientists to estimate the time of evolutionary divergence between two species. On what fundamental observation is the molecular clock based?

(A) Neutral mutations accumulate in DNA (or protein sequences) at a roughly constant rate over evolutionary time

(B) Morphological changes in the fossil record occur at a regular, predictable rate

(C) Speciation events occur at a fixed number per lineage per million years

(D) The tertiary structure of proteins changes at a constant rate during evolution

Q12. Modern forensic DNA fingerprinting (DNA profiling) identifies individuals by analysing highly polymorphic repetitive DNA sequences at multiple loci. Which type of repetitive sequences forms the basis of the current standard STR-based profiling systems (e.g., CODIS in the USA)?

(A) Single nucleotide polymorphisms (SNPs)

(B) Restriction fragment length polymorphisms (RFLPs)

(C) Short tandem repeats (STRs / microsatellites)

(D) Copy number variations (CNVs)

Q13. Biological nitrogen fixation converts atmospheric N_2 into ammonia (NH_3) via the enzyme nitrogenase. Which of the following microorganisms forms a specific symbiotic association with leguminous plants and performs nitrogen fixation within specialised **root nodules**?

(A) *Azotobacter* (free-living, aerobic soil bacterium)

(B) *Clostridium* (free-living, anaerobic soil bacterium)

(C) *Anabaena* (free-living filamentous cyanobacterium)

(D) *Rhizobium* (symbiotic soil bacterium in legume root nodules)

Q14. At the neuromuscular junction (NMJ), a motor neuron releases a specific neurotransmitter into the synaptic cleft, which binds to receptors on the motor end plate of the skeletal muscle fibre and triggers an action potential leading to contraction. This neurotransmitter is:

(A) Dopamine

(B) Acetylcholine (ACh)

(C) Serotonin (5-hydroxytryptamine, 5-HT)

(D) Norepinephrine (noradrenaline)

Q15. Echinoderms (sea stars, sea urchins, sea cucumbers) possess a unique hydraulic network of fluid-filled canals and tube feet used for locomotion, prey capture, gas exchange, and sensory reception. This system, found exclusively in phylum Echinodermata, is called the:

(A) Water vascular system

(B) Open circulatory system

(C) Haemolymph-based transport system

(D) Mantle cavity system

Solutions

Sol.1.

Solution

Concept — Cytoskeleton and Mitotic Spindle: The eukaryotic cytoskeleton comprises three main filament types: microtubules (∼25 nm diameter), actin microfilaments (∼7 nm), and intermediate filaments (∼10 nm). Each has distinct mechanical and regulatory roles.

Step 1 — Microtubules as spindle fibres: The mitotic spindle is assembled from dynamic polymers of α/β-tubulin heterodimers that nucleate at microtubule-organising centres (MTOCs / centrosomes) in animal cells. Three functionally distinct populations form: (i) **kinetochore microtubules** that attach to chromosomal kinetochores at their plus ends and depolymerise at the poles (minus ends) during anaphase, "reeling in" sister chromatids; (ii) **polar microtubules** that overlap at the cell equator and slide past each other, elongating the spindle; and (iii) **astral microtubules** that anchor the spindle to the cell cortex. Drugs such as colchicine (depolymerises tubulin) and taxol (stabilises microtubules) arrest cells in mitosis, confirming the essential role of microtubules.

Why other options are wrong:

- Option A (Intermediate filaments): Provide tensile strength and anchor organelles; they are non-dynamic and do not form spindle fibres. Examples: keratin (epithelia), vimentin (mesenchyme), nuclear lamins.
- Option B (Actin microfilaments): Drive cell shape changes, cell migration, and the cytokinetic contractile ring that cleaves the cell after mitosis; they do not form the spindle itself.
- Option C (Centrioles alone): Centrioles are short barrel-shaped structures of microtubule triplets that organise the centrosome. However, it is the pericentriolar material (PCM) that nucleates spindle microtubules — centrioles themselves do not elongate to become spindle fibres.

Final Answer: Microtubules polymerised from tubulin dimers form the spindle fibres that segregate chromosomes ⇒ D

Answer: (D) Go Back to Q 1

Sol.2.

Solution

Concept — Polygenic Inheritance: Polygenic (quantitative) traits are controlled by two or more independent gene loci whose alleles contribute additively to the phenotype. The result is a continuous range of phenotypes in a population that approximates a normal (bell-shaped) distribution, rather than discrete Mendelian classes.

Step 1 — Skin colour as the classic polygenic example: Human skin colour is determined by the quantity and type of melanin produced by melanocytes, regulated by multiple gene loci — including *MC1R*, *OCA2*, *TYRP1*, *SLC45A2*, *SLC24A5*, and *ASIP* (at least six principal loci). Each locus contributes additively: more "dark" alleles $\rightarrow$ more melanin $\rightarrow$ darker skin. Because no single locus dominates, skin colour in large mixed populations shows a smooth, continuous distribution from very light to very dark, with intermediate shades being most common — the hallmark of polygenic inheritance. Environmental factors (UV exposure causing tanning) further extend the continuous variation.

Why other options are wrong:

- Option A (ABO blood groups): Controlled by a single gene (I locus) with three alleles (I^A, I^B, i); produces four distinct, non-overlapping phenotypic classes. This is an example of multiple allelism at a single locus, not polygenic inheritance.
- Option B (Tongue rolling): Produces only two discrete phenotypes (roller / non-roller); although its genetics are more complex than a simple dominant/recessive trait, it does not show a continuous normal distribution.
- Option D (Albinism): Results from homozygous loss-of-function mutations at a single locus (e.g., *TYR* encoding tyrosinase); it is a discrete recessive Mendelian trait with two phenotypes (albino / pigmented).

Final Answer: Skin colour, governed by multiple additive loci, is the classic polygenic trait with a continuous distribution $\Rightarrow$ C

Answer: (C) Go Back to Q 2

Sol.3.

Solution

Concept — Normal Resting Heart Rate: The heart rate (cardiac frequency, pulse rate) is the number of complete cardiac cycles per minute. It is set by spontaneous depolarisation of the sinoatrial (SA) node — the intrinsic pacemaker — modulated by the autonomic nervous system and circulating hormones.

Step 1 — Standard value per NCERT: NCERT Class 11 Biology (Chapter 18 — Body Fluids and Circulation) explicitly states that the heart of a normal healthy individual beats **70–72 times per minute**. This gives an average resting heart rate of **72 beats per minute (bpm)**. At 72 bpm each cardiac cycle lasts $60/72 \approx 0.83$ seconds (0.3 s systole + 0.5 s diastole). The normal clinical range is 60–100 bpm; values below 60 bpm are bradycardia and above 100 bpm are tachycardia.

Why other options are wrong:

- Option A (40 bpm): Below the lower limit of normal (60 bpm); constitutes bradycardia. Seen in highly trained endurance athletes (increased stroke volume compensates) but is not the standard resting value for a healthy adult.
- Option C (100 bpm): The upper boundary of normal; sustained 100 bpm at rest is considered borderline tachycardia. Occurs transiently during emotional stress or mild fever.
- Option D (120 bpm): Clearly tachycardic; occurs during vigorous exercise, significant fever, pain, or certain arrhythmias — not a normal resting rate.

Final Answer: The normal resting heart rate in a healthy adult is 72 beats per minute $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q 3

Sol.4.

Solution

Concept — Phytochrome and Photomorphogenesis: Phytochrome is a blue-green chromoprotein photoreceptor found in all vascular plants. It detects the ratio of red (R, 660 nm) to far-red (FR, 730 nm) light in the environment and transduces that information into developmental responses: seed germination, shade avoidance, de-etiolation, and flowering.

Step 1 — The Pr/Pfr switch: Phytochrome exists in two photoreversible forms:

- **Pr** (λ_{max} = 660 nm): The inactive ground state, synthesised in darkness.
- **Pfr** (λ_{max} = 730 nm): The physiologically *active* form, produced when Pr absorbs red light.

On absorption of red light by Pr, a rapid photoisomerisation of the covalently bound phytochromobilin chromophore converts it to Pfr. Active Pfr then interacts with transcription factors (e.g., PIFs — phytochrome-interacting factors) in the nucleus to initiate gene expression changes that promote seed germination, hypocotyl shortening, and leaf expansion. Exposure to far-red light (or prolonged darkness via slow thermal reversion) converts Pfr back to Pr, turning off the responses. This is why red light promotes germination and far-red light inhibits it — demonstrated classically with lettuce seeds by Borthwick and Hendricks in the 1950s.

Why other options are wrong:

- Option B (Pr): Pr is the *inactive* precursor that absorbs red light; it does not itself trigger germination responses — only its conversion product Pfr does.
- Option C (Both equally active): The two forms have opposite activities; Pfr is the active signalling form and Pr is inactive. They are not equally active.
- Option D (Phytochrome has no role): Incorrect; phytochrome-mediated red/far-red photoreversibility of seed germination is one of the best-documented responses in plant physiology (NCERT Class 11, Chapter 15).

Final Answer: Pfr (the far-red-absorbing active form), generated by red light absorption, promotes seed germination $\Rightarrow$ A

Answer: (A) Go Back to Q 4

Sol.5.

Solution

Concept — Phylum Chordata: Chordates are defined by four anatomical synapomorphies (shared derived characters) that are present in *every* member at least at some stage (embryonic or adult) of the life cycle. These characters unite an otherwise morphologically diverse group spanning from filter-feeding sea squirts to humans.

Step 1 — The four chordate characters (NCERT Class 11, Chapter 4):

- **Notochord**: A flexible, rod-like mesodermal structure providing support. Present in all chordate embryos; persists in adults of non-vertebrate chor-

dates (Cephalochordata: *Amphioxus*); replaced by the vertebral column in vertebrates.

- **Dorsal hollow nerve cord**: Single, hollow, dorsal neural tube (vs. solid, ventral nerve cord of invertebrates). Develops into brain + spinal cord in vertebrates.
- **Pharyngeal slits / gill pouches**: Present in embryos of all chordates; function as filter-feeding apparatus in lancelets and tunicates; become gill slits in fish; modified into ear, jaw, and neck structures in tetrapods.
- **Post-anal tail**: A muscular tail posterior to the anus, present at some developmental stage in all chordates.

Of these, the **notochord** is the eponymous character of the phylum and is present at some stage in every chordate without exception.

Why other options are wrong:

- Option A (Vertebral column throughout life): The vertebral column is a synapomorphy of Subphylum Vertebrata only; invertebrate chordates (tunicates, lancelets) lack it entirely.
- Option B (Bilateral symmetry + coelom): These features are shared by many non-chordate phyla (Annelida, Mollusca, Arthropoda, Echinodermata); they are not diagnostic of chordates.
- Option C (Endoskeleton of bone): Bone is a feature of Osteichthyes (bony fish) and tetrapods; cartilaginous fish have cartilaginous endoskeletons, and non-vertebrate chordates lack mineralised endoskeletons.

Final Answer: Presence of a notochord at some stage of the life cycle is the defining character of all chordates $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q 5

Sol.6.

Solution

Concept — Mitochondrial Electron Transport Chain: The ETC is a series of four multiprotein complexes (I–IV) embedded in the inner mitochondrial membrane. Electrons from NADH and $FADH_2$ pass through these complexes in order of increasing reduction potential, ultimately reducing O_2 to H_2O at Complex IV. The energy released is harnessed as a proton gradient (chemiosmotic potential) that drives ATP synthesis by Complex V (ATP synthase).

Step 1 — The role of Complex IV (Cytochrome c oxidase, CcO): Complex IV is

the terminal oxidase of the respiratory chain. It accepts four electrons sequentially from four molecules of reduced cytochrome c (a small mobile carrier, Fe^{2+} form) and uses them to reduce one molecule of O_2 to two molecules of water:

$$4\,\text{Cyt}\,c^{2+} + O_2 + 4\,H^{+}_{\text{matrix}} \longrightarrow 4\,\text{Cyt}\,c^{3+} + 2\,H_2O$$

Complex IV contains copper centres (Cu_A, Cu_B) and haem a / a_3 groups that carry out this stepwise four-electron reduction. It also pumps $\sim$2 H^+ per electron pair into the intermembrane space, contributing to the proton gradient.

Why other options are wrong:

- Option A (Complex I): NADH dehydrogenase oxidises NADH and reduces ubiquinone (CoQ) to ubiquinol; it does not reduce O_2 and does not interact with cytochrome c.
- Option B (Complex II): Succinate dehydrogenase (also an enzyme of the TCA cycle) oxidises succinate to fumarate, reducing CoQ to ubiquinol; it does *not* pump protons and does not reduce O_2 directly.
- Option D (Complex III / bc_1 complex): Oxidises ubiquinol ($CoQH_2$) and reduces cytochrome c via the Q-cycle; it passes electrons *to* cytochrome c and does not directly reduce O_2 — that is the exclusive role of Complex IV downstream.

Final Answer: Complex IV (cytochrome c oxidase) accepts electrons from cytochrome c and reduces O_2 to water $\Rightarrow$ C

Answer: (C) Go Back to Q 6

Sol.7.

Solution

Concept — Epigenetics and Gene Silencing: Epigenetic modifications alter chromatin structure and gene accessibility without changing the DNA sequence. They are heritable through cell divisions and include DNA methylation and a wide range of histone modifications (acetylation, methylation, phosphorylation, ubiquitination). Different modifications are associated with distinct transcriptional states.

Step 1 — DNA methylation and stable gene silencing: DNA methylation is the covalent addition of a methyl group ($-CH_3$) to the C5 position of cytosine, predominantly at **CpG dinucleotides** (5′-CG-3′ sites), catalysed by DNA methyltransferases (DNMT1, DNMT3A, DNMT3B). Methylation of CpG islands (CpG-

dense regions, typically 200–2000 bp) in gene promoters represses transcription by two mechanisms: (i) it directly *blocks* binding of transcription factors that require unmethylated CpGs; (ii) it recruits methyl-CpG-binding domain (MBD) proteins (e.g., MeCP2) which assemble repressor complexes containing histone deacetylases (HDACs) and H3K9 methyltransferases, driving the chromatin into a compact, inaccessible heterochromatin state. DNA methylation underlies key silencing events: X-chromosome inactivation (in females), genomic imprinting, and silencing of transposable elements and tumour-suppressor genes in cancer.

Why other options are wrong:

- Option A (Histone acetylation): Acetylation of histone tail lysines (by HATs, histone acetyltransferases) neutralises their positive charge, loosening chromatin into an open (euchromatic) configuration. It is a mark of *transcriptional activation*, not silencing.
- Option C (Histone H3 phosphorylation at Ser10): H3S10 phosphorylation is a marker of chromosome condensation during mitosis and meiosis, not of long-term transcriptional silencing.
- Option D (SWI/SNF remodelling): The SWI/SNF complex uses ATP hydrolysis to slide or eject nucleosomes, generally *increasing* chromatin accessibility. It is associated with gene *activation*, not stable silencing.

Final Answer: DNA methylation at CpG dinucleotide sites is the epigenetic mark most strongly associated with stable gene silencing $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q 7

Sol.8.

Solution

Concept — ABO and Rh Blood Groups: Red blood cells (RBCs) display surface glycolipid antigens (A, B) encoded by the ABO gene, and a protein antigen (Rh D) encoded by the *RHD* gene. Corresponding antibodies (anti-A, anti-B, anti-D) in the plasma cause agglutination (clumping) and haemolysis if incompatible blood is transfused.

Step 1 — Why O negative is the universal donor:

- **Group O**: The *I* gene encodes a non-functional enzyme; no A or B antigens are displayed on the RBC surface. Therefore, neither anti-A nor anti-B antibodies in the recipient react with Group O RBCs.
- **Rh negative (D negative)**: The Rh D antigen is absent from the RBC sur-

face. Transfusing Rh-negative blood into an Rh-positive patient is safe (no anti-D reaction). Importantly, it is also safe for Rh-negative recipients (does not sensitise them to D antigen).

Because O^- blood lacks the A, B, *and* Rh D antigens simultaneously, it can be safely transfused to *any* recipient regardless of their ABO or Rh type, without triggering an immediate haemolytic transfusion reaction. This is why O^- blood is used in emergency settings when the patient's blood type is unknown.

Why other options are wrong:

- Option B (O positive): Lacks A and B antigens but *expresses Rh D*; transfusing to Rh-negative recipients (approximately 15% of the population) risks immune sensitisation and future haemolytic disease.
- Option C (AB positive): AB^+ individuals are the "universal recipients" (not donors); their RBCs carry A, B, and D antigens, which would react with anti-A, anti-B, or anti-D antibodies in recipients of other blood types.
- Option D (AB negative): AB^- RBCs display both A and B antigens (no D), so they would trigger haemolytic reactions in recipients with anti-A or anti-B antibodies (blood groups O, B, and A respectively).

Final Answer: O negative (O^-) individuals are universal donors because their RBCs lack A, B, and Rh D antigens $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q 8

Sol.9.

Solution

Concept — Models of Population Growth: Population ecologists use mathematical models to quantify how population size (N) changes over time. The two fundamental models — exponential and logistic — differ in whether environmental resistance (resource limitation) is incorporated.

Step 1 — The logistic (Verhulst) model: The logistic growth equation is:

$$\frac{dN}{dt} = r_{\max} N \left(\frac{K - N}{K} \right)$$

where $r_{\max}$ = intrinsic rate of natural increase, K = **carrying capacity** (maximum sustainable population size set by available resources). The term $(K - N)/K$ is the "unused" fraction of K; as $N \to K$, this fraction $\to 0$ and growth stops. This produces the characteristic **S-shaped (sigmoidal)** curve with three phases: (i)

slow initial growth (few individuals), (ii) rapid exponential-like growth at $N = K/2$ (inflection point of maximum dN/dt), and (iii) slowing deceleration phase as N approaches K, where density-dependent factors (competition, predation, disease) increase.

Step 2 — Contrast with the exponential model: The exponential model $dN/dt = rN$ assumes unlimited resources; the per-capita growth rate is constant, producing the J-shaped curve with no upper limit.

Why other options are wrong:

- Option A (Exponential/Malthusian): Produces a J-shaped curve; does not incorporate carrying capacity; growth rate accelerates continuously.
- Option B (Arithmetic/linear): A constant increment per time unit; not a standard ecological model and does not reflect biological mechanisms of reproduction.
- Option C (Hyperbolic): Would imply accelerating (not decelerating) growth; not a recognised ecological population model and incompatible with density-dependent regulation.

Final Answer: The logistic (Verhulst) model produces the S-shaped curve incorporating carrying capacity $K \Rightarrow \boxed{\text{D}}$

Answer: (D) Go Back to Q 9

Sol.10.

Solution

Concept — Seed Dispersal Mechanisms: Dispersal of seeds away from the parent plant reduces intraspecific competition for resources and enables colonisation of new habitats. Plants have evolved fruits and seeds with structural adaptations matched to specific dispersal agents (wind, water, animals, explosive self-dispersal).

Step 1 — Coconut and hydrochory (water dispersal): *Cocos nucifera* is the textbook example of **hydrochory**. The fruit has layered structural adaptations for flotation and protection during extended sea or river travel:

- **Fibrous mesocarp (coir)**: Thick, spongy layer of air-filled fibres (density $<$ 1 g/cm^3) that provides buoyancy. This is the defining adaptation.
- **Hard, waterproof endocarp (coconut shell)**: Protects the seed and endosperm from prolonged saltwater immersion.

- **Large liquid endosperm (coconut water)**: Provides metabolic reserves during dispersal and early germination.

Coconuts can remain viable floating at sea for 110+ days and travel hundreds of kilometres, explaining the pan-tropical coastal distribution of coconut palms across the Indo-Pacific — a textbook example of hydrochorous colonisation of oceanic islands.

Why other options are wrong:

- Option A (Anemochory, wind): Wind-dispersed diaspores are lightweight and often have aerodynamic structures (pappus: dandelion; wing/samara: maple, ash; or tiny seeds: orchid). A large, heavy coconut ($\sim$1–2 kg) is entirely unsuitable for wind dispersal.
- Option C (Zoochory, animals): Zoochorous fruits have nutritious, fleshy or palatable flesh (endozoochory) or hooked surface structures that cling to fur/feathers (epizoochory). While some animals (e.g., sea turtles, humans) transport coconuts, the primary evolutionary mechanism is hydrochory.
- Option D (Autochory, self-dispersal): Self-dispersal involves explosive dehiscence (squirting cucumber, *Impatiens*), elasticity (witch-hazel), or hygroscopic movements. Coconuts have none of these mechanisms.

Final Answer: Coconut is dispersed by water (hydrochory) owing to its buoyant fibrous husk $\Rightarrow$ B

Answer: (B) Go Back to Q 10

Sol.11.

Solution

Concept — The Molecular Clock: The molecular clock is a method in molecular evolution that uses the rate of molecular change (mutations in DNA or amino acid substitutions in proteins) to estimate the timing of evolutionary events, such as when two lineages diverged from a common ancestor.

Step 1 — Basis: constant rate of neutral mutation accumulation: Emile Zuckerkandl and Linus Pauling (1965) observed that the number of amino acid differences in homologous proteins (e.g., haemoglobin, cytochrome c) between pairs of species was approximately proportional to the time of divergence estimated from the fossil record. This suggested that sequence change accumulates at a roughly *constant rate* over time. Motoo Kimura's neutral theory of molecular evolution (1968) provided the theoretical basis: most DNA sequence changes at

synonymous sites and in non-coding regions are **neutral** (neither beneficial nor deleterious), invisible to natural selection, and drift to fixation at a rate equal to the mutation rate μ. Therefore:

$$\text{Divergence time} = \frac{\text{Number of sequence differences between species}}{2\mu}$$

(Factor of 2 because both lineages accumulated mutations since divergence.) Calibration from fossil-dated divergences allows the rate μ to be estimated for specific genes.

Why other options are wrong:

- Option B (Rate of morphological change in fossils): Morphological evolution is highly variable (mosaic, punctuated) and does not tick at a constant rate; it provides calibration points for the molecular clock but is not the clock itself.
- Option C (Rate of speciation per lineage): Speciation rates vary enormously between lineages (radiations vs. living fossils) and cannot serve as a uniform clock.
- Option D (Rate of protein structural change): Three-dimensional protein structure is highly conserved relative to sequence; structural change rates are not constant and cannot serve as a reliable clock.

Final Answer: The molecular clock is based on the approximately constant rate of neutral mutation accumulation in DNA over evolutionary time $\Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q 11

Sol.12.

Solution

Concept — DNA Fingerprinting: DNA fingerprinting (DNA profiling, genetic fingerprinting) identifies individuals by detecting polymorphic patterns in their genome. Since all humans share ∼99.9% of their DNA sequence, forensic identification relies on the ∼0.1% that varies between individuals, particularly highly polymorphic repetitive regions.

Step 1 — Short Tandem Repeats (STRs / microsatellites): STRs are tandemly repeated sequences of 2–7 base pairs (e.g., AGAT repeated n times at a given locus). The number of repeats (n) varies enormously between individuals due to slippage of DNA polymerase during replication, creating many alleles per locus (high heterozygosity). Modern forensic systems (e.g., **CODIS** — Combined DNA

Index System in the USA, which uses 20 STR loci) exploit this multi-locus polymorphism: the probability that two unrelated individuals share identical alleles at all loci simultaneously is vanishingly small ($< 10^{-15}$). STRs replaced older RFLP/VNTR methods because: (i) STR alleles can be amplified by PCR from minute or degraded samples; (ii) results are obtained quickly with automated capillary electrophoresis; (iii) allele sizes are standardised across laboratories.

Why other options are wrong:

- Option A (SNPs): Single nucleotide polymorphisms are biallelic (two alleles per locus), providing less individual identification power per locus than multi-allelic STRs. SNP arrays are used for ancestry and disease association studies but not for standard forensic profiling.
- Option B (RFLPs): RFLP analysis using minisatellite (VNTR) probes was the original DNA fingerprinting method (Alec Jeffreys, 1984). It required large quantities of high-molecular-weight DNA, making it unsuitable for degraded or trace evidence samples; largely superseded by PCR-based STR profiling.
- Option D (CNVs): Copy number variations (large duplications/deletions, >1 kb) are studied using array CGH or whole-genome sequencing; they are not used in standard forensic DNA fingerprinting panels.

Final Answer: Short tandem repeats (STRs / microsatellites) are the basis of modern forensic DNA fingerprinting $\Rightarrow$ C

Answer: (C) Go Back to Q 12

Sol.13.

Solution

Concept — Biological Nitrogen Fixation: Atmospheric N_2 ($\sim$78% of air) is inert to most organisms because its triple bond (N$\equiv$N; bond energy $\approx$ 945 kJ mol^{-1}) is extremely stable. Only prokaryotic diazotrophs possessing the enzyme **nitrogenase** can fix N_2 into biologically usable NH_3.

Step 1 — Rhizobium: symbiotic nitrogen fixation in root nodules: *Rhizobium* (and related genera: *Bradyrhizobium*, *Sinorhizobium*, *Mesorhizobium*) are aerobic, Gram-negative soil bacteria that form highly specific mutualistic symbioses with plants of the family **Leguminosae** (Fabaceae: peas, beans, lentils, soybeans, alfalfa, clover). The infection process involves:

- Root hairs curl around *Rhizobium* cells, which enter via an *infection thread*.
- Bacteria differentiate into **bacteroids** inside cortical cells of the developing

root nodule.

- The nodule produces **leghaemoglobin** (encoded jointly by plant and bacterial genes), which buffers O_2 to micro-aerobic levels: high enough for bacteroid respiration (energy for nitrogenase), low enough to prevent O_2-mediated nitrogenase inactivation.
- Nitrogenase fixes $N_2 \rightarrow NH_3$, which is assimilated into amino acids (asparagine, ureides) and exported to the plant.

Why other options are wrong:

- Option A (*Azotobacter*): Free-living, aerobic, heterotrophic soil bacterium that fixes N_2 directly in the soil without forming root nodule symbioses.
- Option B (*Clostridium*): Free-living, anaerobic, spore-forming soil bacterium (*Clostridium pasteurianum*) that fixes N_2 under anaerobic conditions; no symbiotic root nodule association.
- Option C (*Anabaena*): Filamentous cyanobacterium with specialised nitrogen-fixing cells called **heterocysts**; forms symbioses with the aquatic fern *Azolla* and the angiosperm *Gunnera* — but *not* with leguminous plants.

Final Answer: *Rhizobium* performs symbiotic nitrogen fixation within root nodules of leguminous plants $\Rightarrow$ D

Answer: (D) Go Back to Q 13

Sol.14.

Solution

Concept — Neuromuscular Junction (NMJ): The NMJ is the specialised chemical synapse between the axon terminal of a somatic (lower) motor neuron and the motor end plate of a skeletal muscle fibre. Efficient neurotransmitter release and receptor activation at the NMJ is essential for voluntary movement (NCERT Class 11 Biology, Chapter 21).

Step 1 — Acetylcholine (ACh) as the NMJ neurotransmitter: When an action potential propagates to the axon terminal (pre-synaptic bouton), voltage-gated Ca^{2+} channels open; Ca^{2+} influx triggers exocytosis of synaptic vesicles containing **acetylcholine (ACh)**. ACh diffuses across the synaptic cleft ($\sim$50–100 nm) and binds to **nicotinic acetylcholine receptors (nAChR)** — ligand-gated cation (Na^+/K^+) ion channels on the motor end plate. This generates an *end-plate potential (EPP)* which, if large enough, triggers a muscle action potential. The action potential propagates along the sarcolemma and T-tubules, stimulating Ca^{2+}

release from the sarcoplasmic reticulum and initiating cross-bridge cycling (contraction). ACh is rapidly degraded by **acetylcholinesterase (AChE)** anchored in the synaptic cleft, terminating the signal within milliseconds. This prevents sustained depolarisation and allows repetitive signalling.

Why other options are wrong:

- Option A (Dopamine): A catecholamine neurotransmitter active in the brain's reward pathways (mesolimbic dopamine system), motor control (nigrostriatal pathway), and prefrontal cortex. Dopamine does not act at somatic NMJs.
- Option C (Serotonin, 5-HT): A monoamine neurotransmitter important in mood, sleep, appetite regulation (CNS), and gut motility (enteric nervous system). It is not released at the skeletal muscle NMJ.
- Option D (Norepinephrine): Released by postganglionic sympathetic neurons at smooth muscle (e.g., blood vessels) and cardiac muscle, and from the adrenal medulla. It is not the neurotransmitter at the somatic NMJ for skeletal muscle.

Final Answer: Acetylcholine (ACh) is the neurotransmitter released at the neuromuscular junction $\Rightarrow$ B

Answer: (B) Go Back to Q 14

Sol.15.

Solution

Concept — Phylum Echinodermata: Echinoderms (Greek: *echinos* = spiny; *derma* = skin) are exclusively marine, deuterostome invertebrates with pentaradial (five-fold) symmetry in adults (bilateral as larvae). Major classes include Asteroidea (sea stars), Echinoidea (sea urchins, sand dollars), Holothuroidea (sea cucumbers), Ophiuroidea (brittle stars), and Crinoidea (feather stars / sea lilies). NCERT Class 11 Biology, Chapter 4 identifies the water vascular system as the defining feature of this phylum.

Step 1 — The water vascular system (WVS): The WVS is a unique coelomic hydraulic network filled with seawater (modified), unique to Echinodermata. Its principal components:

- **Madreporite**: Sieve-like plate on the aboral surface, the entry point for seawater.
- **Stone canal**: Connects madreporite to ring canal; has a calcified wall.

- **Ring canal**: Encircles the oesophagus; connects to five radial canals.
- **Radial canals**: Extend into each arm/radius, giving off lateral canals to each tube foot.
- **Tube feet (podia)**: Each consists of an ampulla (muscular bulb) and a podium (elongated cylinder). Ampulla contraction forces fluid into podium, extending it; sucker at tip adheres to substrate; retraction of podium by longitudinal muscles allows locomotion.

Functions: locomotion, prey capture (sea stars pry open bivalves), gas exchange (thin-walled podia allow diffusion), osmoregulation, and sensory reception.

Why other options are wrong:

- Option B (Open circulatory system): Characteristic of most arthropods and many molluscs, where haemolymph flows into body sinuses. Echinoderms do have a haemal system (open, reduced), but the defining, eponymous locomotory system is the WVS.
- Option C (Haemolymph-based transport): A feature of arthropods (insects: haemolymph bathing tissues in the haemocoel); not present in echinoderms.
- Option D (Mantle cavity): Found exclusively in Mollusca; the mantle folds enclose a cavity housing the gills (ctenidia) and receiving excretory and reproductive products. Echinoderms have no mantle.

Final Answer: The water vascular system — a unique hydraulic network of canals and tube feet — defines phylum Echinodermata $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q 15

Answer Key

Q	Ans	Q	Ans	Q	Ans	Q	Ans	Q	Ans
1	D	2	C	3	B	4	A	5	D
6	C	7	B	8	A	9	D	10	B
11	A	12	C	13	D	14	B	15	A