A.3.2 · Classification and cladistics · supported focus

International Baccalaureate · IB Diploma · Biology · HL

Scope and prerequisites

Supported HL focus. First assessment 2025; current subject brief acquired; full Biology guide not acquired. Remaining guide, assessment and practical requirements retain their recorded holds.

Prerequisites: diversity of organisms from A.3.1 and DNA sequences from A.1.2. Each lesson develops its own method before independent transfer.

These are original or explicitly fictional teaching examples, not actual measurements or completed assessed learner investigations.

Classification and cladistics

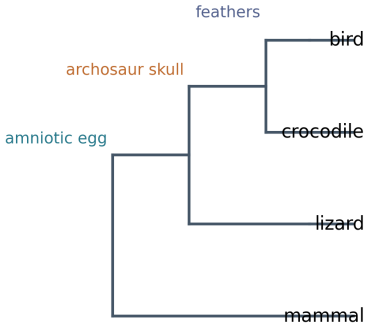
■ What would explain this observation?

- Birds were once classed far from reptiles, yet their DNA and skull bones place them next to crocodiles. Which evidence should decide the grouping?
- Start with a prediction. State the quantities or features you would compare, then decide what evidence could distinguish two explanations.

■ Build the model

- **Classification** places every species in the nested hierarchy: domain, kingdom, phylum, class, order, family, genus, species, named by the **binomial system** (genus + species, as in Homo sapiens). **Cladistics** groups organisms by **shared derived characters** – features that appeared in a common ancestor – drawn as a **cladogram** whose nodes mark those characters.
- Molecular evidence such as DNA sequence differences usually decides between competing trees. Rotating two branches at a node changes nothing: the branching pattern, not the left-right order, records the relationships.
- classification: Placing organisms into nested groups by shared features; binomial system: The two-part naming of species by genus and species; shared derived character: A feature inherited from the group's most recent common ancestor; cladogram: A branching diagram of relationships built from shared derived characters.

A cladogram: shared derived characters define each clade



Rotating at a node changes nothing about the relationships

Molecular evidence counts differences

8 differences in 50 aligned sites
8/50 × 100 = 16%

fewer differences →
a more recent shared ancestor

An observed percentage is not a molecular clock without rate assumptions

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■ Choose evidence that can test it

- Build the tree from a character matrix first, then ask whether a NEW dataset (for example a DNA sequence) reproduces the same groupings; independent agreement is the strongest support.
- A single visible feature can mislead through convergent evolution – distantly related animals evolve similar shapes for similar lives – so one trait alone never defines a clade.

■ Work from known quantities

- State the known values and their units. Choose the relation because its assumptions fit this case, then rearrange before substitution.
- Known: two aligned DNA sequences differ at 8 of 50 sites. Percentage difference = differences / sites × 100 = 8/50 × 100 = 16%. A third species differing at only 5 of 50 sites (10%) shares a more recent ancestor with the second sequence than the first does.

Example:

Another alignment shows 6 differences in 40 sites. Find the percentage difference using the same sequence: known quantities → model → relation → substitution → unit and interpretation. (Answer: 6/40 × 100 = 15%. The percentage is an observed comparison, not a calibrated molecular clock – dating a split needs rate assumptions.)

■ Check the conclusion and its limits

- A cladogram is a hypothesis of relationships, revisable when better evidence arrives. The observed percentage difference ignores multiple changes at the same site, so it underestimates true divergence for distant pairs.
- Return to the original observation. Explain what the result supports, which conditions it assumes, and one way to test a competing explanation.

Warn:

A modern species at one branch tip is the ancestor of the species at another tip. This claim is false: every tip is a modern descendant; the nodes represent shared ancestors that no longer exist. Birds are descended from archosaur ancestors – they are not descended from today's crocodiles.

Key:

Classification and cladistics: nested groups from domain to species, named binomially; cladograms group by shared derived characters, with molecular differences as decisive evidence. Count differences as a percentage, and read the branching – never the tip order – as the relationship.