

Reading Evolutionary Trees:

An Introduction for Learners and Educators



Trees show evolutionary relationships, organize biodiversity, and support real-world work



Applications span health, agriculture, conservation, biotechnology, and forensics



Course roadmap: tree anatomy, clades, tree shapes, classification, tree-building, classroom strategies



By the end: identify clades, trace common ancestors, compare relatedness, evaluate claims



Core framing: a tree is a testable hypothesis about shared ancestry, not a ladder of progress



Why Trees Are Misread: Everyday Intuitions and Their Limits

- **Misreading phylogenetic trees is predictable, not careless**

- Documented across students, teachers, and the public
- Four recurring patterns:
 - Reading across tips: proximity equals relatedness
 - Node counting: fewer nodes means closer relatives
 - Ladder thinking: progress toward a target
 - Similarity equals relatedness

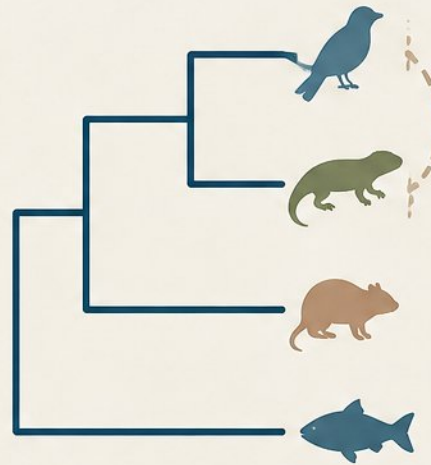
- **Theory-based misconceptions resist change more than graphic-reading errors**

- **Teach by contrasting intuition with scientific interpretation**

- **Design tip: avoid edge placements and diagonal layouts**

Intuitive (misleading) reading

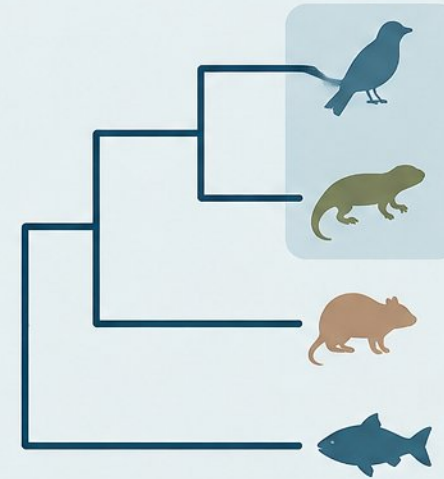
Closest tip = closest relative



These two look close,
so they must be closely
related.

Scientific interpretation

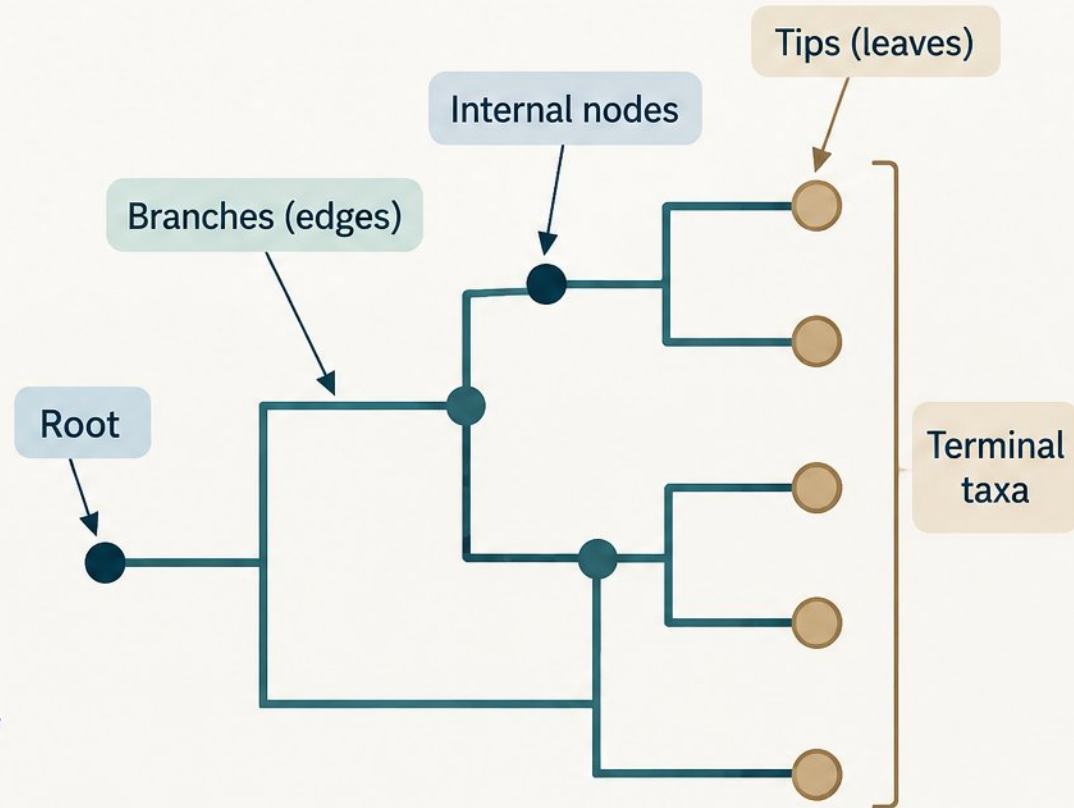
Clades show true relatedness



These two are part of
the same clade and are
more closely related.

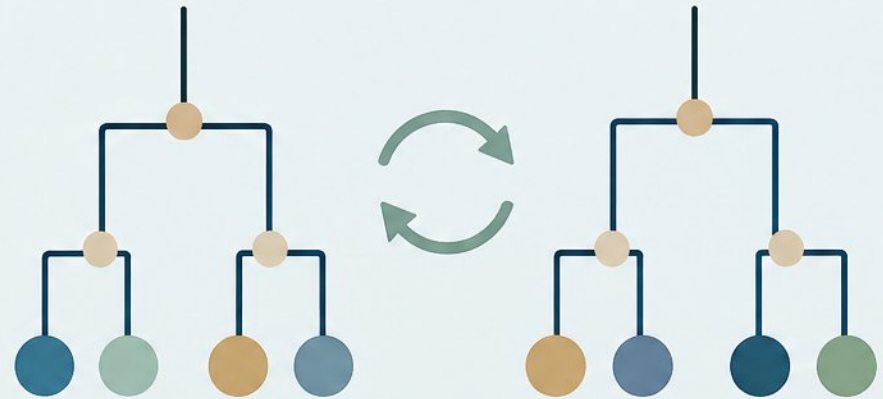
Tree Anatomy and Core Vocabulary

- Parts: root, branches (edges), internal nodes, tips (leaves), terminal taxa
- Root = most recent common ancestor of all taxa in the tree
- Internal nodes = inferred ancestral populations, not observed directly
- Rooted trees show ancestry direction; unrooted trees show relatedness only
- Rooting usually uses an outgroup; Newick notation writes trees linearly
- Rotating branches around nodes reorders taxa but changes no relationships



Practice: Rotate, Reread, and Reinterpret

- Hands-on task: build or rotate a simple tree; confirm relationships stay the same
- Nodes are shared ancestors; terminal taxa are cousins, not parent-child pairs
- Rotating branches dissolves the illusion of a 'main line' with side tracks
- Use straws, cards, mobiles, or tree software so learners feel rotation
- Preempt the error: leftmost or bottom-most tip is not ancestral to the rest

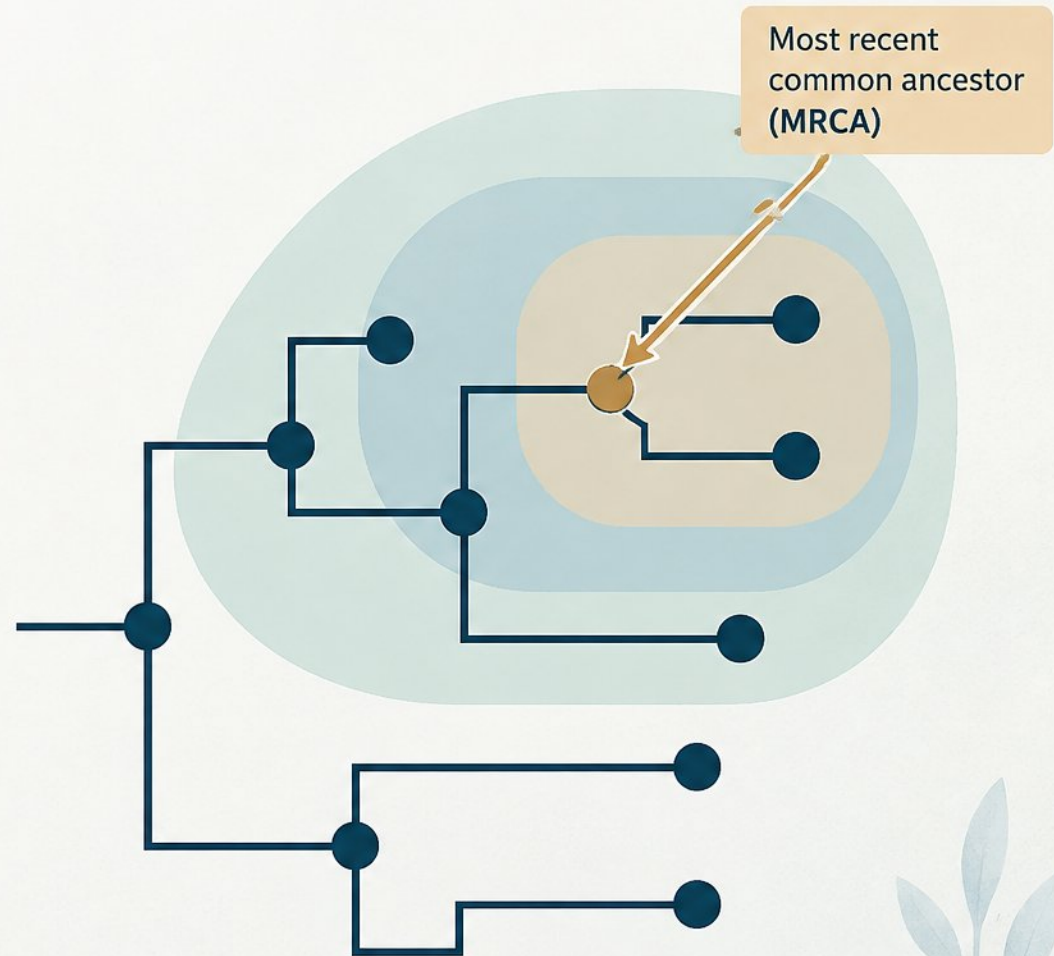


Same relationships, different tip order



Clades and Common Ancestors: Determining Relatedness

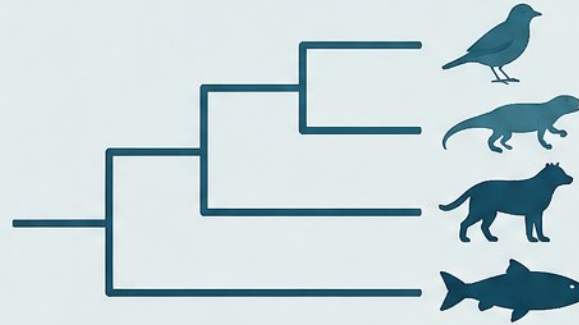
- A clade = an ancestor plus all its descendants (monophyletic group)
- Only clades are valid groups in phylogenetic classification
- Relatedness = age of the most recent common ancestor
- Not tip proximity, not the number of nodes between taxa
- Sister taxa share a more recent common ancestor than any other group
- Nested clades: cut one branch to remove a complete clade
- Practice: trace two tips back to their MRCA



What Trees Do and Do Not Tell Us

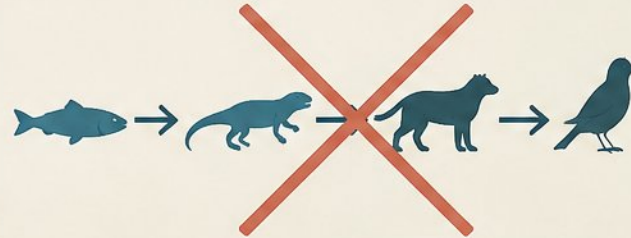
- A tree shows relative relatedness and branching order, not one tip evolving into another
- Bird and bat wings: analogous as wings, homologous as forelimbs
- Homoplasy, convergence, parallelism, and reversal can mislead tree reading
- Parsimony is the criterion for choosing among competing explanations
- Trees are hypotheses supported by morphology, DNA, and fossils — revised as evidence grows
- Trees are not pedigrees: they do not identify specific direct ancestor-descendant lineages

A tree shows relatedness



A tree shows relative relatedness and branching order, not one tip evolving into another.

Not a pedigree



Trees are not pedigrees: they do not identify specific direct ancestor-descendant lineages.

Bird and bat wings



Bird wing

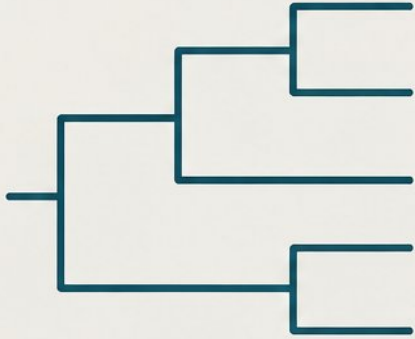


Bat wing

Bird and bat wings: analogous as wings, homologous as forelimbs.

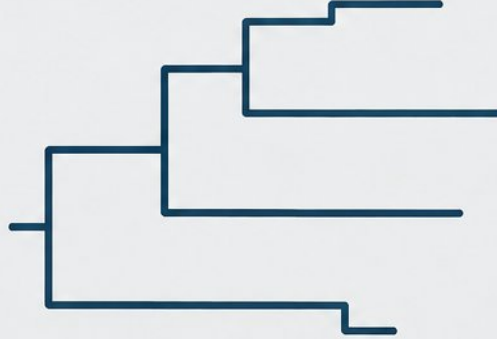
Tree Shapes, Branch Lengths, and Time

Cladogram



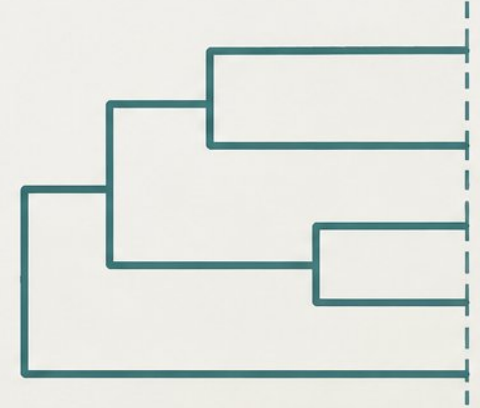
Cladogram: topology only;
branch lengths carry no meaning

Phylogram



Phylogram: branch length equals
amount of evolutionary change

Chronogram



Chronogram: branch length equals time;
tips align

- Phylograms hold the same time information as cladograms
- Balanced or unbalanced shapes imply nothing about advancement
- Branching order is not divergence timing without a time scale
- Time flows root to tips; events on separate branches are not comparable

—————→
TIME

From Trees to Taxonomy: Classification in Practice



Phylogenetic classification names only clades, not artificial Linnaean ranks



Linnaean ranks imply false equivalence: Felidae and Orchidaceae both "family"



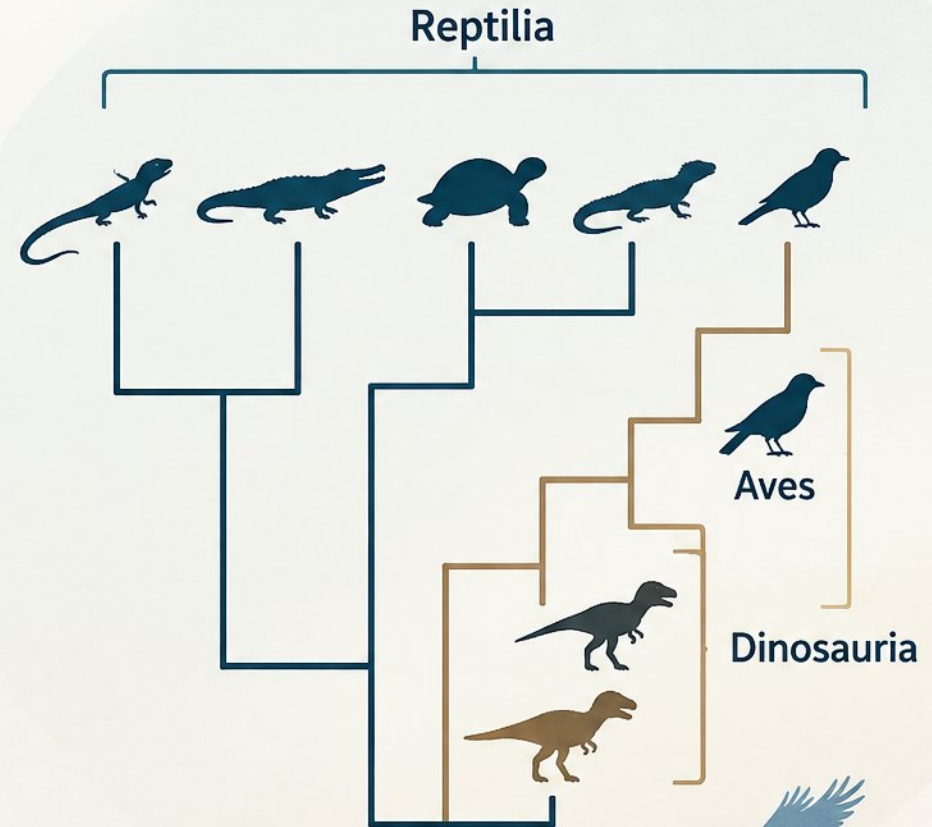
Birds are dinosaurs: Aves nested within Dinosauria; Reptilia valid only with birds



Rank-free names reduce disruption as evolutionary relationships are revised

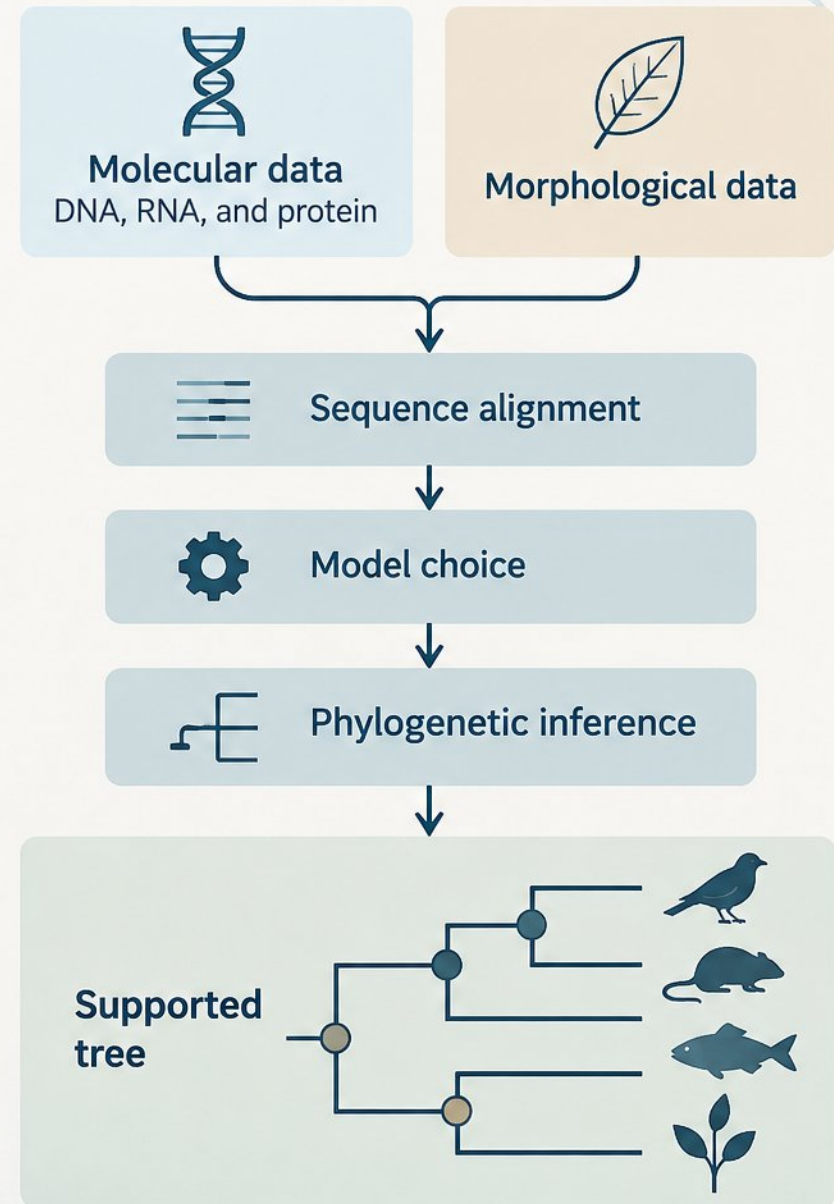


Aves vs. Avialae debate shows nomenclature as a living scientific process



How Trees Are Built: Evidence and Methods

- **Data sources:** morphology plus DNA, RNA, and protein — molecular data dominate today
- **Distance methods** (neighbor joining) vs. character-based methods
- **Character-based:** maximum parsimony, maximum likelihood, Bayesian inference
- **Support values:** bootstrap, ultrafast bootstrap, posterior probabilities — weak clades are unreliable
- **Gene trees $\neq$ species trees:** discordance from incomplete lineage sorting, hybridization, duplication and loss
- **Teaching tools:** MEGA, BEAST, MrBayes, IQ-TREE, R packages, MAFFT



Classroom Strategies for Teaching Tree Reading



Active learning is essential: passive or no instruction yields no significant gains



Sequence by difficulty: rectangular trees first, then diagonal and circular



Proven activities: Great Clade Race, drinking-straw trees, mobiles, seashell sorting



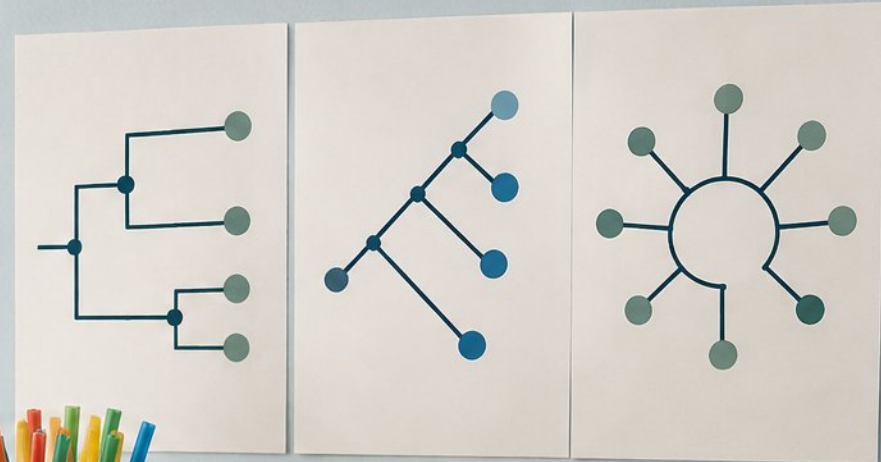
Target stubborn misconceptions: rotation, MRCA tracing, homology vs. analogy



Assess with BETTSI, the Phylogeny Assessment Tool, and forced-choice items

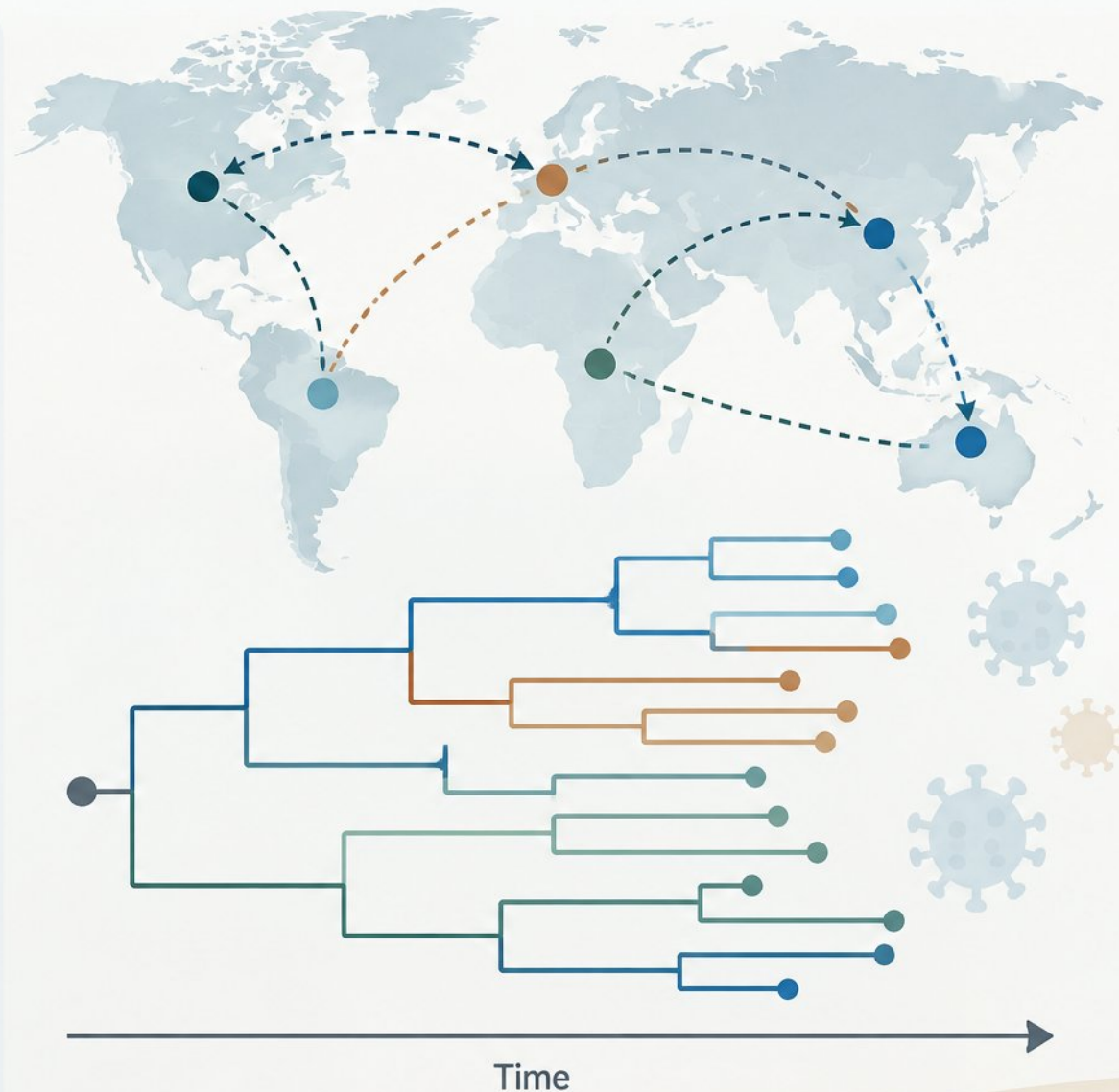


Tactile and universal design approaches reduce barriers and benefit all learners



Real-World Applications I: Disease Tracking and Public Health

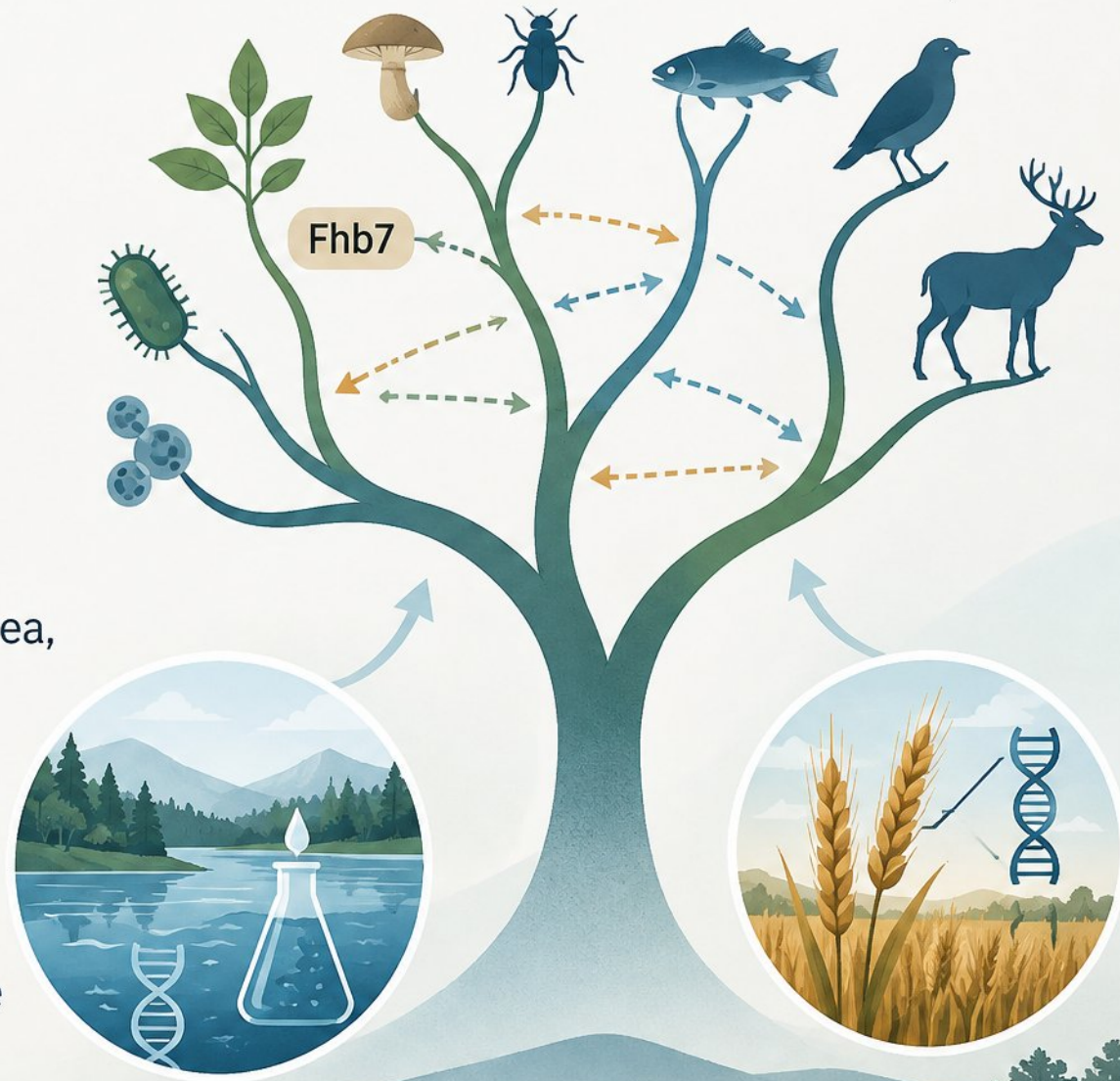
- Phylogenetics drives outbreak response: dating origins, tracing spread, and flagging concerning lineages
- Nextstrain delivers continuously updated genomic surveillance for 21 viruses and tuberculosis
- Delphy (2026) brings near-real-time Bayesian analysis to laptop-scale outbreak datasets
- Pandemic-scale methods (MAPLE, UShER, SPRTA) handle millions of genomes and sequencing errors
- Pango lineage nomenclature now extends beyond SARS-CoV-2 to chikungunya and other viruses



Real-World Applications II:

Conservation, Biotechnology, and the Evolving Tree of Life

- Conservation genomics: prioritize populations, monitor biodiversity, apply eDNA surveillance
- Agriculture: domestication studies, crop improvement, Fhb7 resistance gene in wheat
- Horizontal gene transfer challenges a strictly branched tree model
- HGT widespread in bacteria and archaea, increasingly documented in plants and fungi
- Frontiers: reticulate evolution, hybridization, gene tree discordance
- Data quality and methods matter more than simply adding taxa



Practice Studio: Reading Novel Trees and Explaining Relatedness

1



Guided practice: on an unfamiliar tree, label root, nodes, branches, tips

2



Circle two nested monophyletic groups; state one synapomorphy for each

3



Tracing: find the most recent common ancestor of two taxa and justify in words

4



Tree comparison: do two different drawings show the same relationships?

5

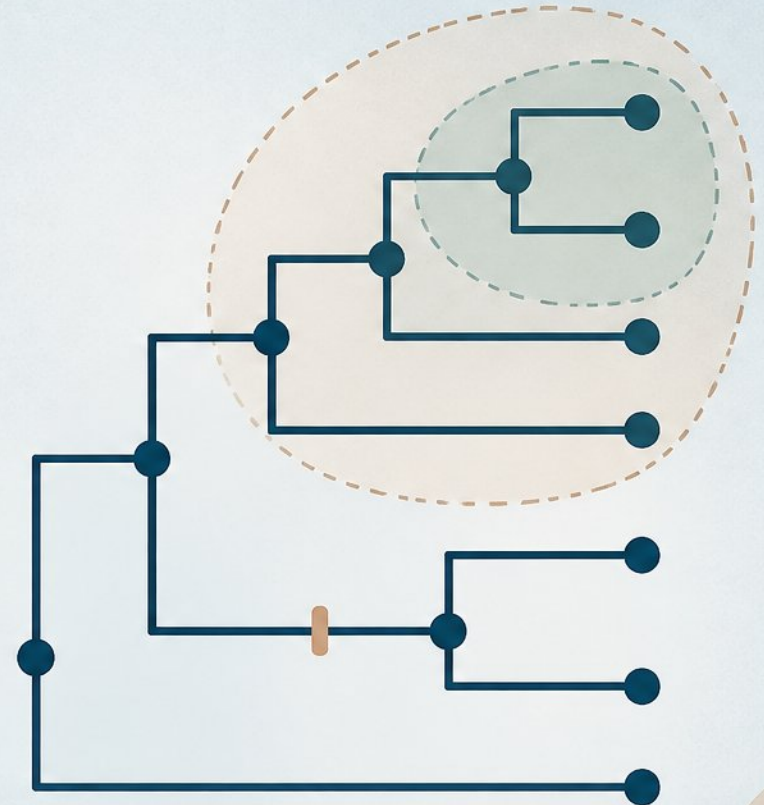


Character mapping: mark where a trait arose or was lost; explain the most parsimonious reconstruction

6



Peer critique: strengthen explanations and surface leftover misconceptions



Wrap-Up: Key Takeaways and Resources for Continued Practice



Core skills: identify clades, trace common ancestors, read branch lengths



Avoid ladder thinking and proximity reasoning; trees are revisable hypotheses



Free tools to practice: OneZoom, iTOL, and HHMI BioInteractive modules



Self-check with BETTSI, the Phylogeny Assessment Tool, and published trees



Educators: integrate scaffolded tree tasks using real research trees



Learners: pick a group you care about and trace it on a public tree



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