

Phylogenetics 101

part A



the diversity of living beings

- All life shares a common genetic history
- phylogenies provide a framework for studying diversity

the Tree of Life

- A branching diagram that illustrates evolutionary history
- A representation of the evolutionary relationships among biological entities
- A fundamental tool to investigate evolutionary processes

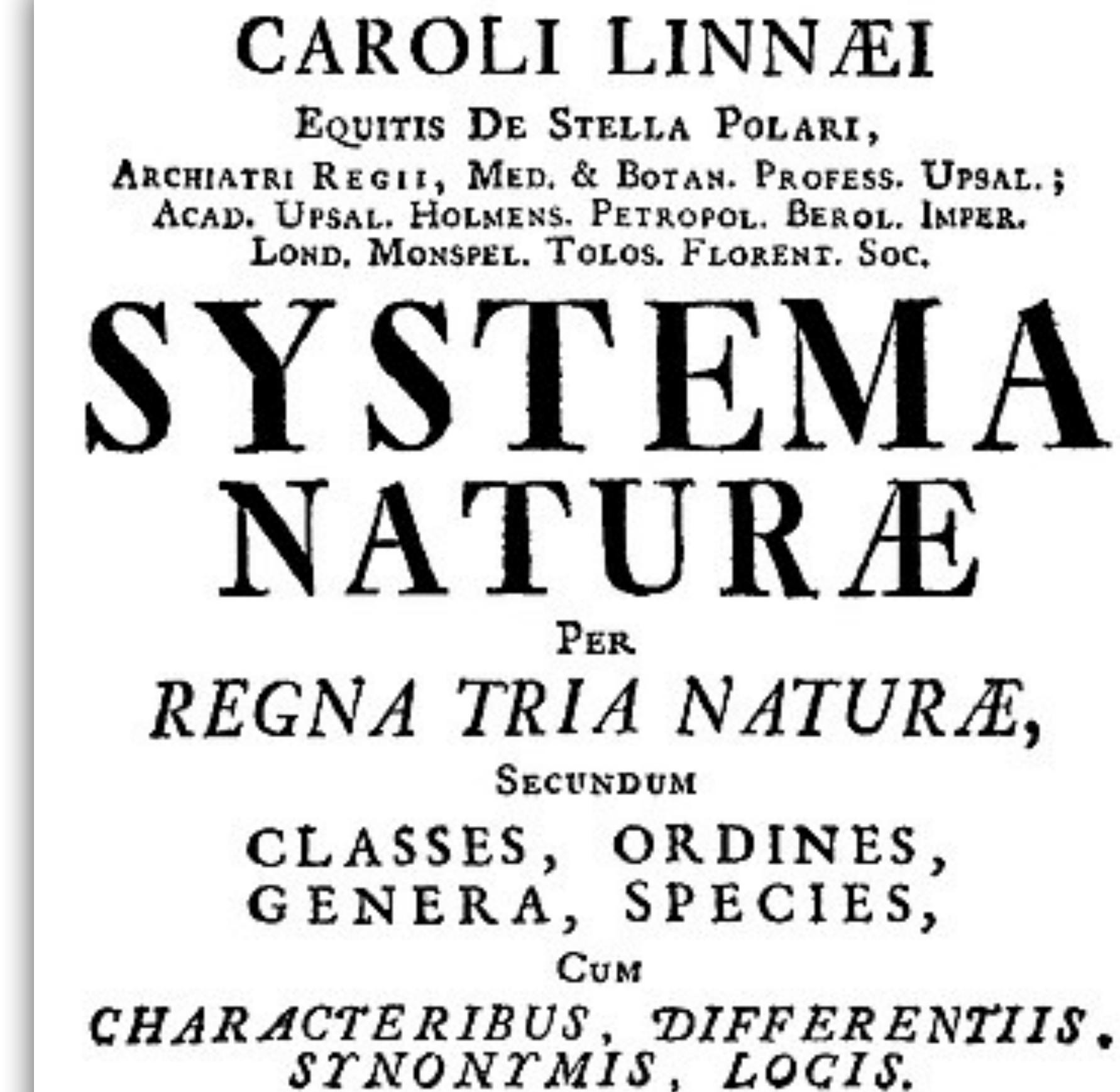
why it matters?

- Helps classify organisms based on shared ancestry
- Reveals patterns of diversification and adaptation
- Provides insights into gene and genome evolution
- Essential for comparative genomics, ecology, and conservation

LINNEUS

Nested hierarchy (groups within groups)

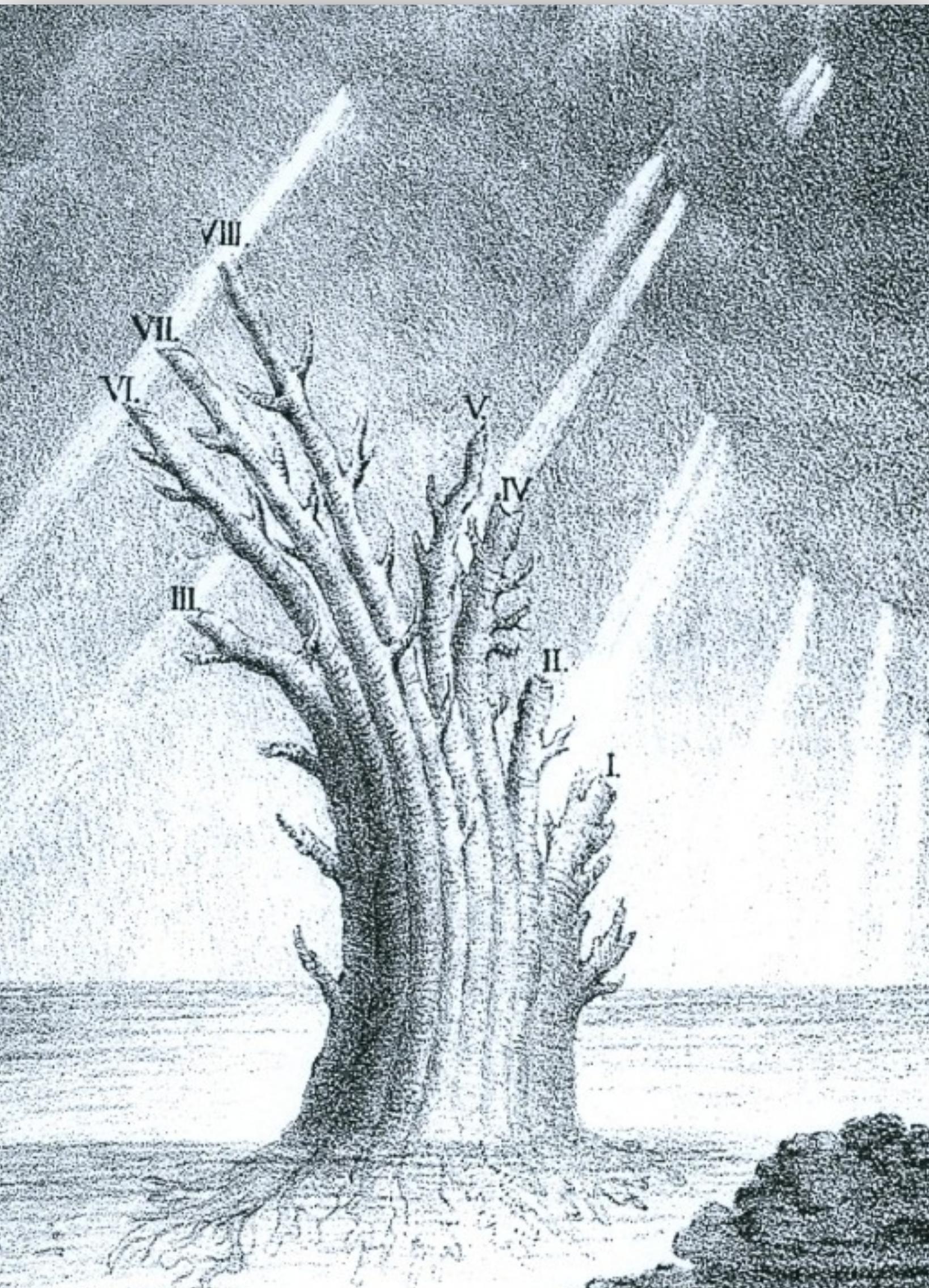
- Kingdom
- Phylum
- Class
- Order
- Family
- Genus
- Species



TOMUS I.

EDITIO DECIMA, REFORMATA.

Cum Privilegio S:æ R:æ M:æ S:æ.



Tree of animal life, from the *Zoologia specialis*
of Carl Edward von Eichwald (1829).

A D D I T I O N S.

463

T A B L E A U

*Servant à montrer l'origine des différens
animaux.*

Vers.

Infusoires.

Polypes.

Radiaires.

Insectes.

Arachnides.

Crustacés.

Annelides.

Cirrhipèdes.

Mollusques.

Poissons.

Reptiles.

Oiseaux.

Monotrèmes.

M. Amphibies.

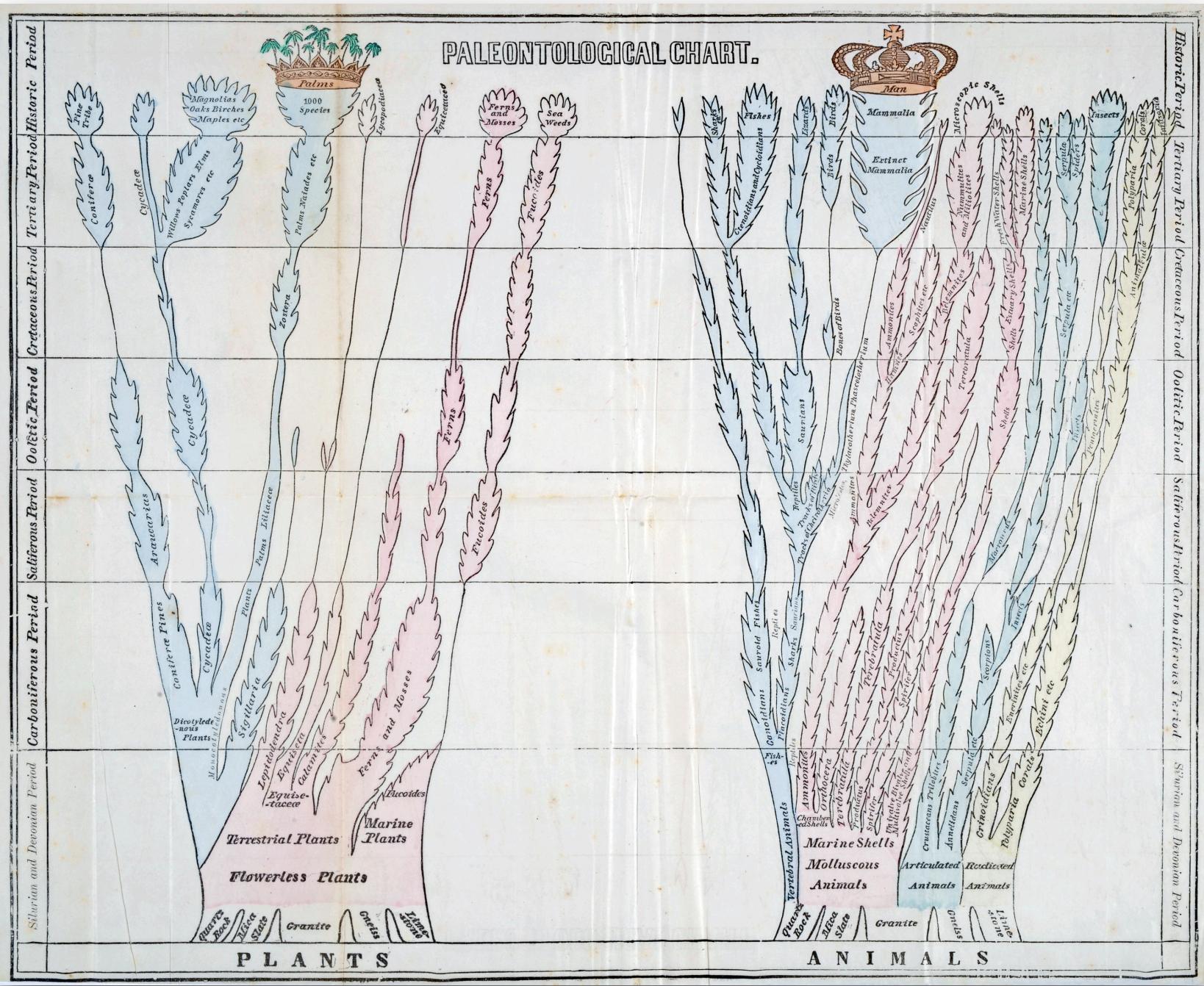
M. Cétacés.

M. Ongulés.

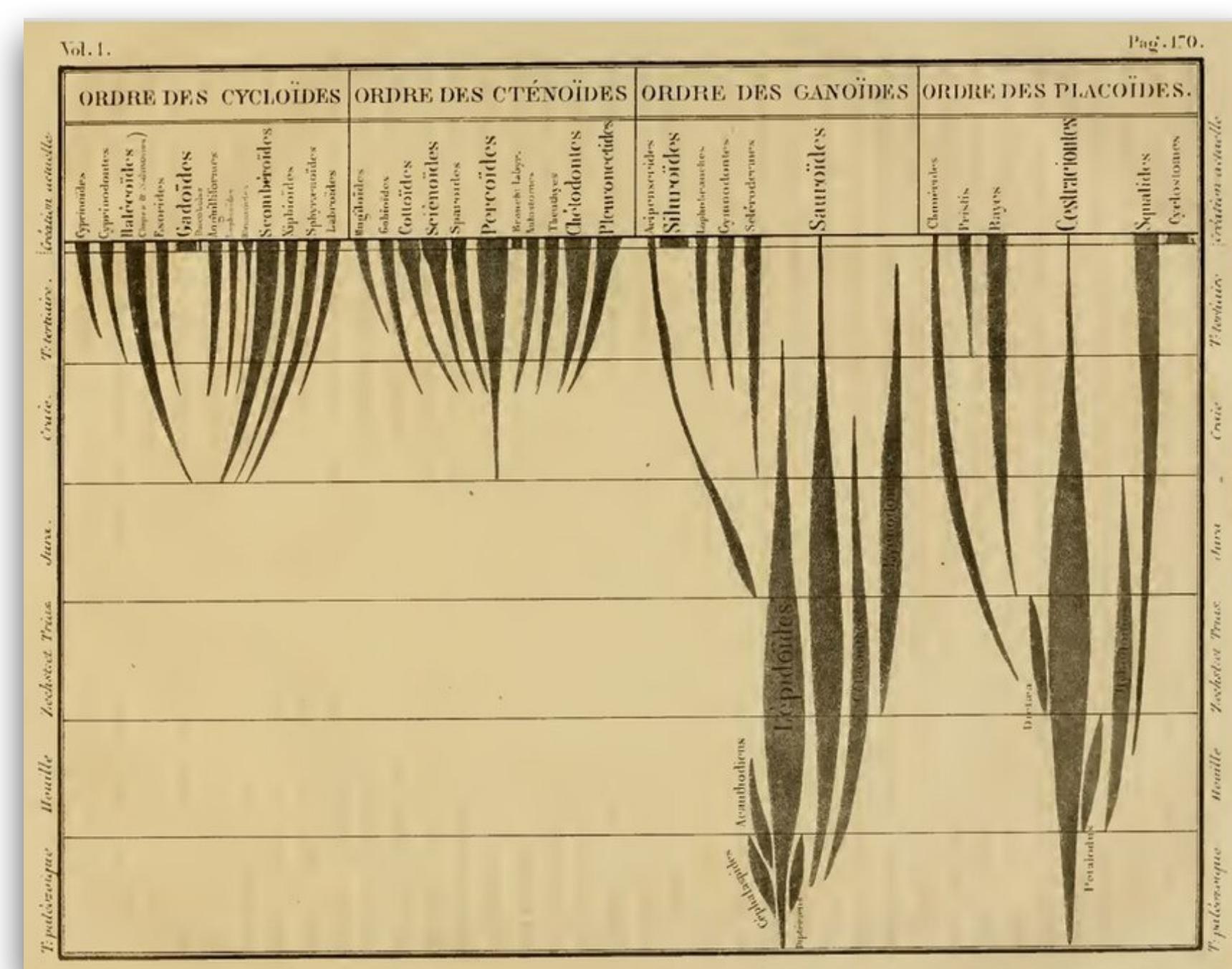
M. Onguiculés.

Cette série d'animaux commençant par deux.

Tree depicting the origin of animals, from the *Philosophie zoologique* of Jean-Baptiste Lamarck (1809).



The Paleontological Chart in the publication 'Elementary Geology'
by Edward Hitchcock (1840).

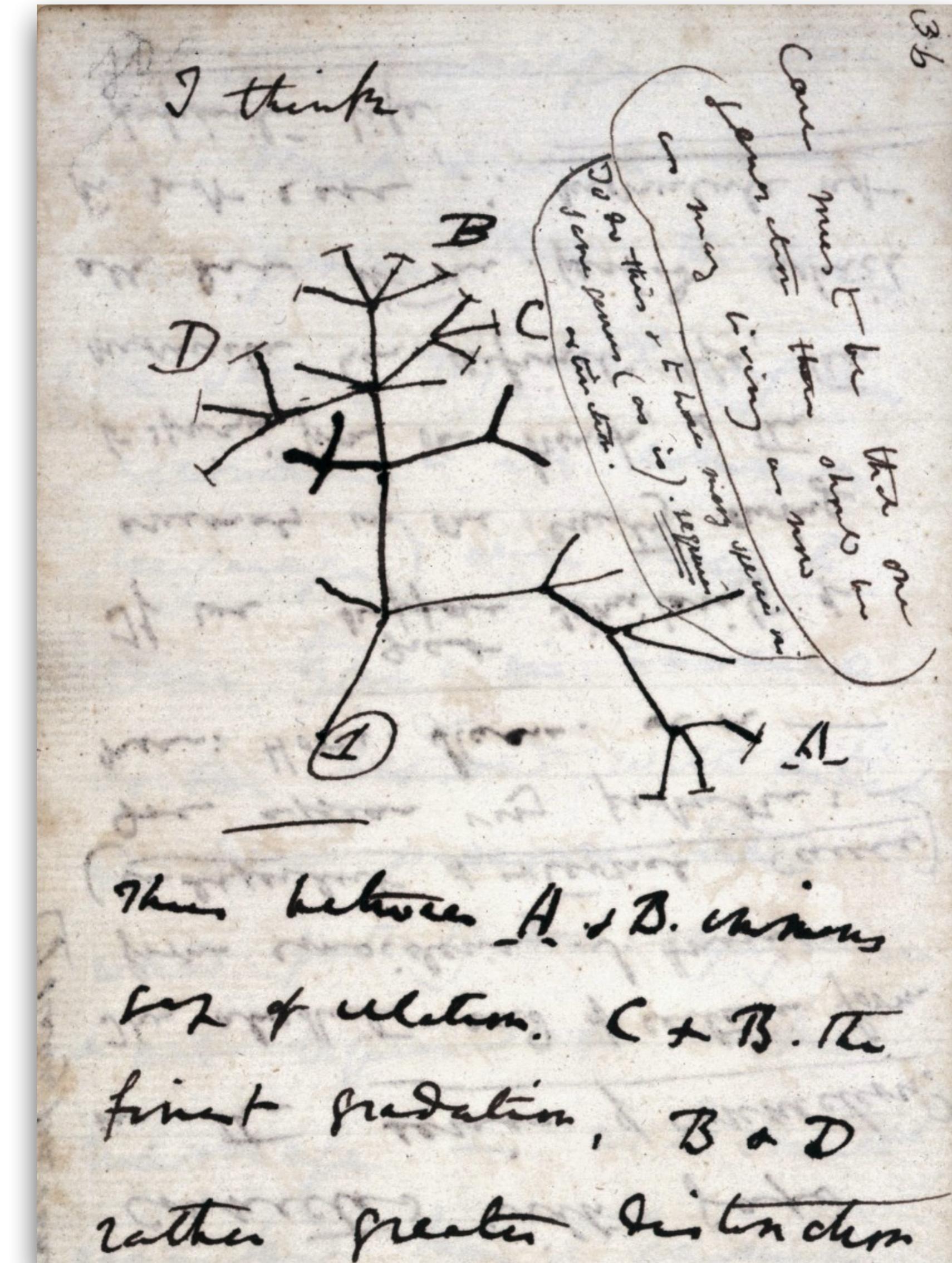


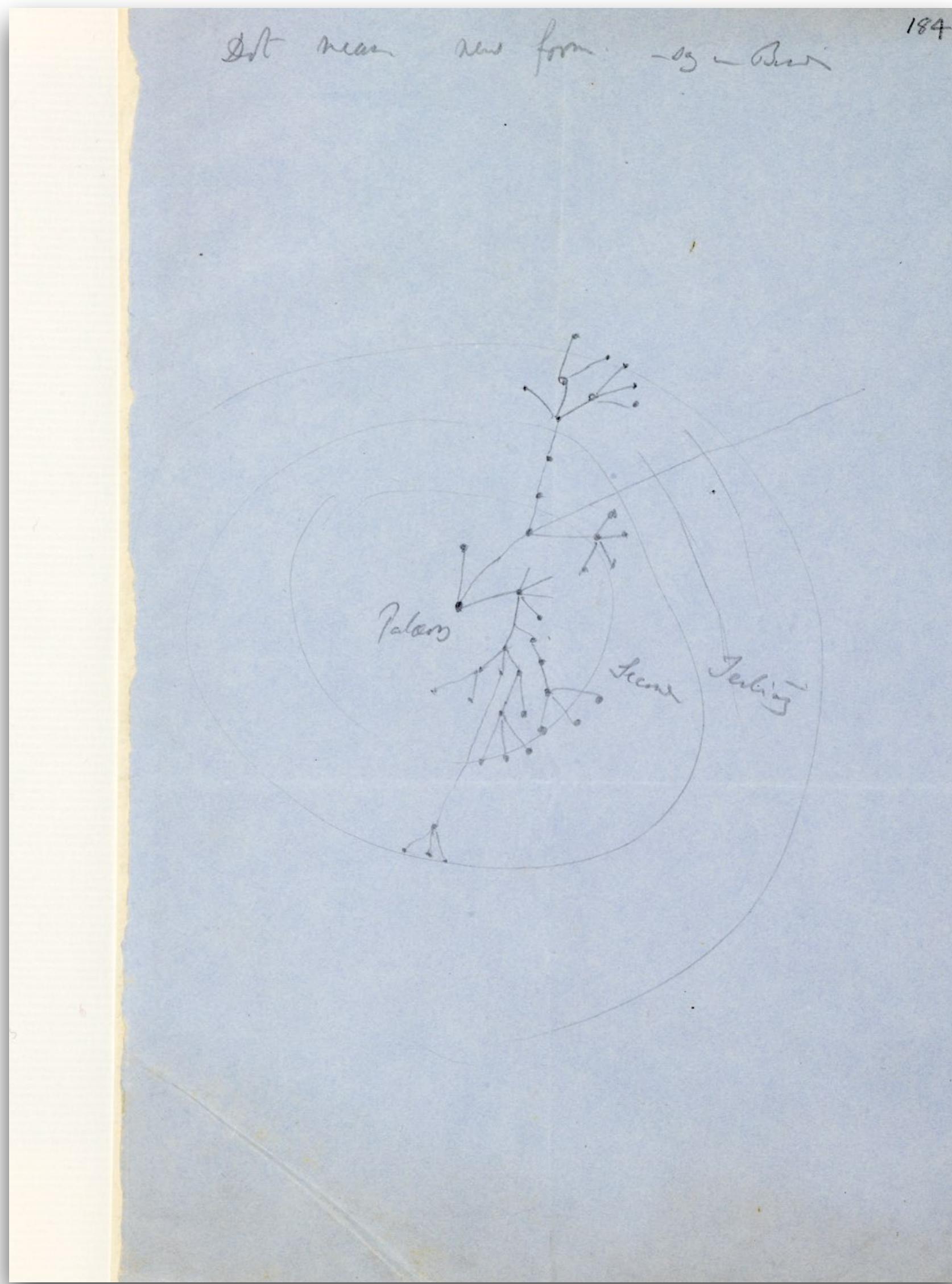
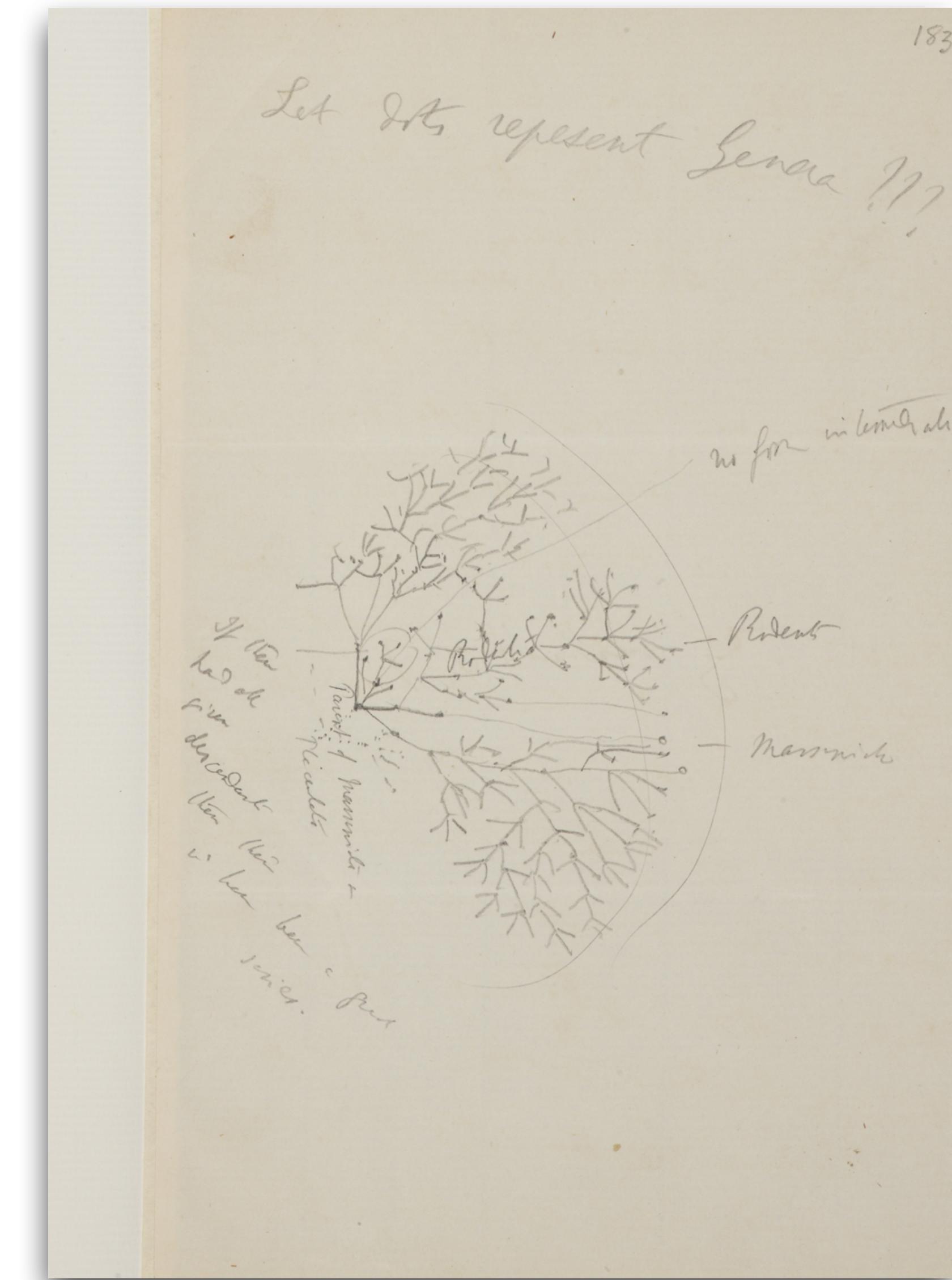
Généalogie de la classe des poissons" in Recherches sur les poissons
fossiles by Louis Agassiz (1833).

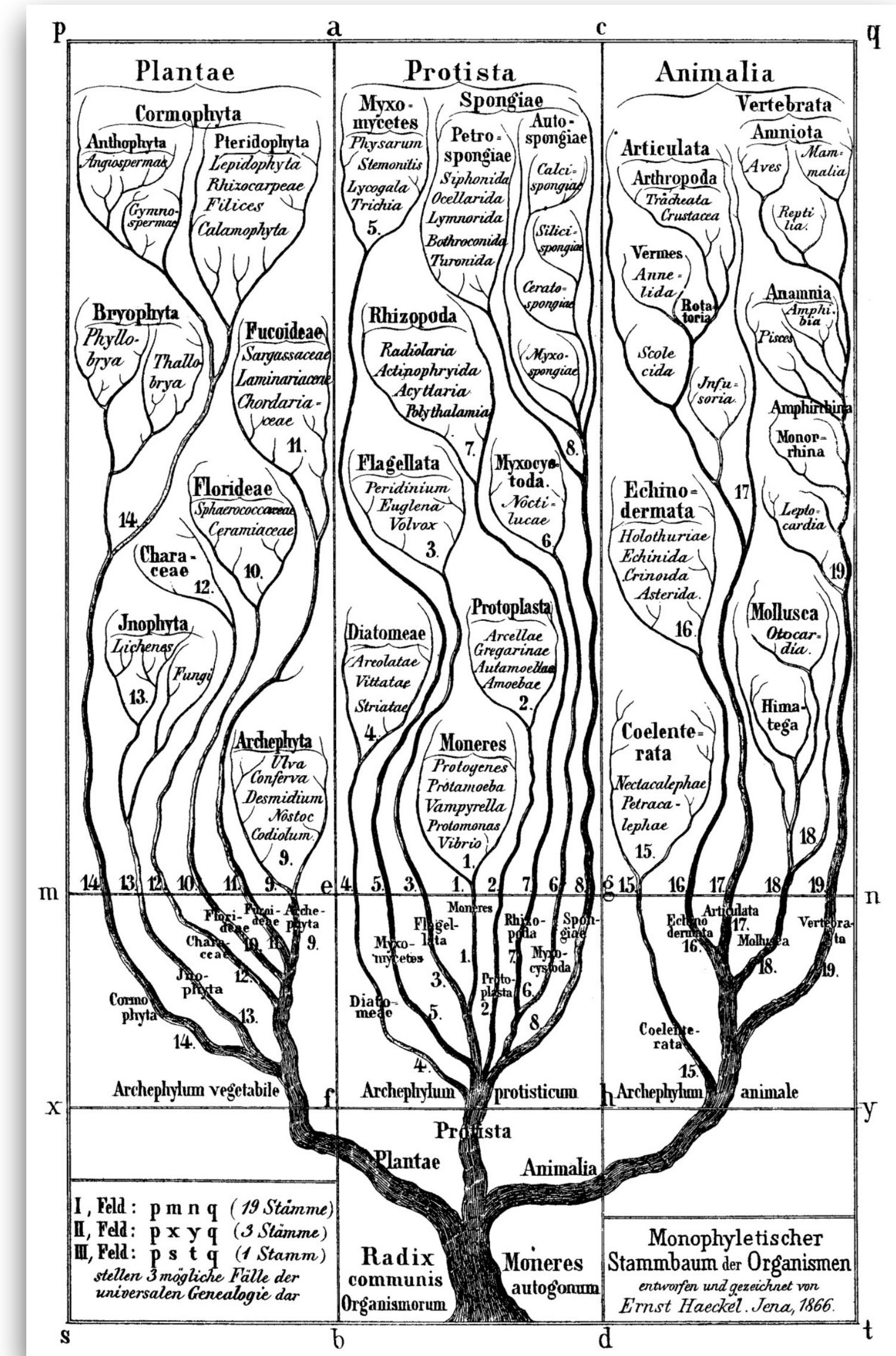
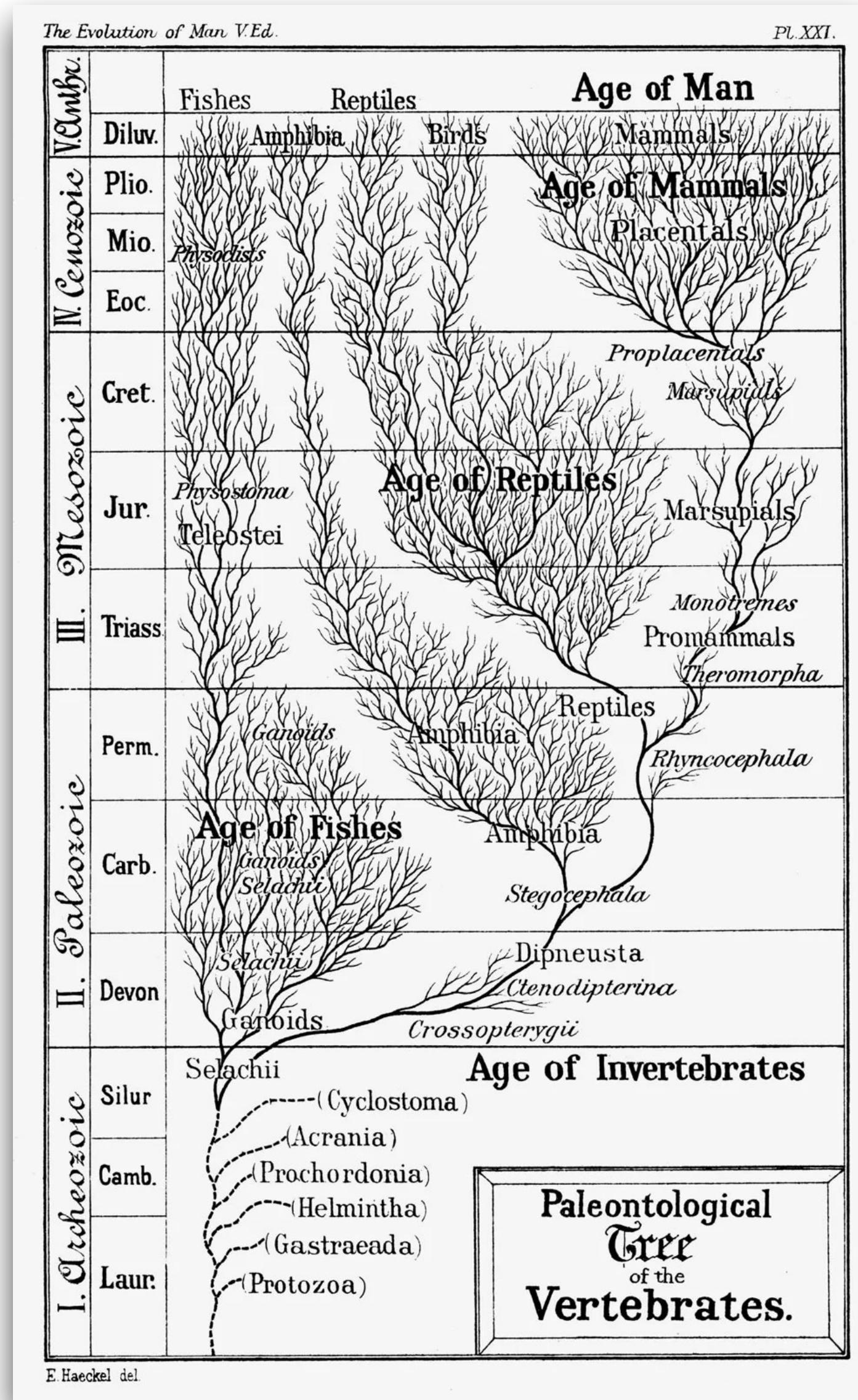
DARWIN

"The affinities of all the beings of the same class have sometimes been represented by a great tree . I believe this simile largely speaks the truth" ...

(Charles Darwin, The Origin of Species) .



darwin manuscript [ms.dar.205.5.184r](#)darwin manuscript [ms.dar.205.5.183r](#)



WHAT IS A TREE?

a branching diagram

a representation of the inferred evolutionary relationships among various biological entities

a tool to investigate the evolutionary processes

TYPES OF PHYLOGENETIC TREES

1.DNA mutations:

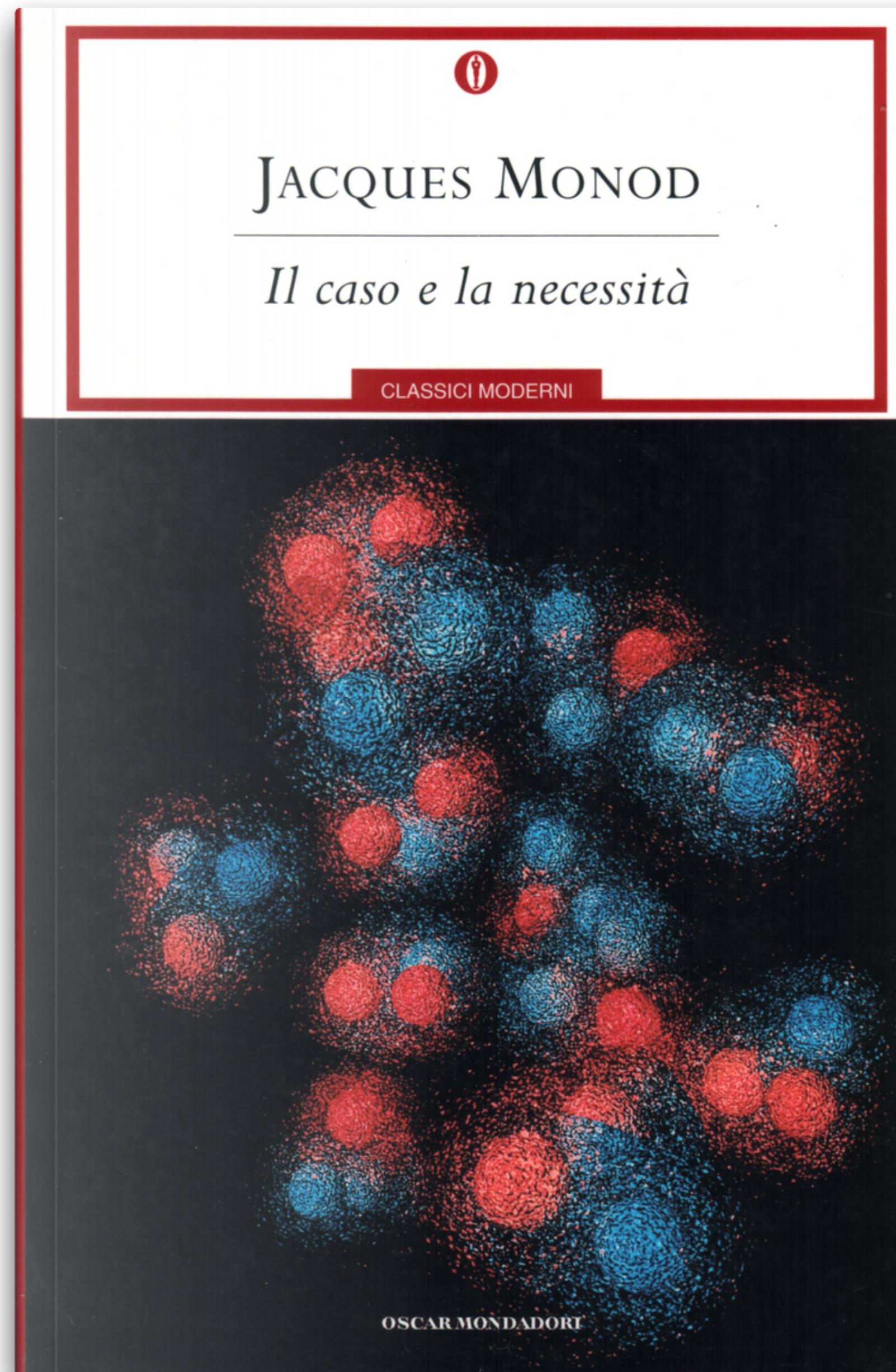
Random generation of diversity

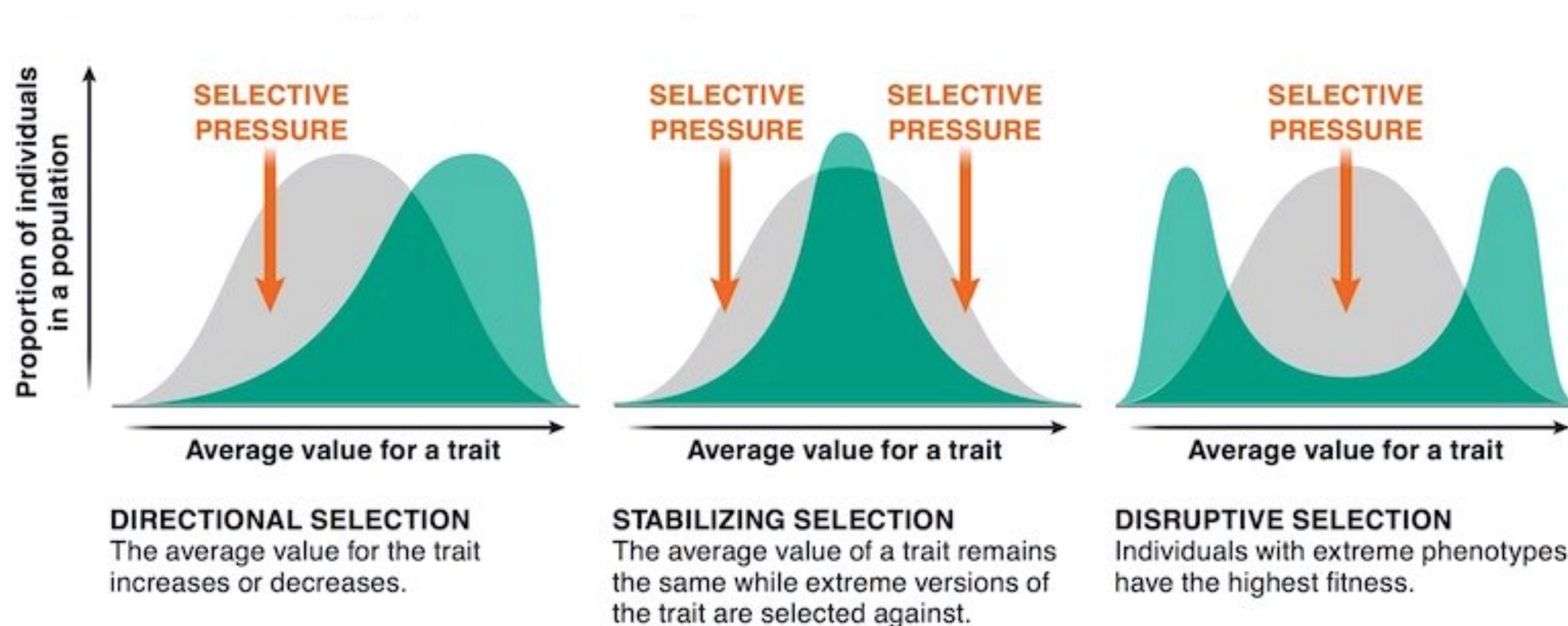
2. Natural Selection:

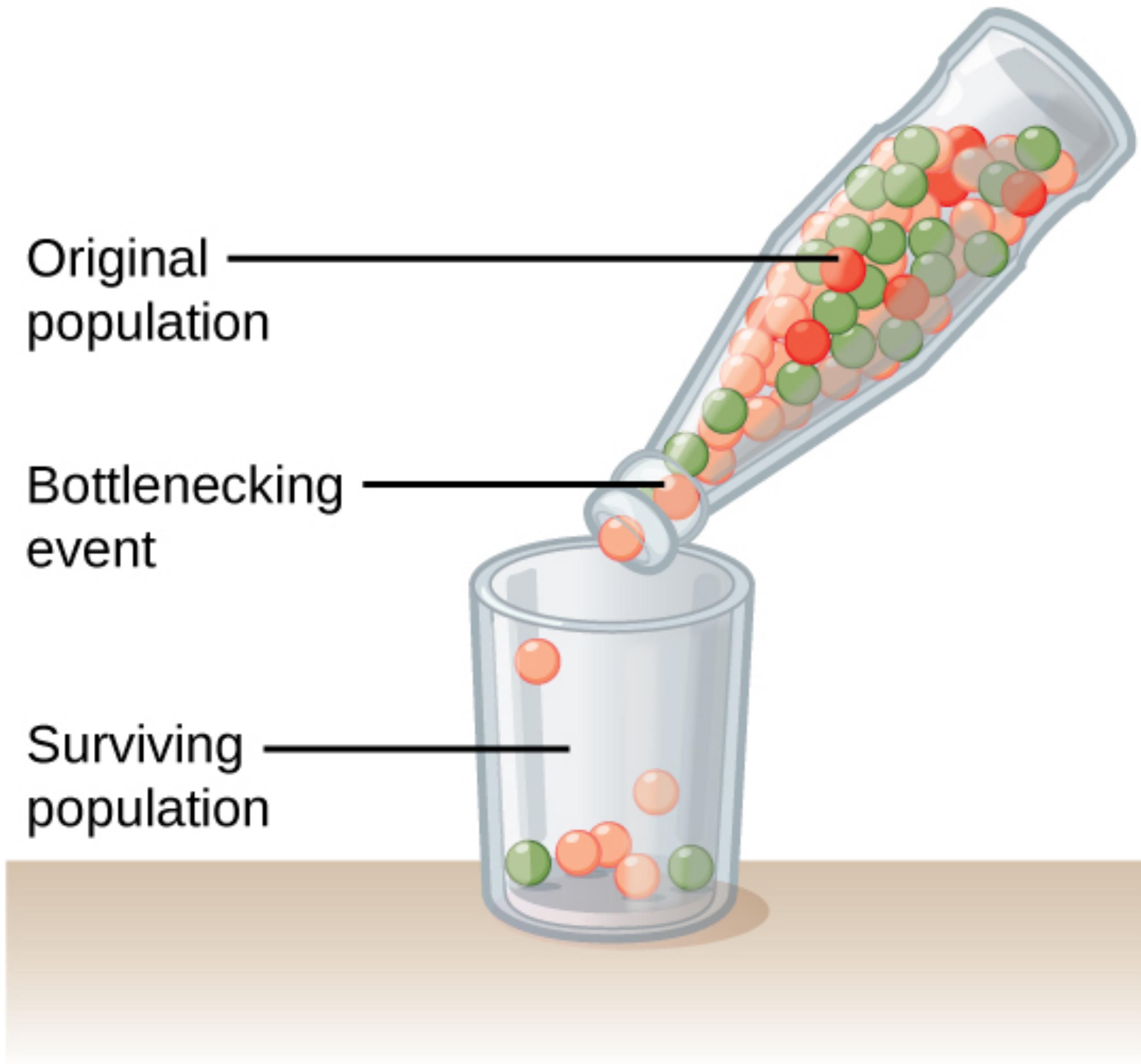
**Von-random, differential survival and
reproduction of variants**

Selection

phylogenetic neutrality



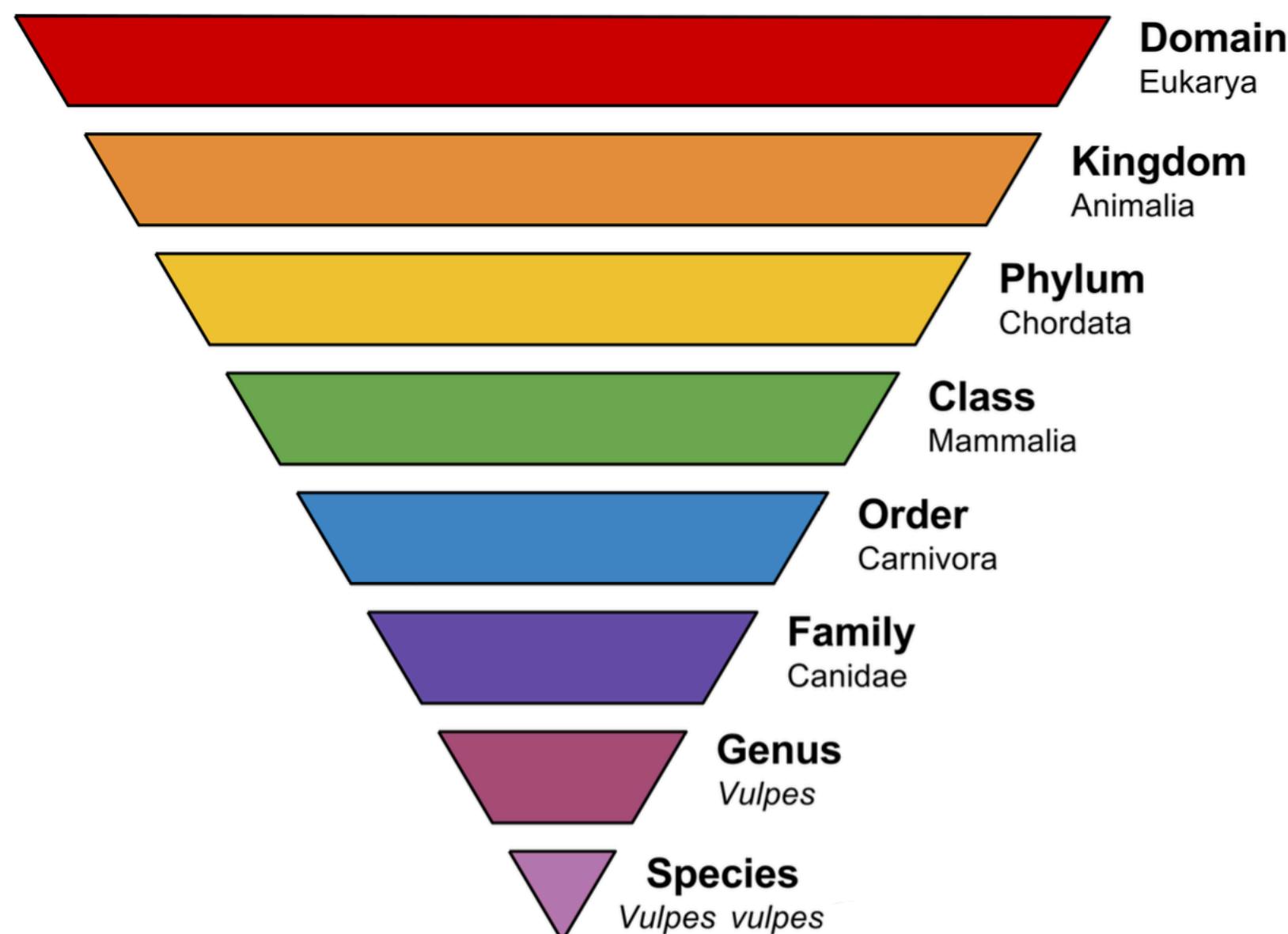




taxonomy and systematics

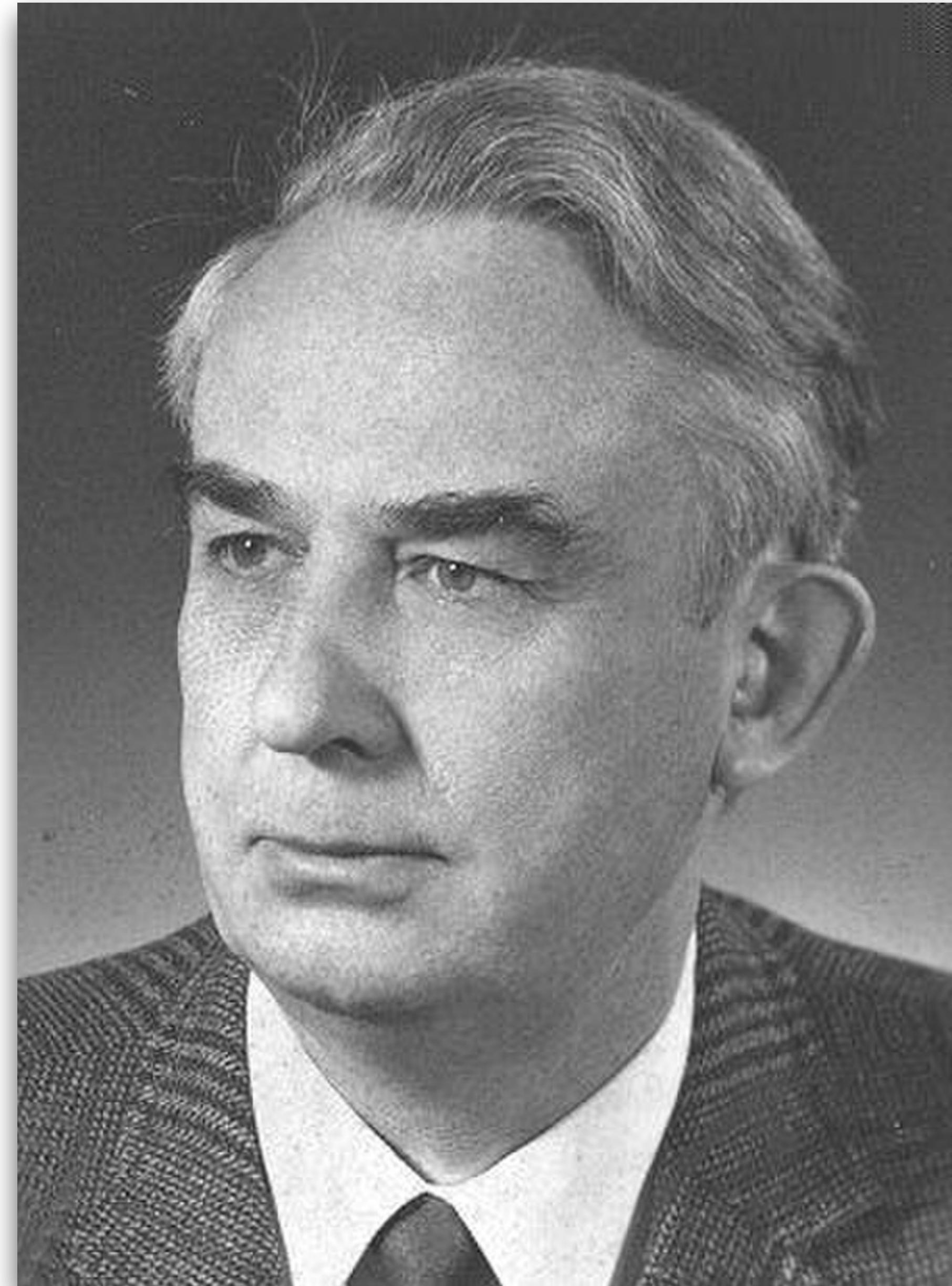
Taxonomy is the theory and practice of identifying, describing, naming, and classifying organisms.

Systematics may be defined as the study of the kinds and diversity of organisms and the relationships among them.



Phylogenetics

- Evolutionary theory states that groups of similar organisms are descended from a common ancestor.
- Phylogenetic systematics (cladistics) is a method of taxonomic classification based on their evolutionary history.
- It was developed by Willi Hennig, a German entomologist, in 1950.



BIOLOGY

Phylogenetic Systematics**WILLI HENNIG**

Translated by D. Dwight Davis and Rainer Zangerl

Foreword by Donn E. Rosen, Gareth Nelson, and Colin Patterson

Phylogenetic Systematics, first published in 1966, marks a turning point in the history of systematic biology. Willi Hennig's influential synthetic work, arguing for the primacy of the phylogenetic system as the general reference system in biology, generated significant controversy and opened possibilities for evolutionary biology that are still being explored.

"A landmark in the development of cladistic systematics."

— *Biological Abstracts*

"This book should be read by all practicing systematists as well as other biologists interested in the analysis of relationships of organisms."

— *The Biologist*

"The ideas put forth in this far-reaching study, and the author's treatment of the subject, should introduce new perspectives to scientists in all areas of biology." — *Scientia*

"English-speaking systematists should be glad to have an opportunity to be exposed to the views of the foremost proponent of the cladistic school. Indeed, no thinking systematist can afford not to have read this volume."

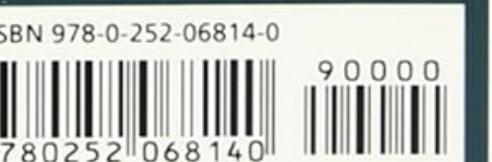
— Robert R. Sokal, *Science*

"This is required reading for all interested in biosystematics." — *Plant Life*

"*Phylogenetic Systematics* is a difficult, stimulating, and controversial work . . . indispensable to the thoughtful systematist." — *Journal of Paleontology*

The late Willi Hennig was director of phylogenetic research at the State Museum of Natural Science, Stuttgart. His honors included the Gold Medal of the Linnaean Society and the Gold Medal for Distinguished Achievement in Science of the American Museum of Natural History.

An Illinois Reissue from the University of Illinois Press

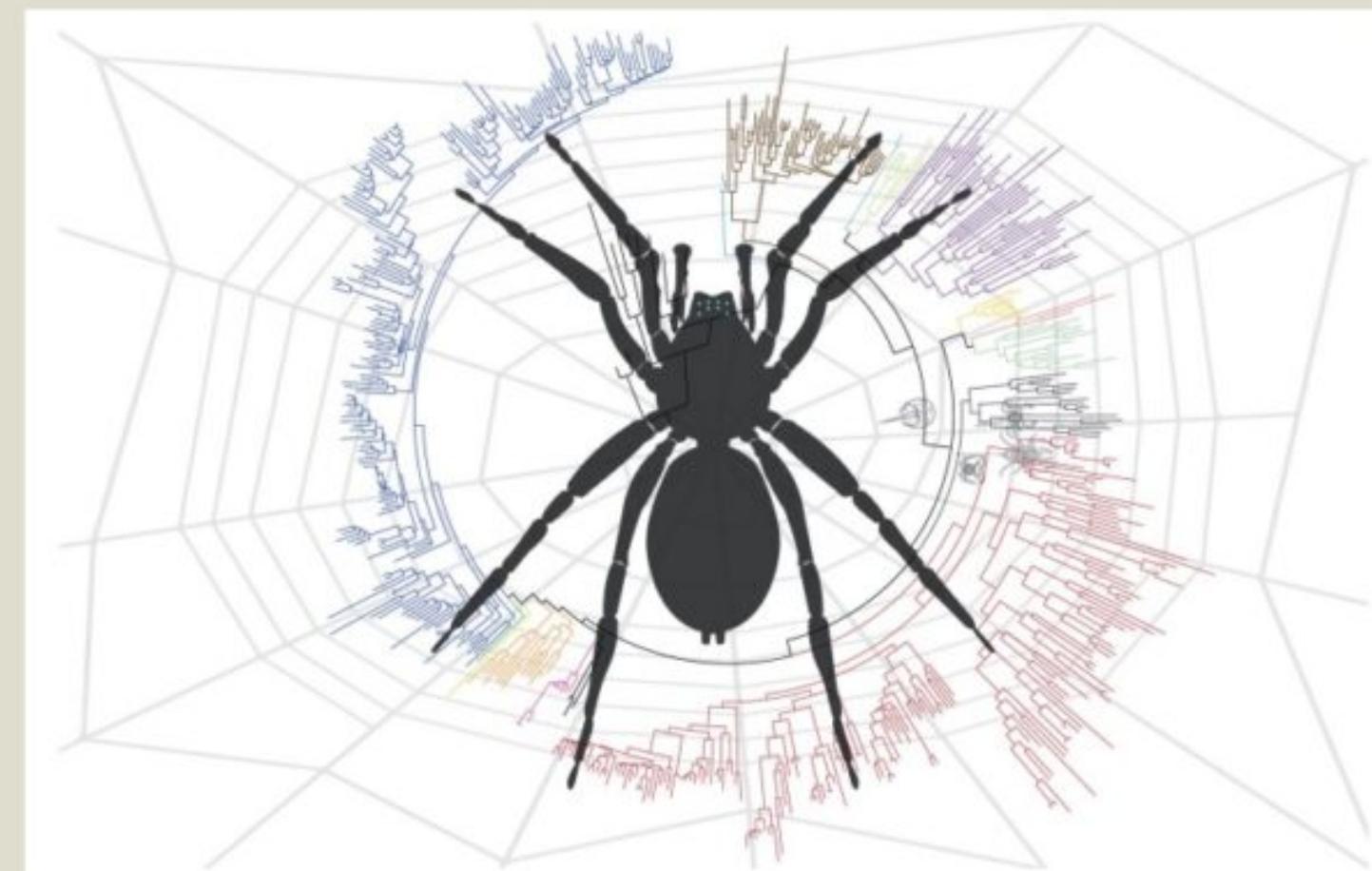


Cladistics

VOLUME 39 • NUMBER 6 • DECEMBER 2023

ISSN 0748-3007

The International Journal of the Willi Hennig Society



WILEY

wileyonlinelibrary.com/journal/cla

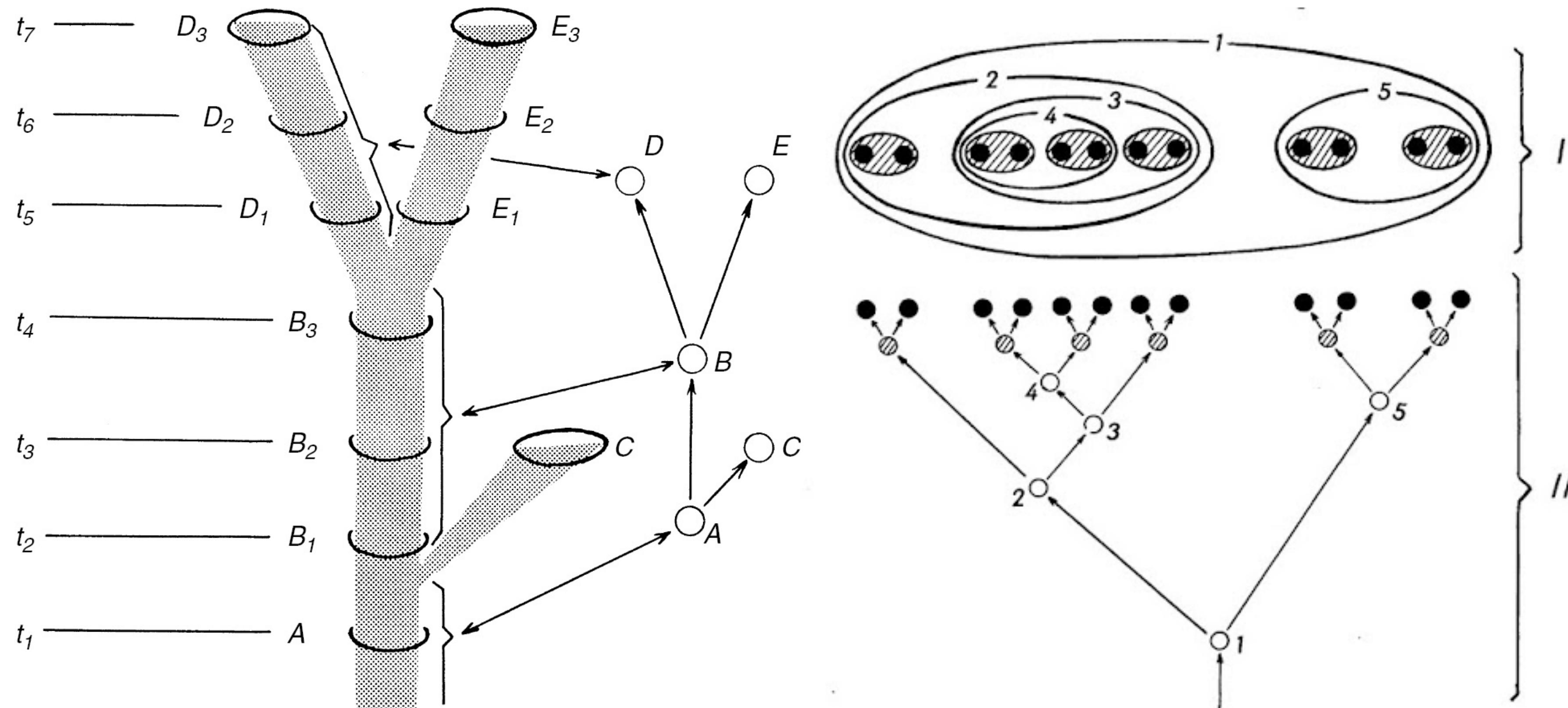


Figure 18. The phylogenetic kinship relations between the species of a monophyletic group, represented in two different ways.

What is phylogenetics?

Phylogenetics is the study of evolutionary relationships among biological entities – often species, individuals or genes (which may be referred to as taxa).

Why use molecular data?

Today, almost all evolutionary relationships are inferred from molecular sequence data. This is because:
DNA is the inherited material We can now easily, quickly, inexpensively and reliably sequence genetic
material Sequences are highly specific and are often information rich

Cladistics

from Ancient Greek κλάδος kládos 'branch') is an approach to biological classification in which organisms are categorized in groups ("clades") based on hypotheses of most recent common ancestry.

The evidence for hypothesized relationships is typically shared derived characteristics (synapomorphies) that are not present in more distant groups and ancestors.

Synapomorphies (Shared Derived Traits)

Synapomorphies are evolutionary traits that are **shared by two or more taxa** and inherited from their most recent common ancestor. These traits define **monophyletic groups (clades)** and provide strong evidence of evolutionary relationships. **Example:** The presence of feathers in birds is a synapomorphy that distinguishes them from other reptiles.

Autapomorphies (Unique Derived Traits)

Autapomorphies traits **unique to a single taxon** and not shared with any other group. While they help in distinguishing individual lineages, they do not provide information about shared ancestry among multiple taxa. **Example:** The elongated neck of giraffes (*Giraffa camelopardalis*) is an autapomorphy, as it is not found in closely related species.

Symplesiomorphies (Shared Ancestral Traits)

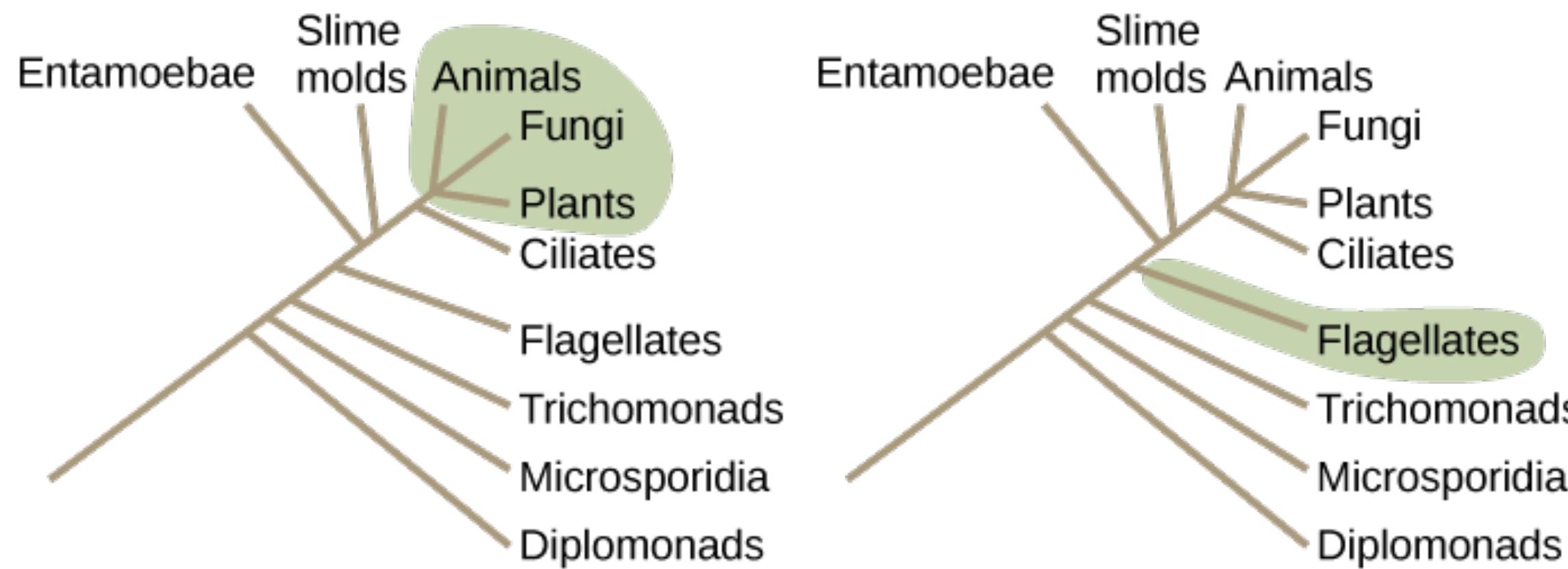
Symplesiomorphies are **ancestral traits shared by multiple taxa** that were inherited from a common ancestor predating the focal clade. These traits are misleading for phylogenetic classification, as they do not indicate close relationships among the taxa that possess them. **Example:** four limbs in mammals, reptiles, and amphibians is a symplesiomorphy inherited from the common ancestor of tetrapods.

Plesiomorphies (Ancestral Traits)

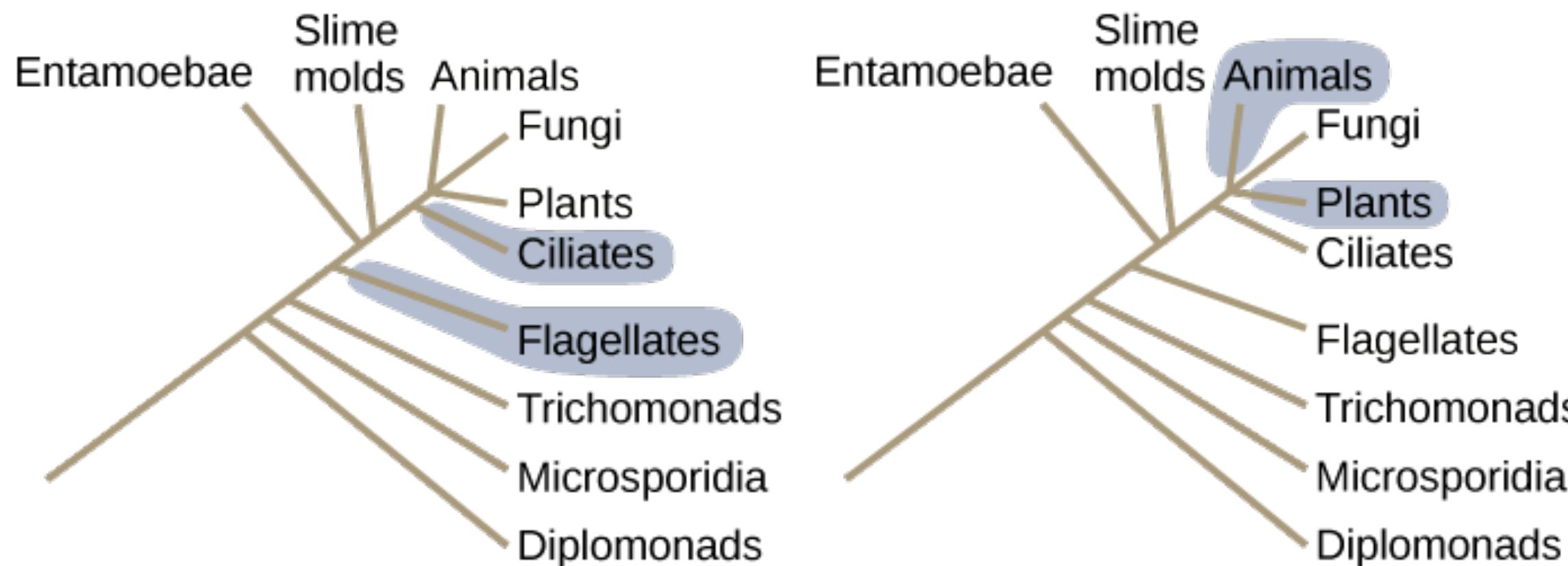
Plesiomorphic traits **originated in a distant ancestor** and are retained by multiple taxa, but they do not define a specific clade. It is a symplesiomorphy discussed in relation to a more derived state. **Example:** vertebrae in mammals is a plesiomorphy because it was inherited from early vertebrates and is also found in fish, amphibians, and reptiles.

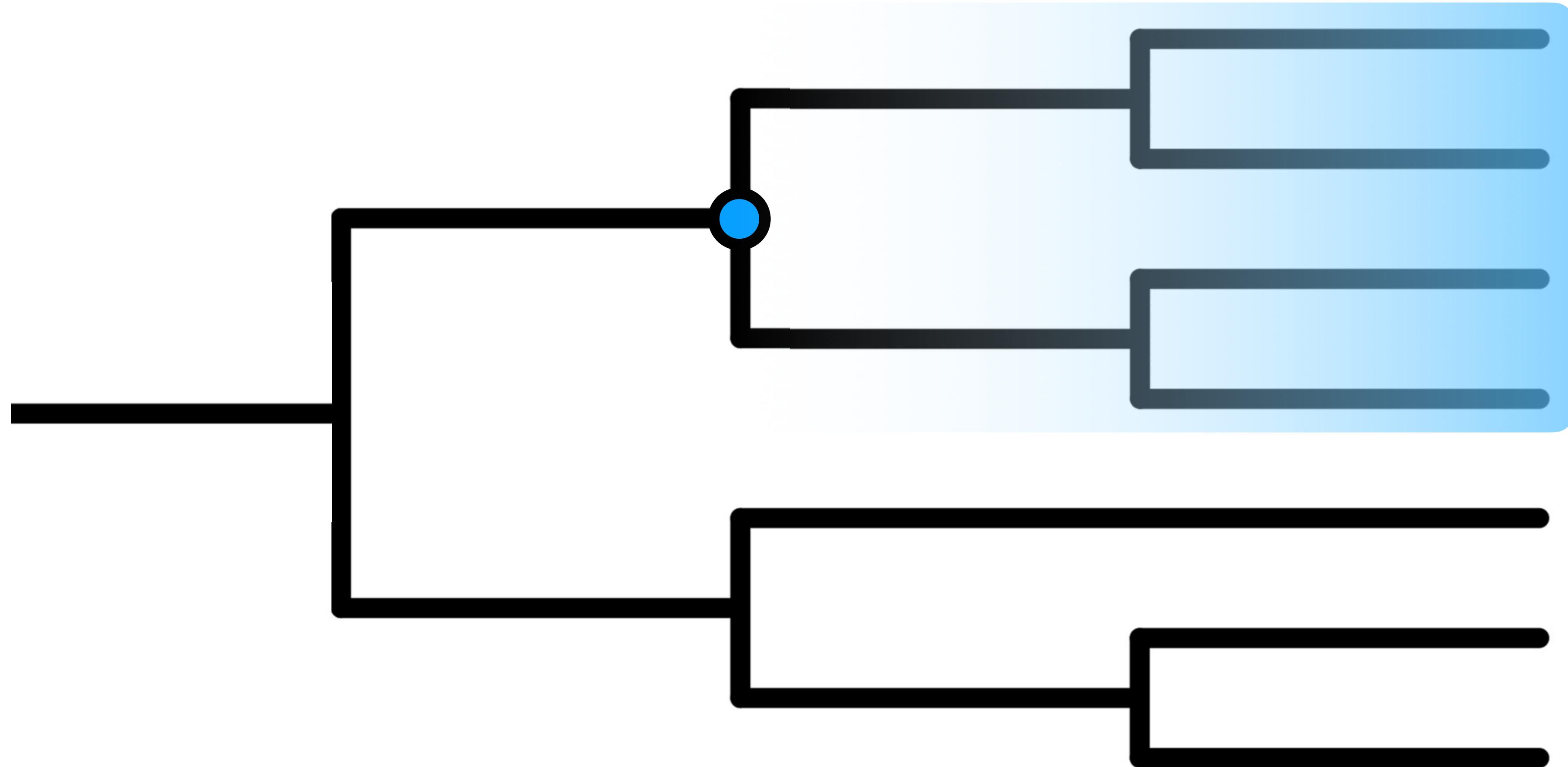
Synapomorphies define clades

Clades



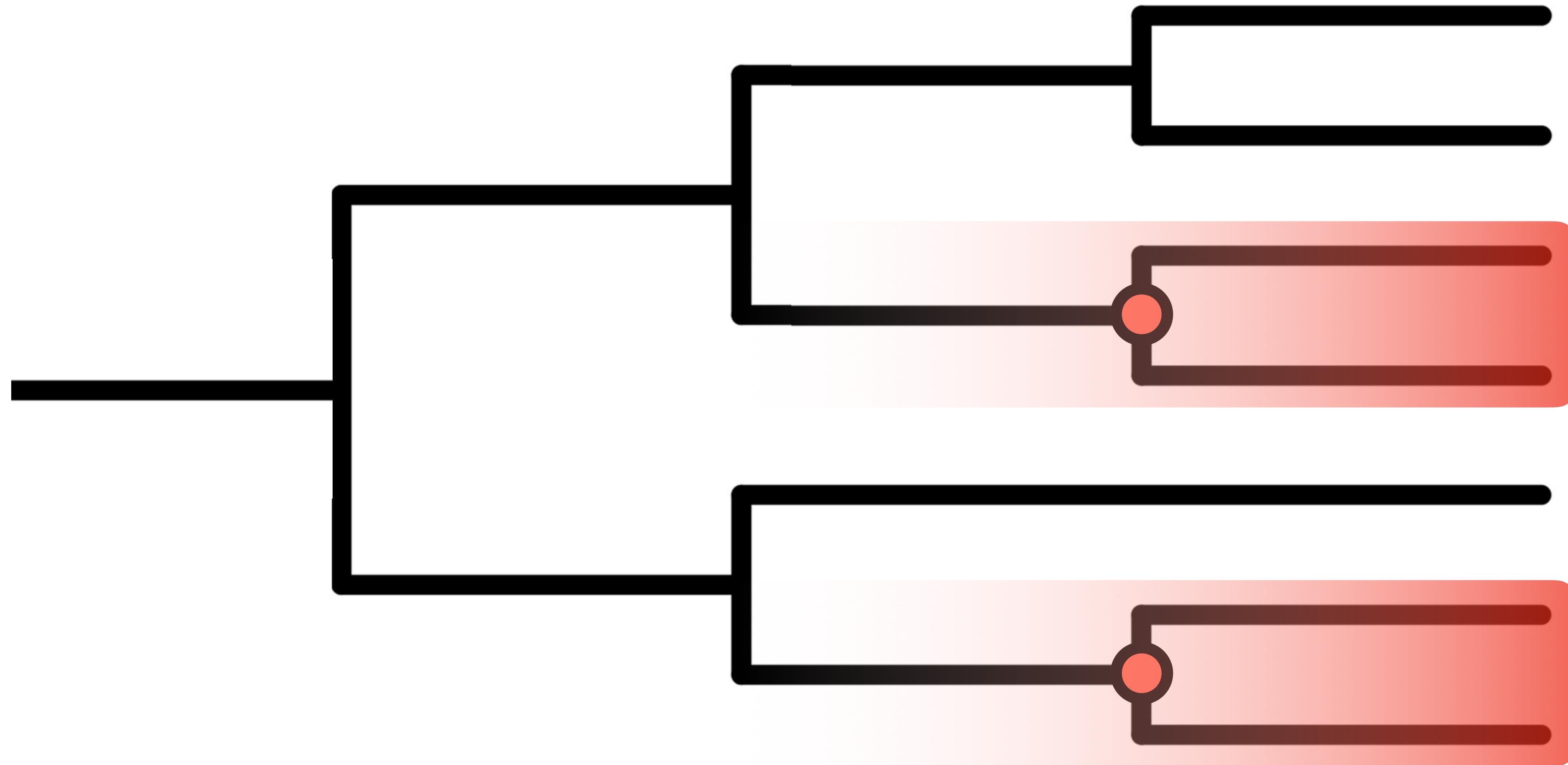
Not Clades





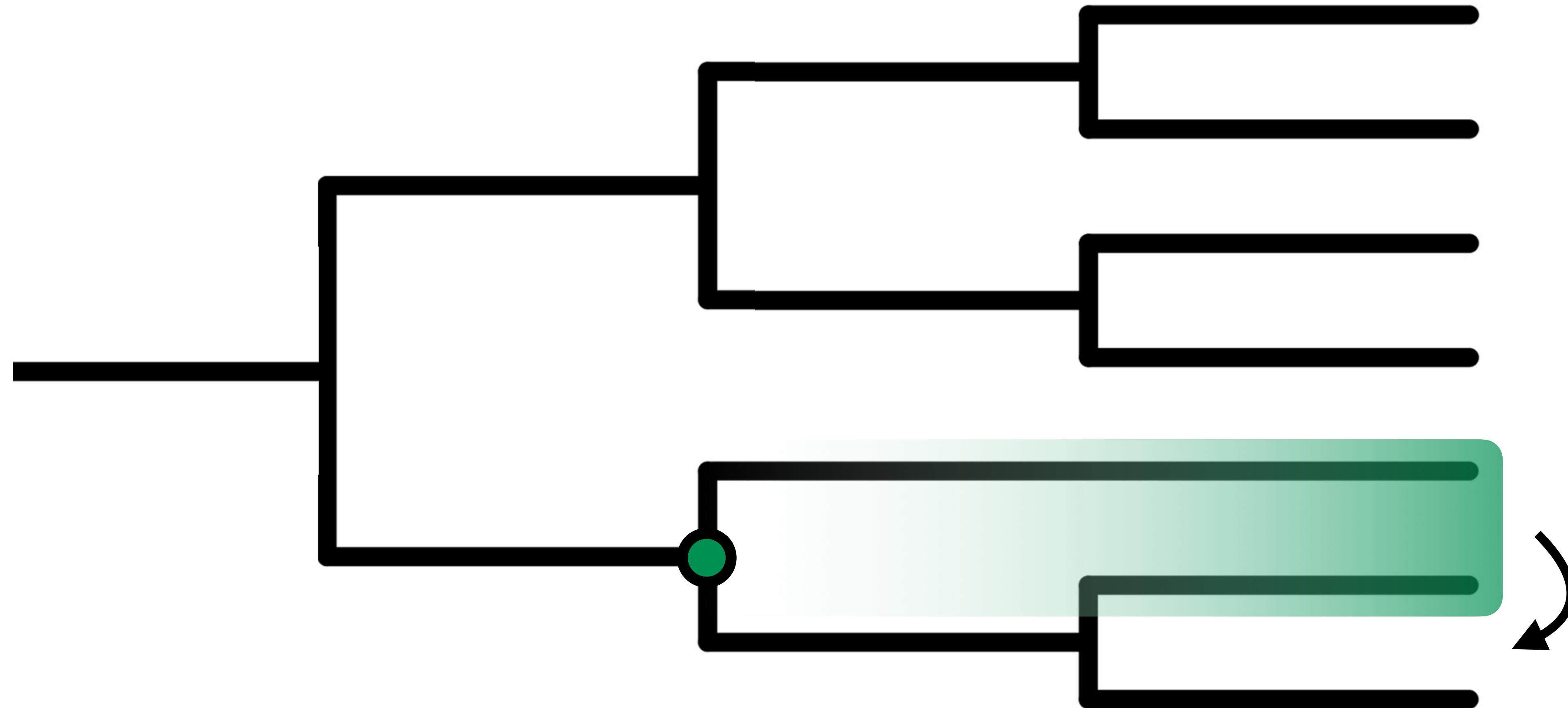
monophily

A grouping of organisms which meets these criteria and contains: **(1)** its own most recent common ancestor, i.e. excludes non-descendants of that common ancestor; **(2)** all the descendants of that common ancestor, without exception. The condition of a taxonomic grouping being a clade.



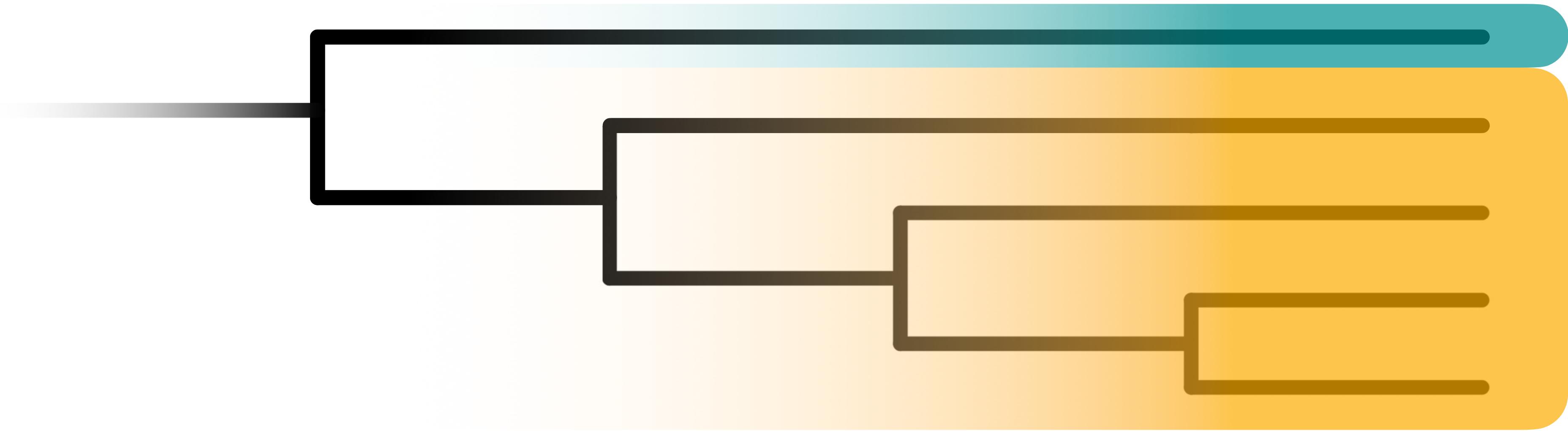
polyphyly

A polyphyletic group is an assemblage that includes two or more separate groups, each with a **separate common ancestor**. The most recent common ancestor of the species in the polyphyletic assemblage would be the ancestor also of species not included in them.



parafly

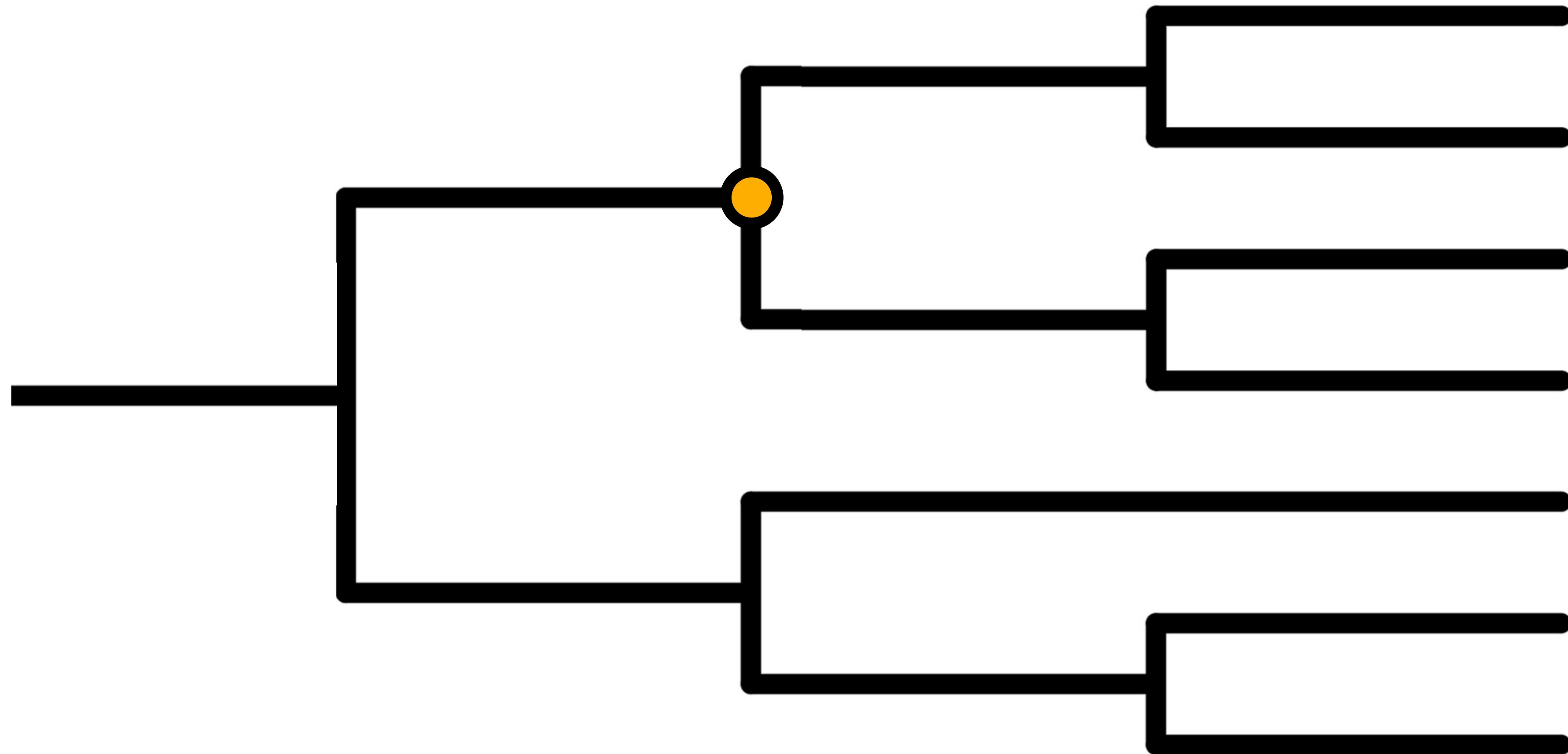
A group that consists of the grouping's **last common ancestor and some but not all of its descendant** lineages. The grouping is said to be paraphyletic with respect to the excluded subgroups.



node (internal)

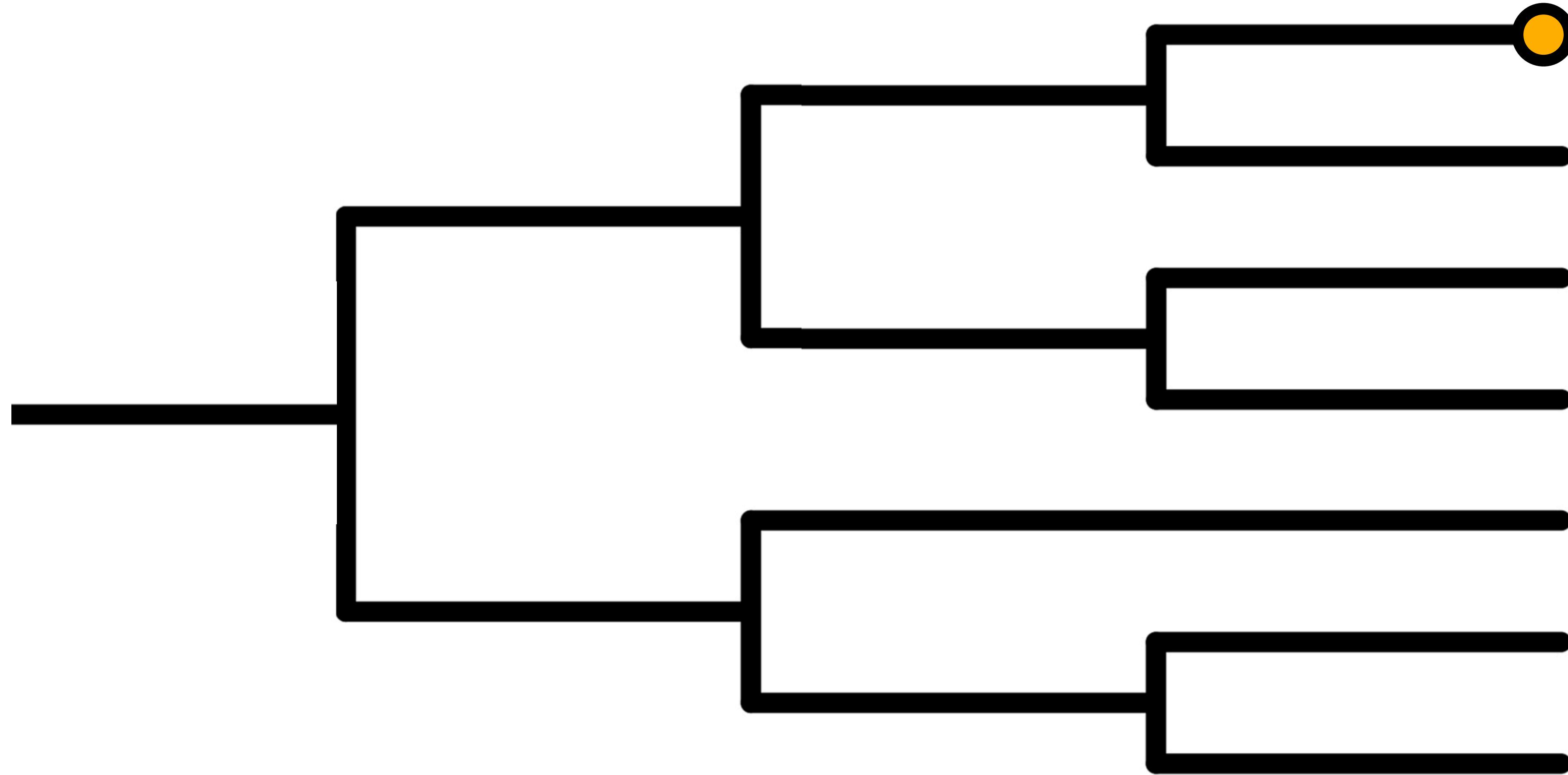
ingroup the OTU under analysis

outgroup a group of OTU assumed a priori to lie outside the monophyly of the OTU under analysis; used to give direction to determination of



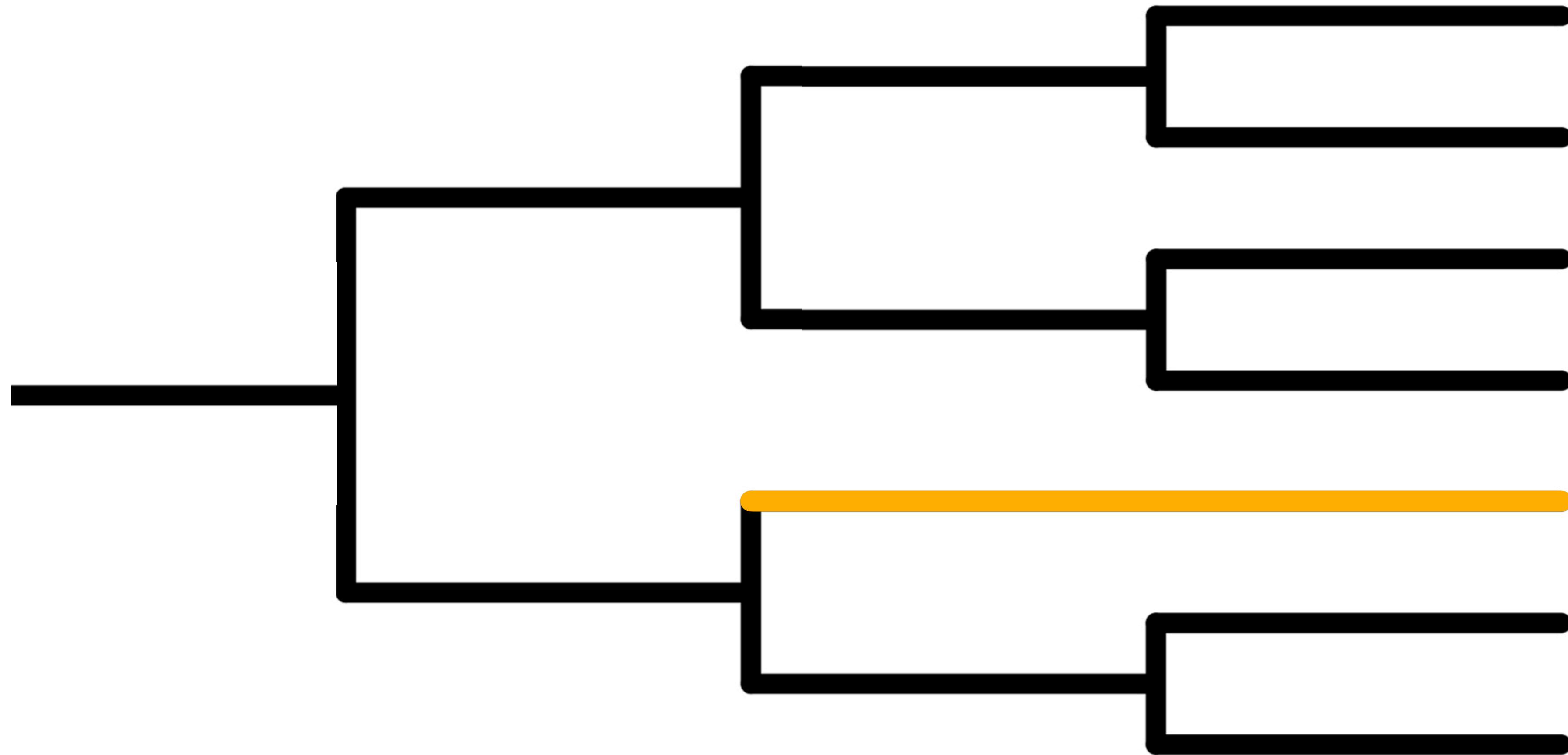
node (internal)

Nodes are the points at the ends of branches which represent **real sequences** or **hypothetical sequences** at various points in evolutionary history. In a tree of species an internal node in a tree is, biologically, an **ancestor**. You can also thin to nodes as **bipartitions or splits**.



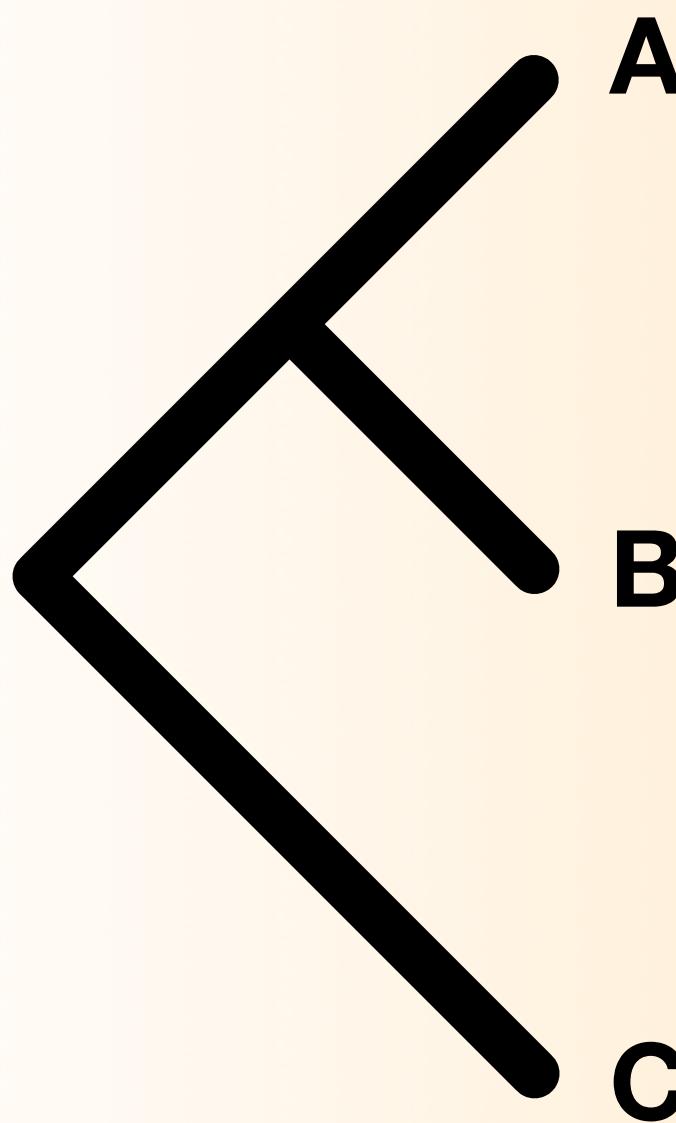
node (terminal or external)

The sequence that we sampled and used to construct our phylogeny occur on single terminal branches, known as tips or leafs. Often referred to as OTU, which stands for Operational Taxonomic Unit, a noncommittal term used for the objects of study (be they species, populations or individuals).

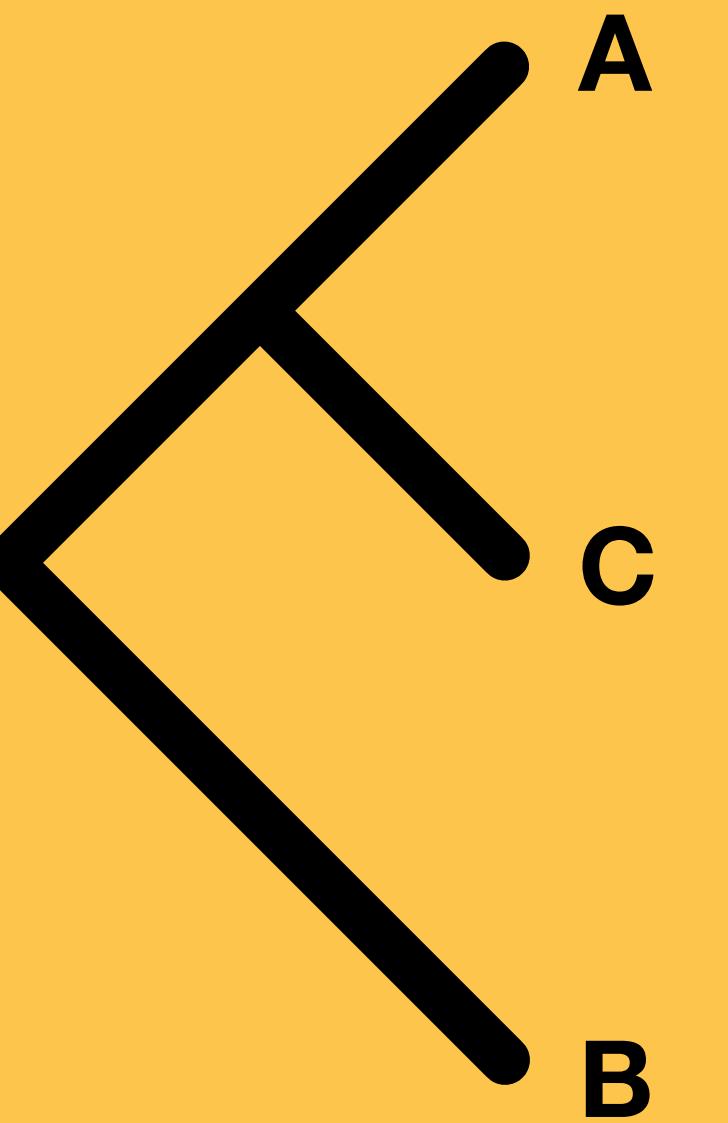
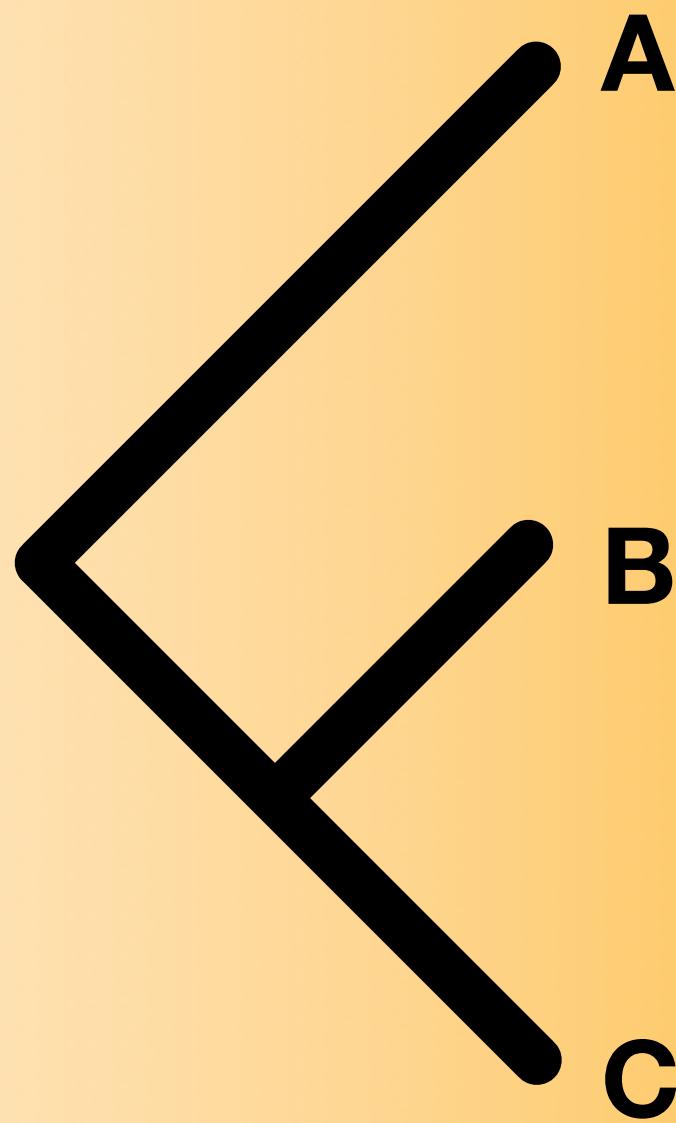
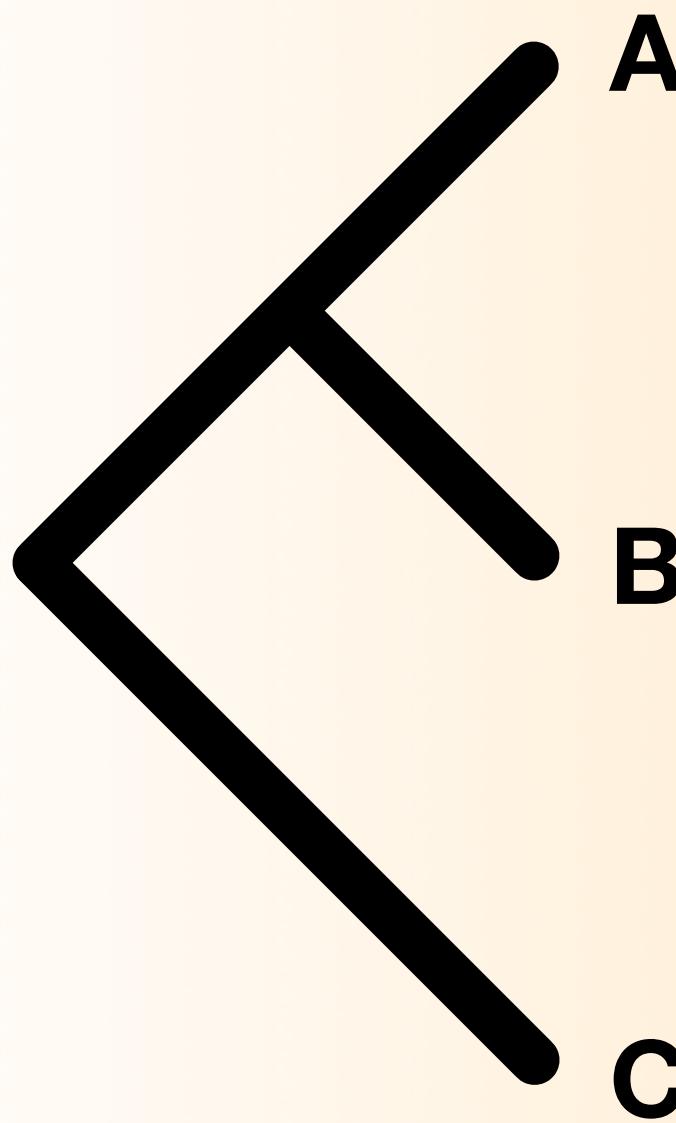


branch

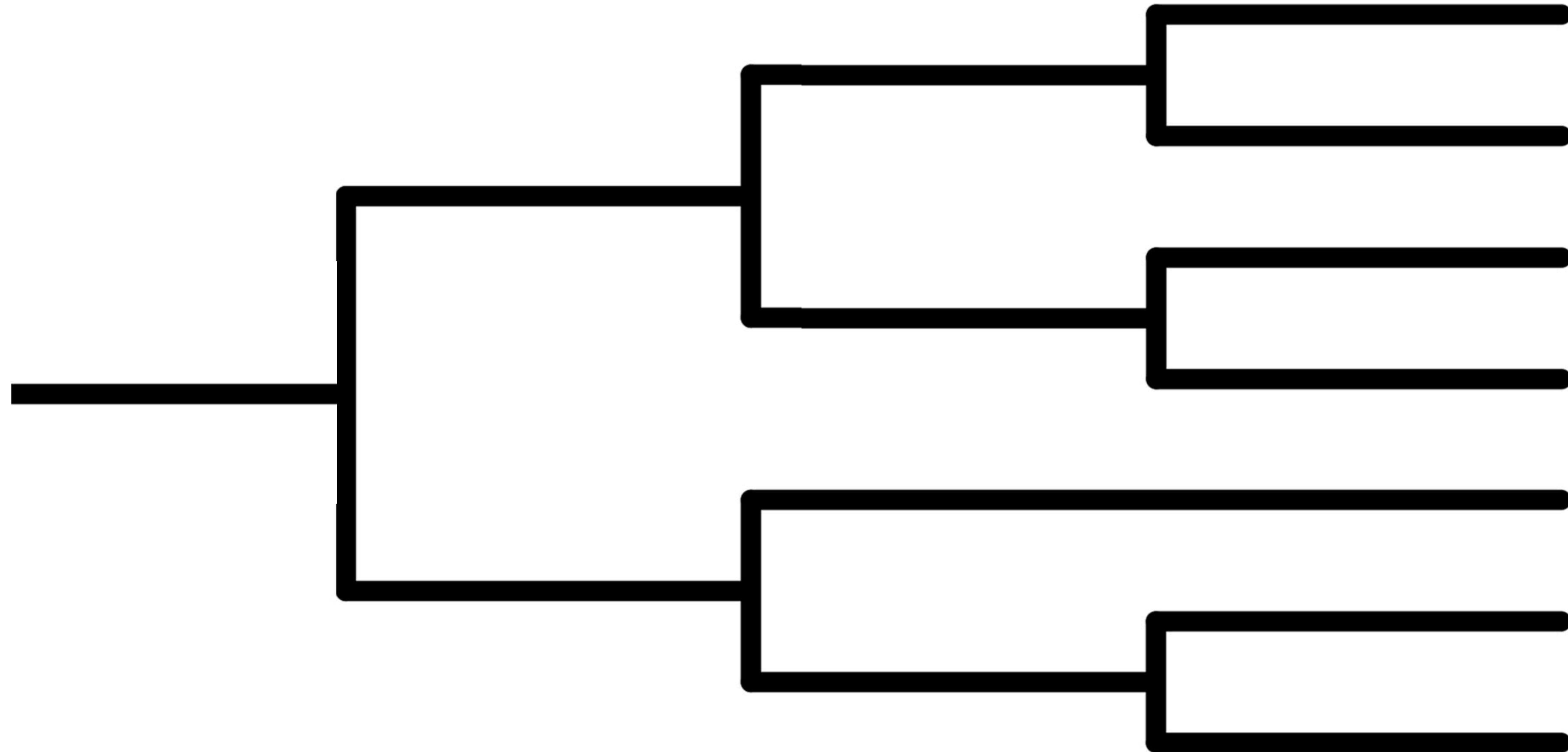
The branching structure of the tree is its topology. It is of particular significance because it indicates patterns of relatedness among taxa. **Beware:** any internal node can be rotated and the tree is the same.



SAME TREES

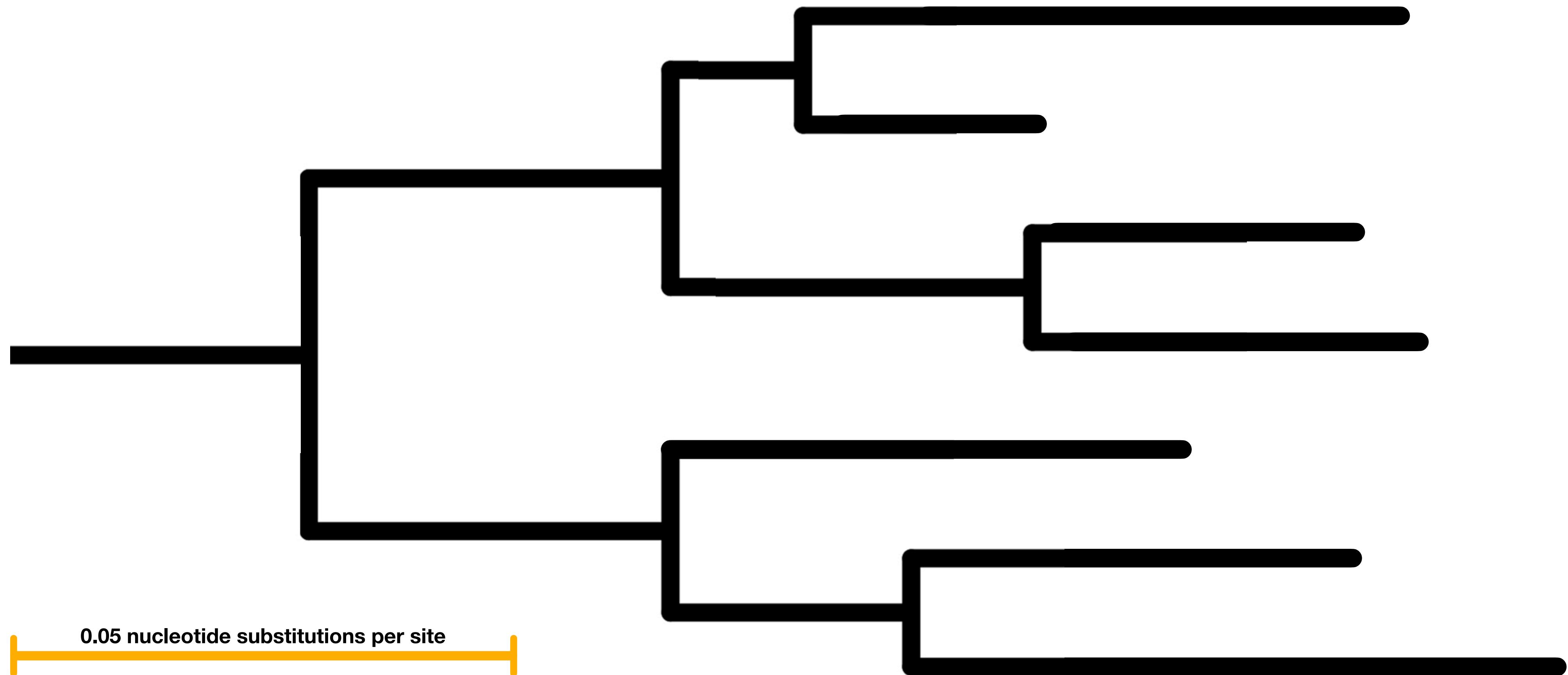


DIFFERENT TREES



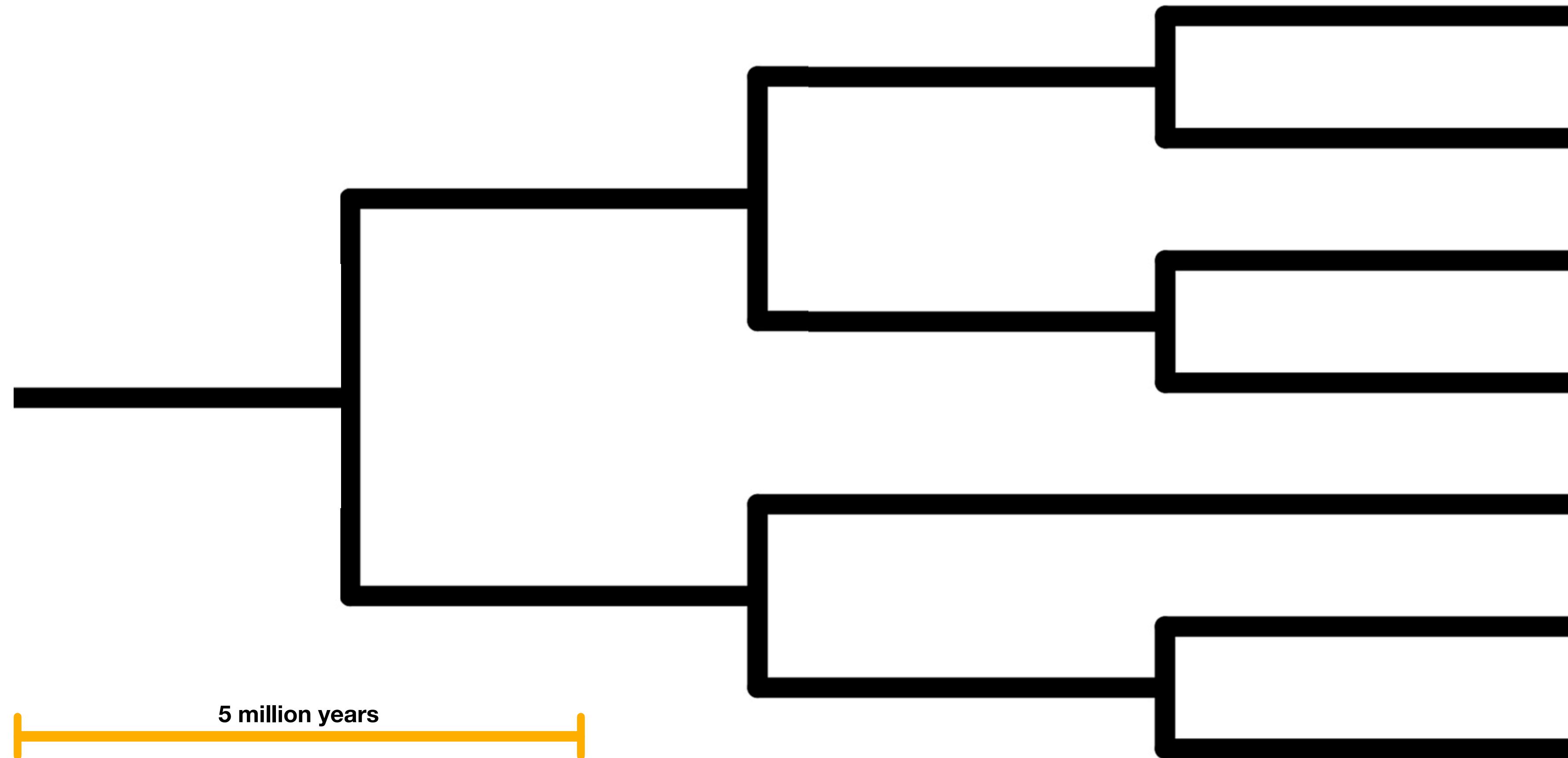
Cladogram

A cladogram only represents a branching pattern; **branch lengths do not have a meaning** and do not represent either time or relative amount of character change.



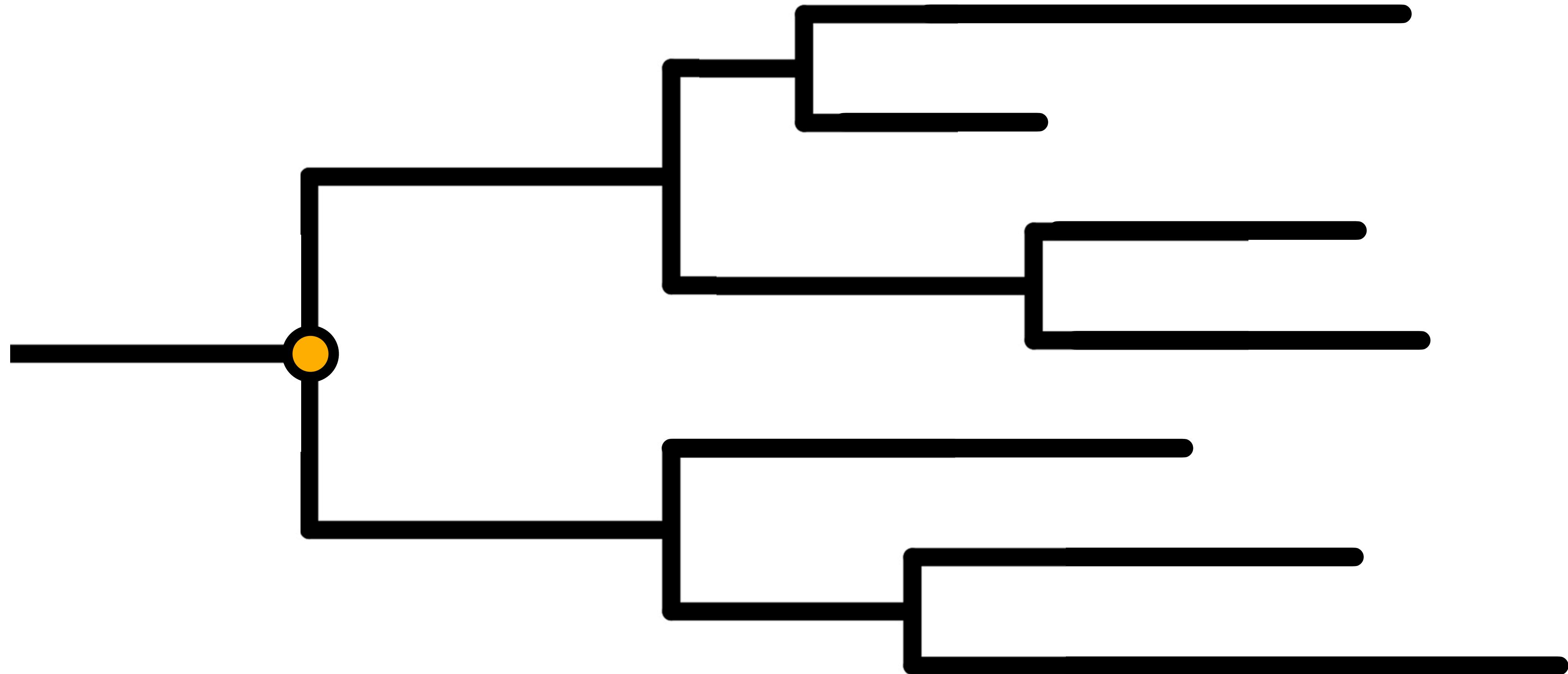
Scale: evolutionary change

The line segment shows the length of branch that represents an amount of change of 0.05. The vertical dimension in this figure has no meaning and is used simply to lay out the tree visually with the labels evenly spaced vertically. This tree is a **phylogram**.



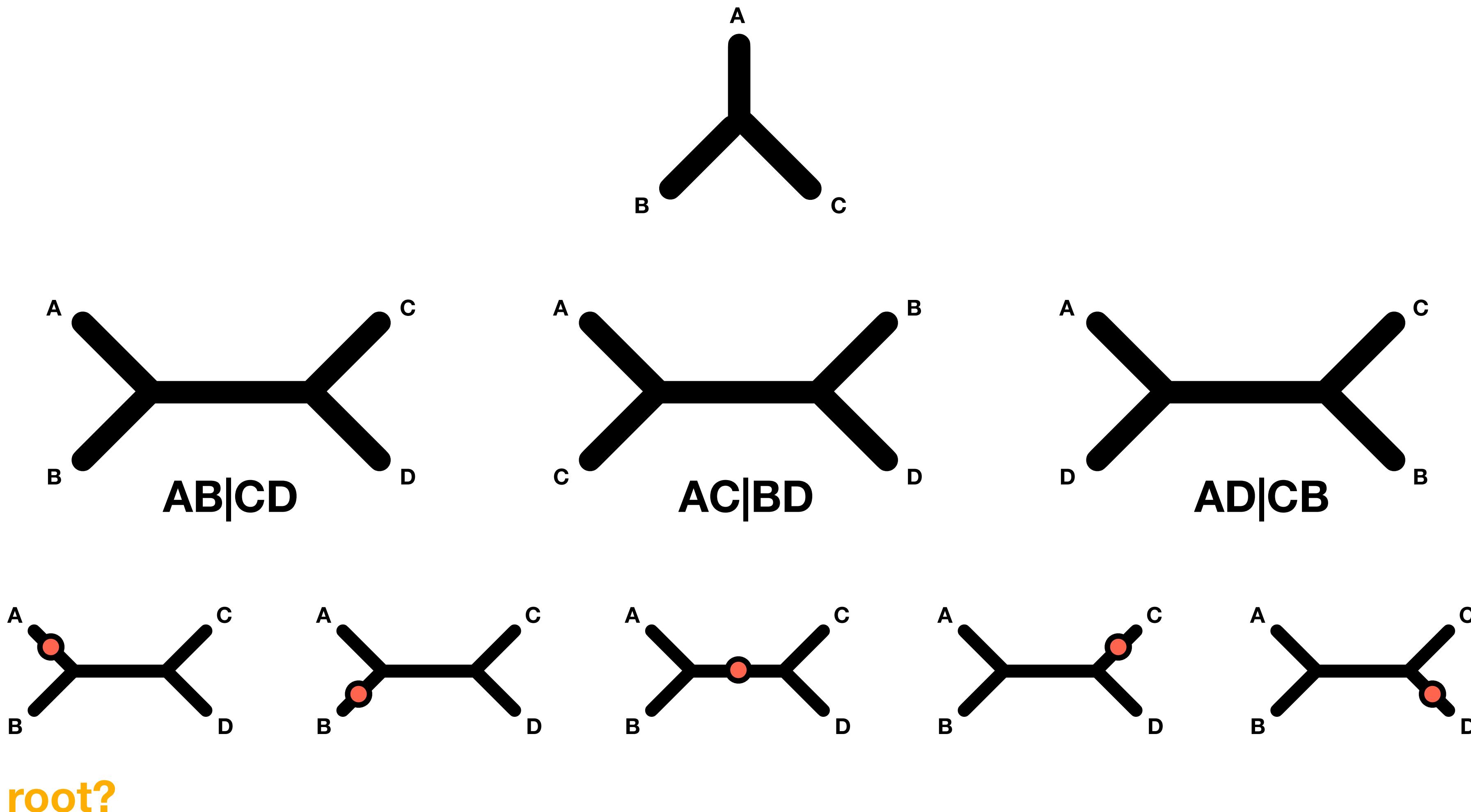
scale: time

A chronogram is a phylogenetic tree that explicitly represents time through its branch lengths. This tree is a **chronogram** or **timetree**. The process of obtaining such a phylogeny is often called a **divergence time analysis**.

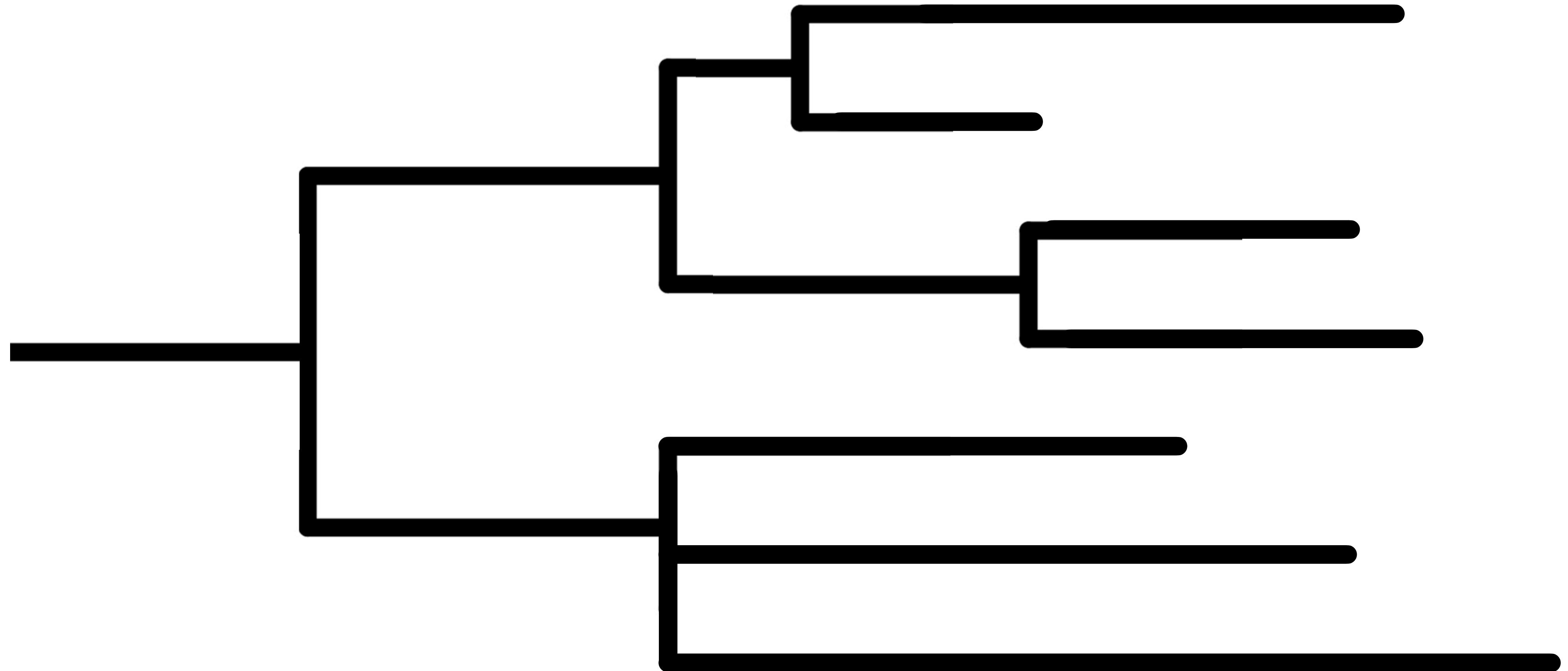


root

The root is a specific internal node representing **the most recent common ancestor** of all tips in the tree. It is therefore the oldest part of the tree and tells us the direction of evolution. There are two main approaches that we can use to root a tree: **outgroup rooting** and **midpoint rooting**.

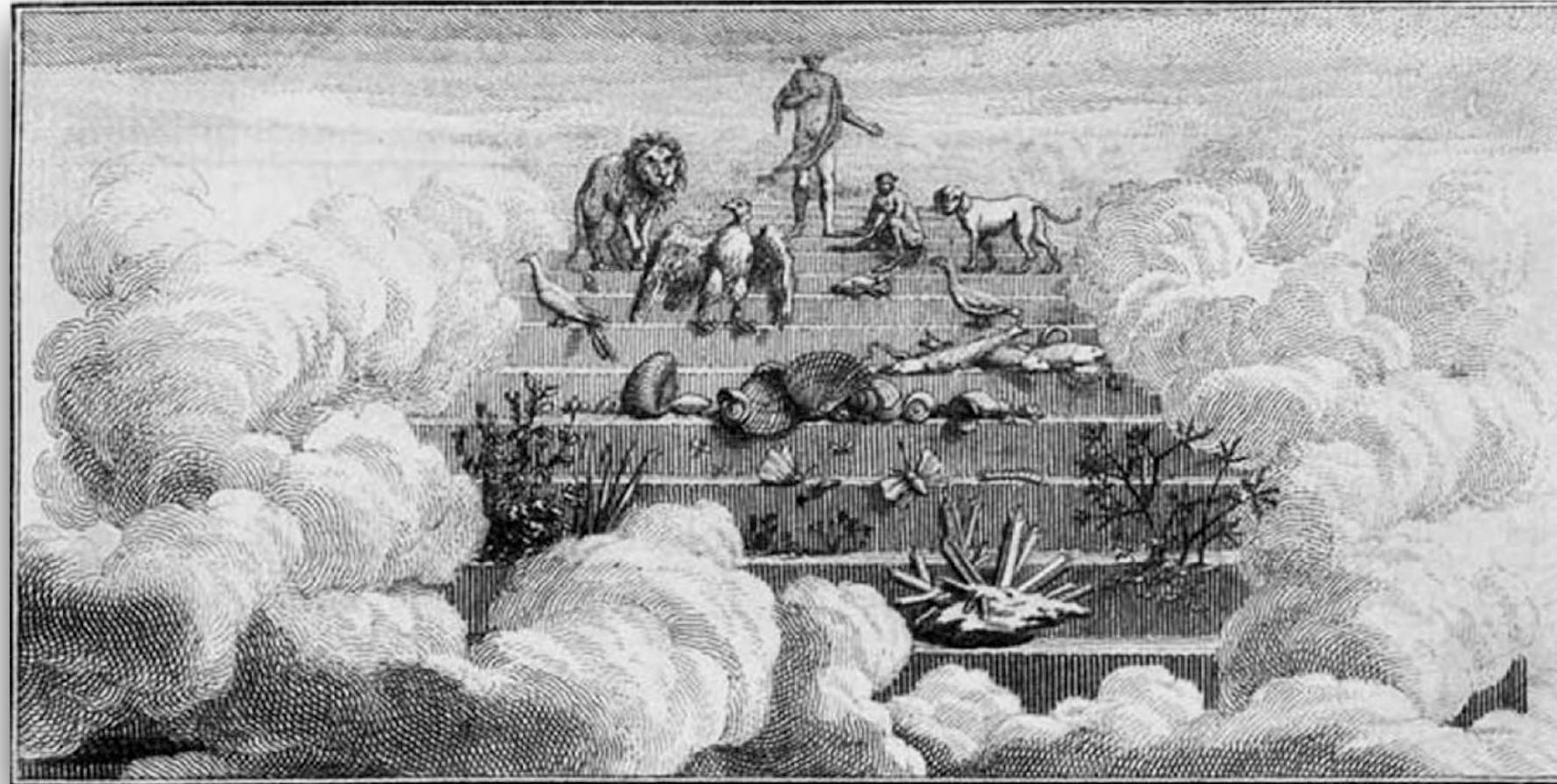


The simplest ambiguous tree is also known as a **quartet**. Phylogenetic trees may be rooted or unrooted. In a rooted phylogenetic tree, each node with descendants represents the inferred most recent common ancestor of those descendants.



polytomy

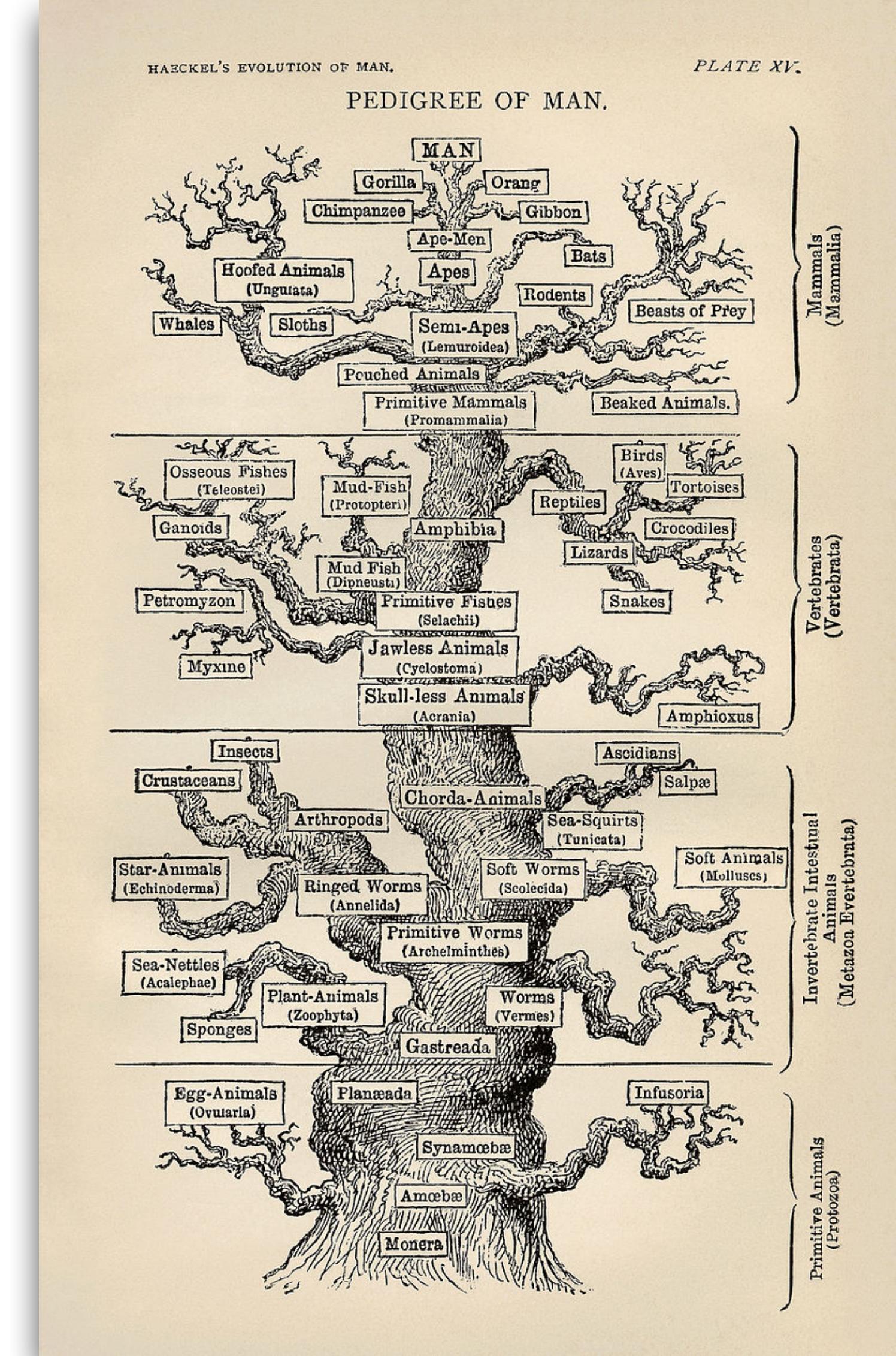
Bifurcating versus multifurcating Both rooted and unrooted trees can be either bifurcating or multifurcating.



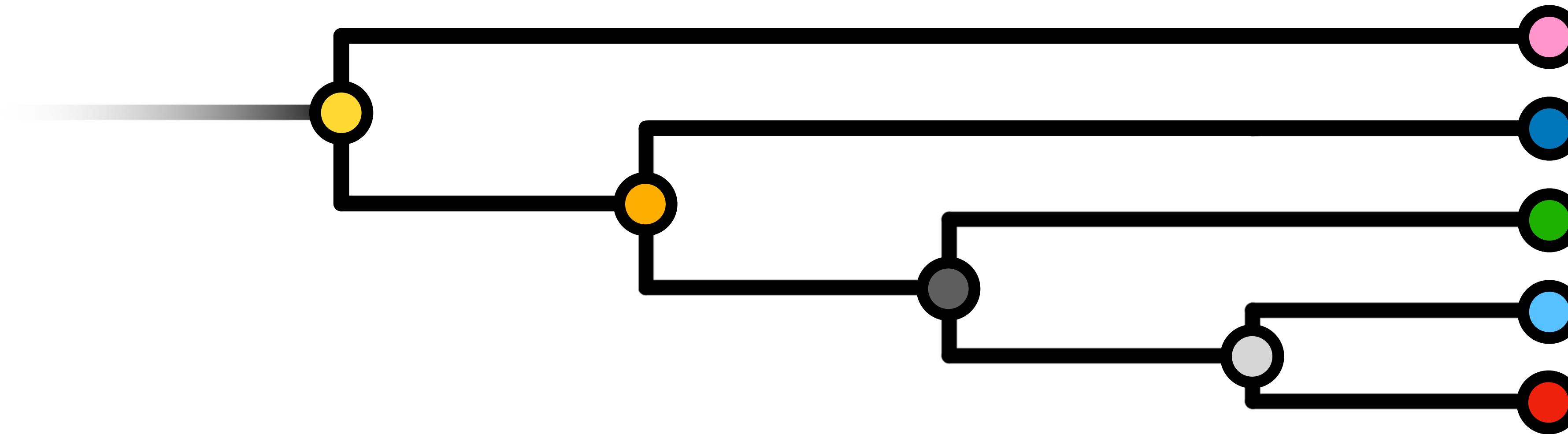
Kette der Wesen, Scala Naturae by Charles Bonnet (1781).

trees are not ladders

The ladder concept (*Scala Naturae*) is an old view that tends to organize ancestry based on complexity or some putative evolutionary superiority. Terms such as “primitive”, “ancient” or “lower” referred to a lineage are misleading as they imply ladder-thinking.



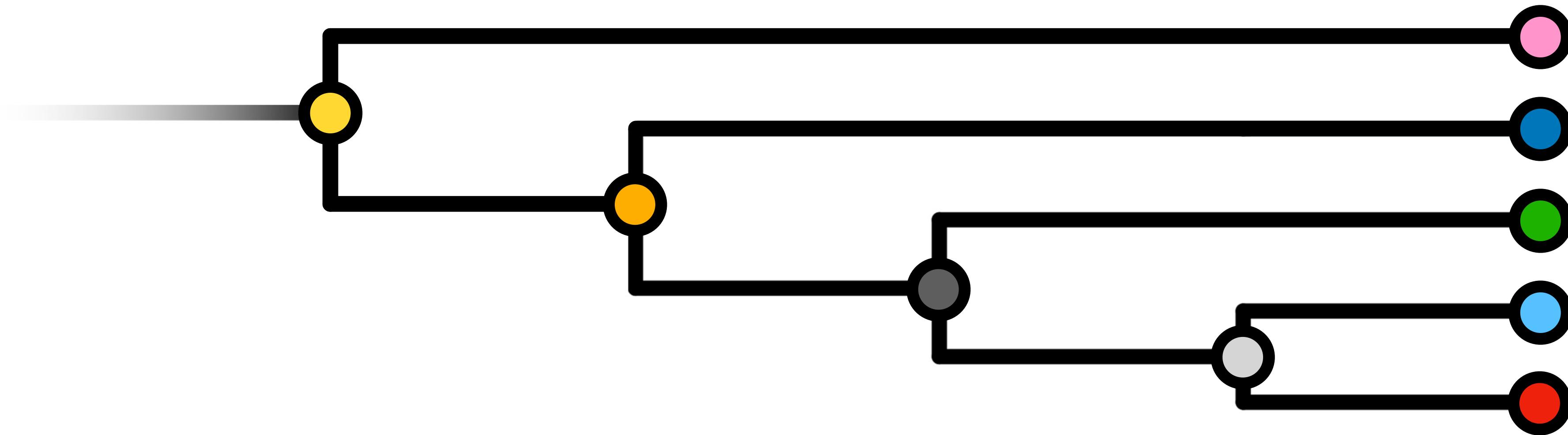
Ernst Haeckel's tree from 'The Evolution of Man' (1879).



The **red tip** is more closely related to the **blue tip** than to the **green tip** because it shares a common ancestor more recently with the **blue tip** (ancestor = light gray node) than they do with the **green tip** (ancestor = dark gray node).

The **purple tip** is more closely related to the **green tip** than they are to the **pink tip** because the **purple tip** shares a common ancestor with the **green tip** more recently (ancestor = **orange node**) than they do with the **pink tip** (ancestor = **yellow node**).

The **pink tip** is equally related to blue as they are to the **purple tip**. This is less intuitive, but if you trace back to the MRCA's you will see why: the **blue tip** and **purple tip** share the same common ancestor (**yellow node**) with **pink tip**, so neither species is more closely related to **pink tip**.



COMMON MISCONCEPTIONS

SOME LEXICON:

rooted *versus* unrooted tree

clade

polytomy

monophily

poliphily

parafyly

internal node

terminal node

branch

bipartitions

cladogram

phylogram

chronogram or timetree

dicotomous *versus* non-dicotomous

automorphy

sinapomorphy