

Cladogenesis, Coalescence and the Evolution of the Three Domains of Life

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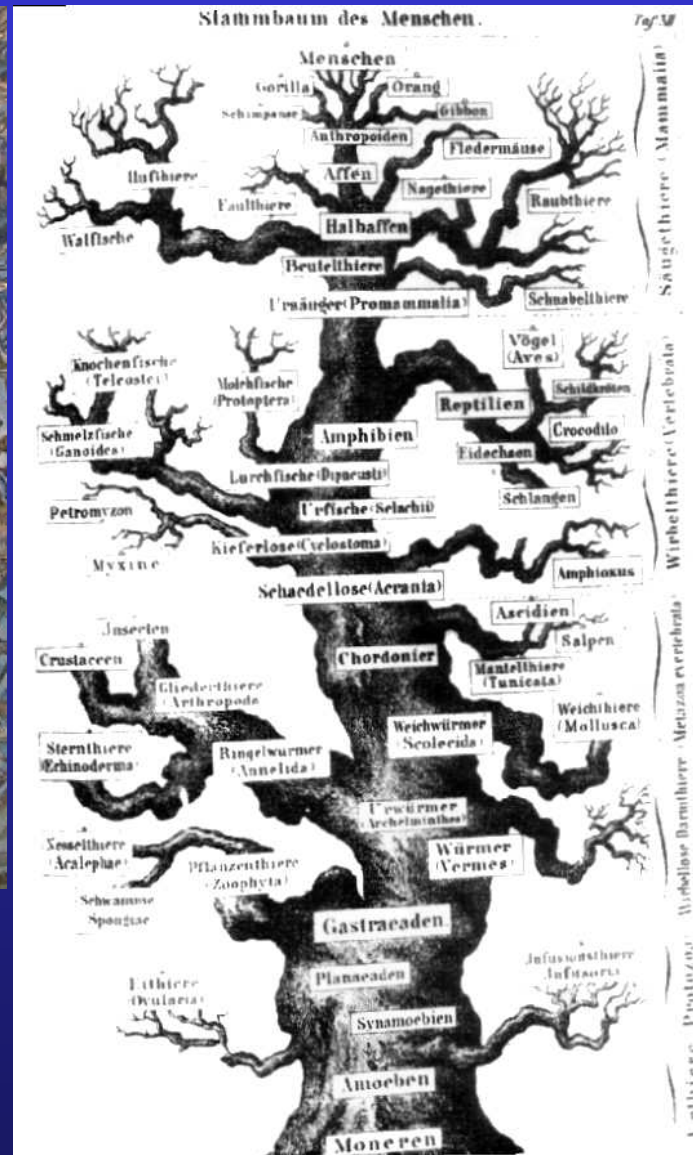
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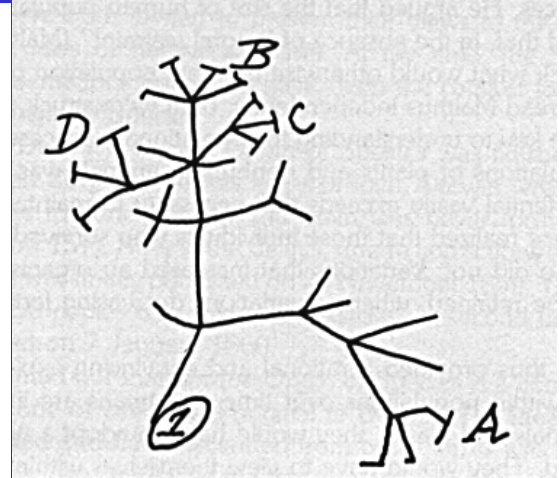
Trees as a Visualization of Evolution



Genealogy
(Church Ceiling,
Santo Domingo, Oaxaca)

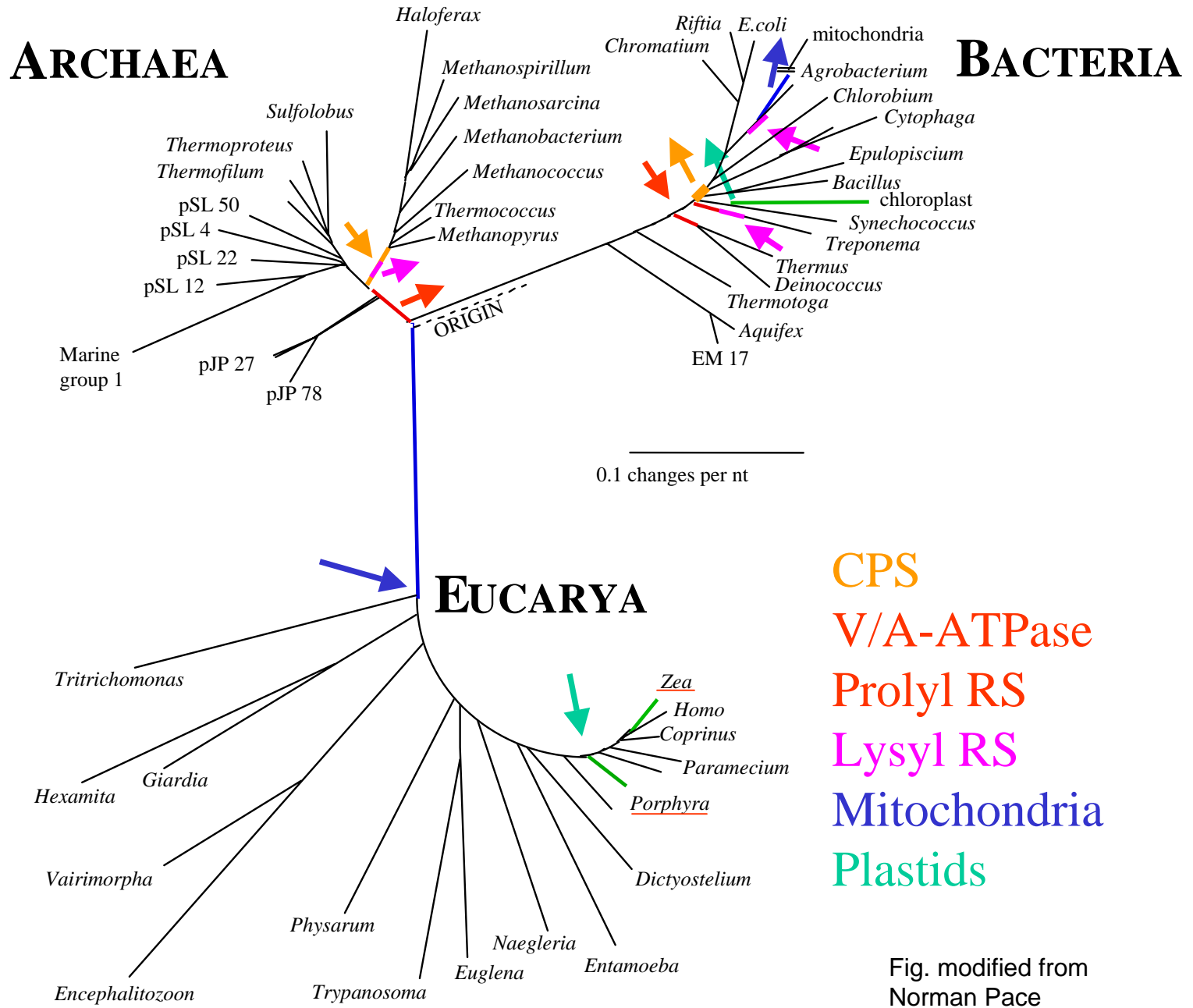


Lebensbaum (German for “Tree of Life”) from Ernst Haeckel, 1874



Charles Darwin (1837)

SSU-rRNA Tree of Life



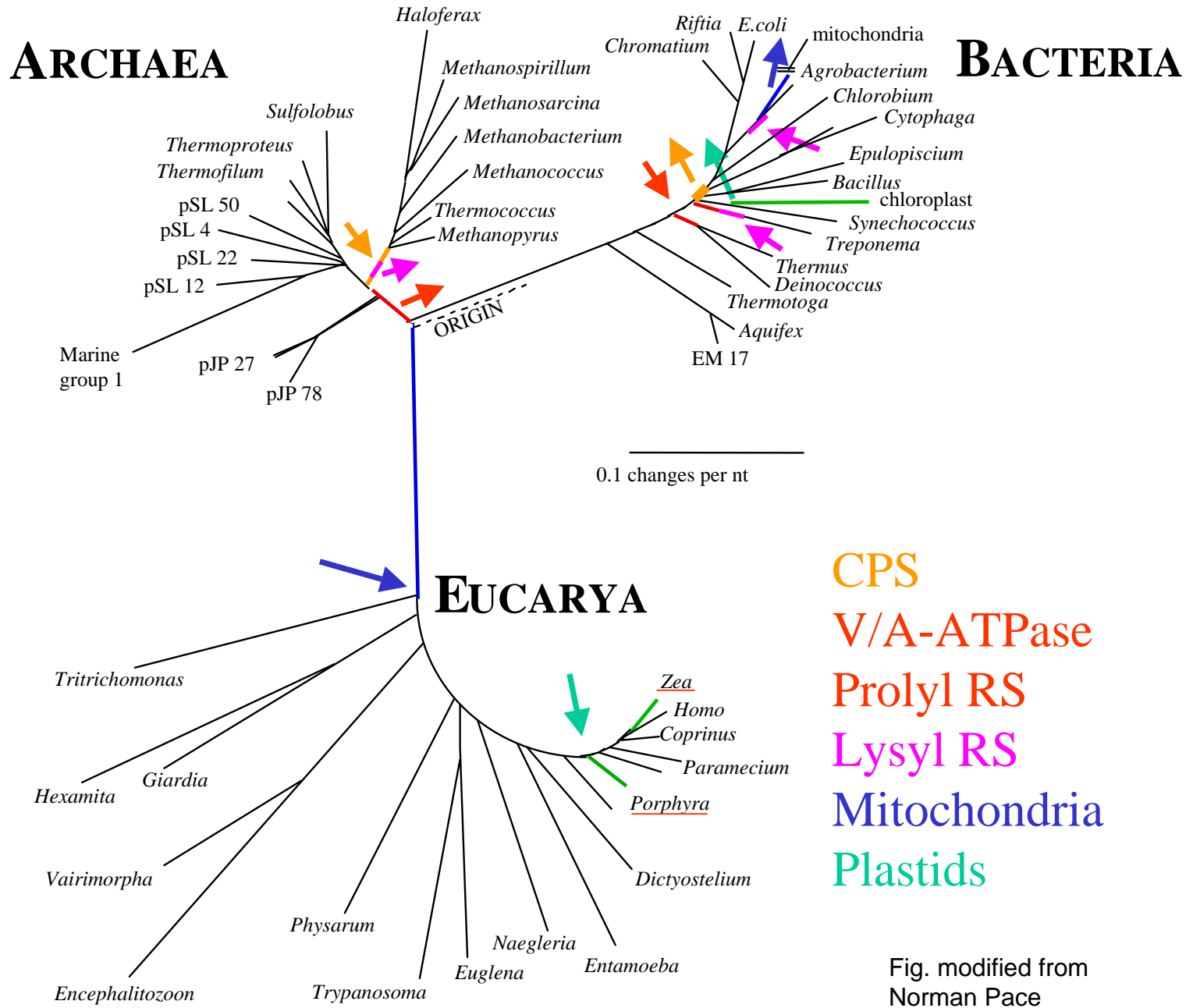
All life forms on Earth share common ancestry

Cenancestor – (from the Greek “kainos” meaning recent and “koinos” meaning common) – the most recent common ancestor of all the organisms that are alive today. The term was proposed by Fitch in 1987.

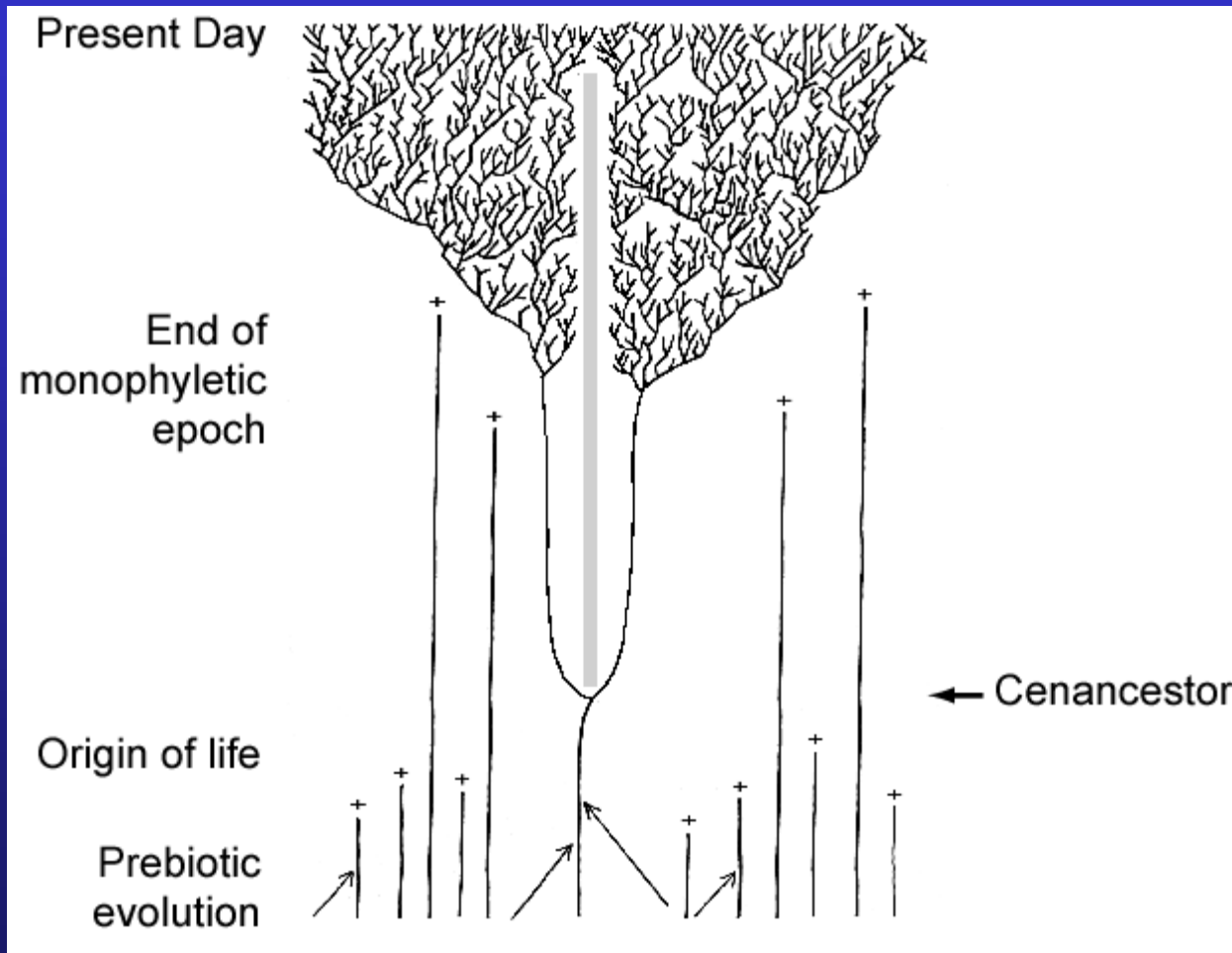
Where is the root of the tree of life?

- On the branch leading to Bacteria
(Gogarten, J.P. *et al.*, 1989; Iwabe, N. *et al.*, 1989)
- On the branch leading to Archaea (Woese, C.R., 1987)
- On the branch leading to Eukaryotes
(Forterre, P. and Philippe, H., 1999; Lopez, P. *et al.*, 1999)
- Under aboriginal trifurcation (Woese, C.R., 1978)
- Inconclusive results (Caetano-Anolles, G., 2002)

SSU-rRNA Tree of Life



Hypotheses to explain the long empty branches connecting the three domains of life



Early evolution prior to the split of the three domains was following different mechanisms.

- Wolfram Zillig, 1992
- Otto Kandler, 1994
- Carl Woese, 1998
- Arthur Koch, 1994

Hypotheses to explain the long empty branches connecting the three domains of life (cont.)

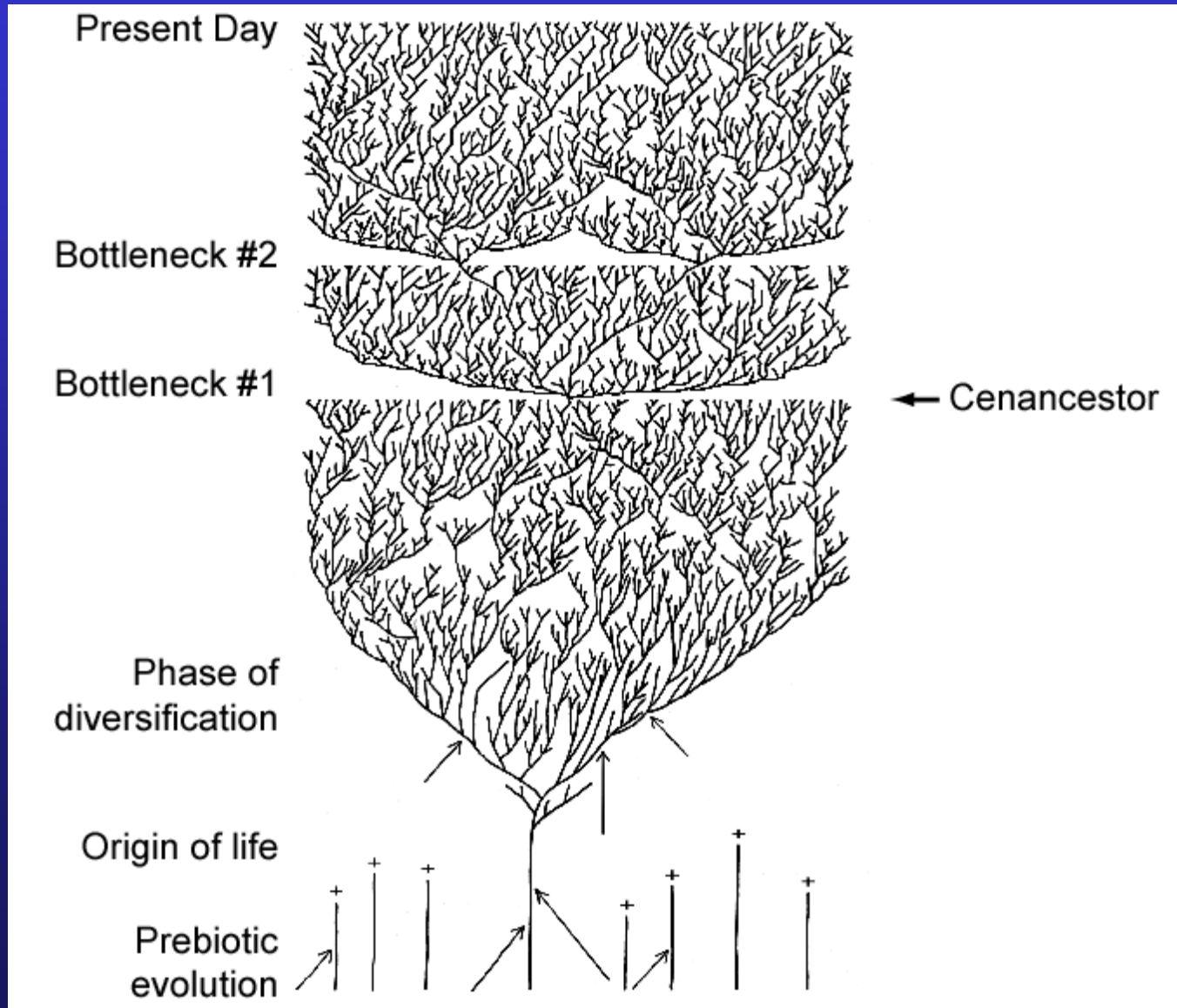


There were major catastrophic events in the past that led to a bottleneck with only few survivors

For example:

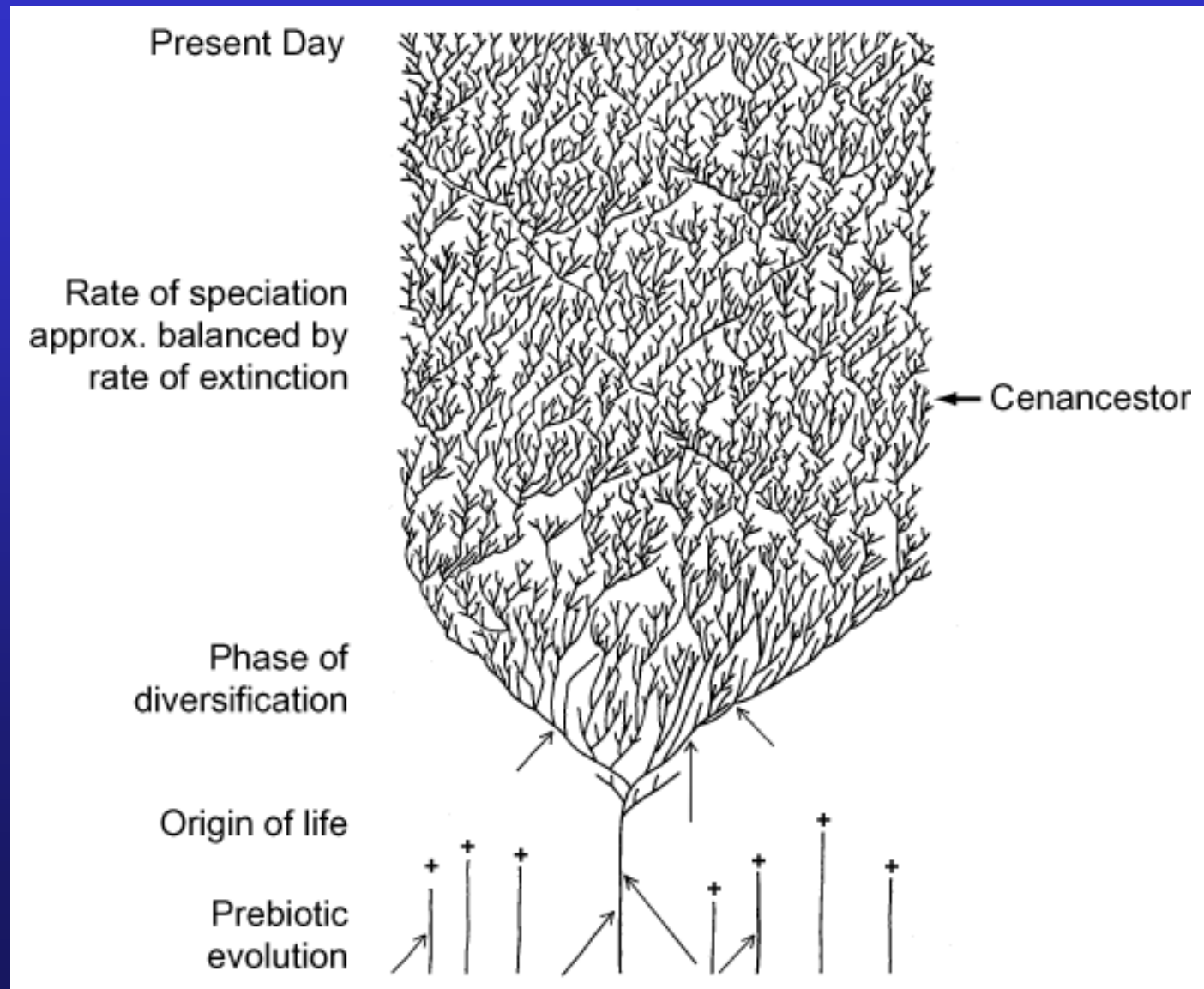
- Tail of early heavy bombardment
- Rise of oxygen

Hypotheses to explain the long empty branches connecting the three domains of life (cont.)



There were major catastrophic events in the past that led to a bottleneck with only few survivors

Hypotheses to explain the long empty branches connecting the three domains of life (cont.)



Coalescence – the process of tracing lineages backwards in time to their common ancestors. Every two extant lineages coalesce to their most recent common ancestor. Eventually, all lineages coalesce to the cenancestor.

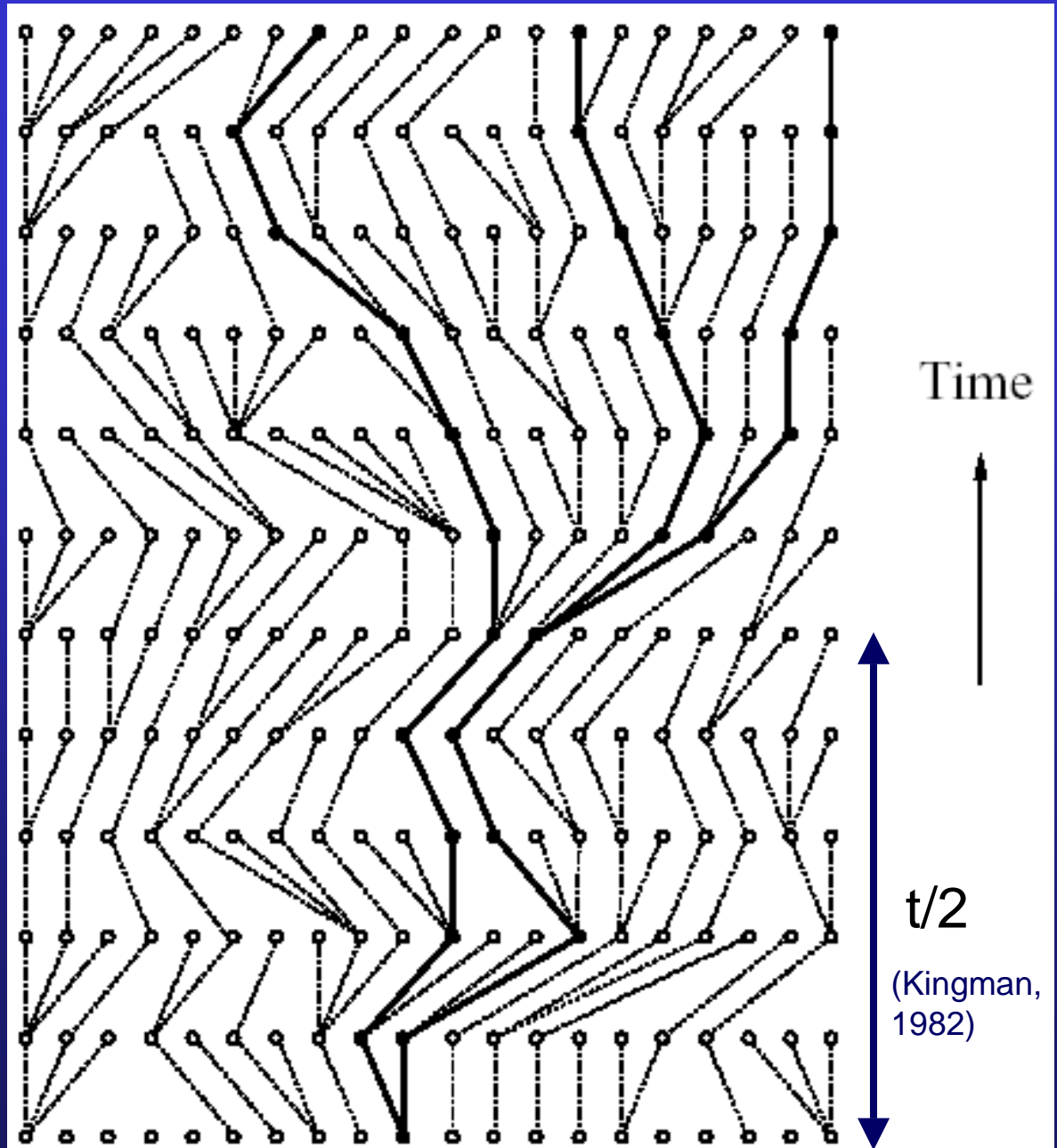
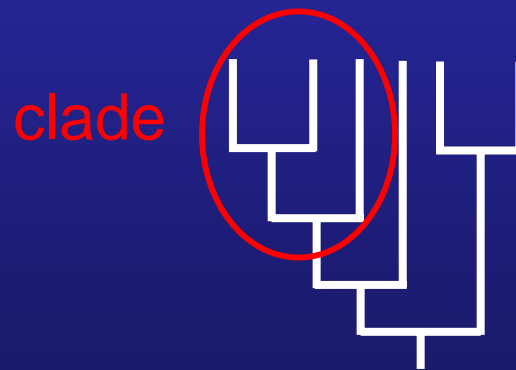


Illustration is from J. Felsenstein, "Inferring Phylogenies", Sinauer, 2003

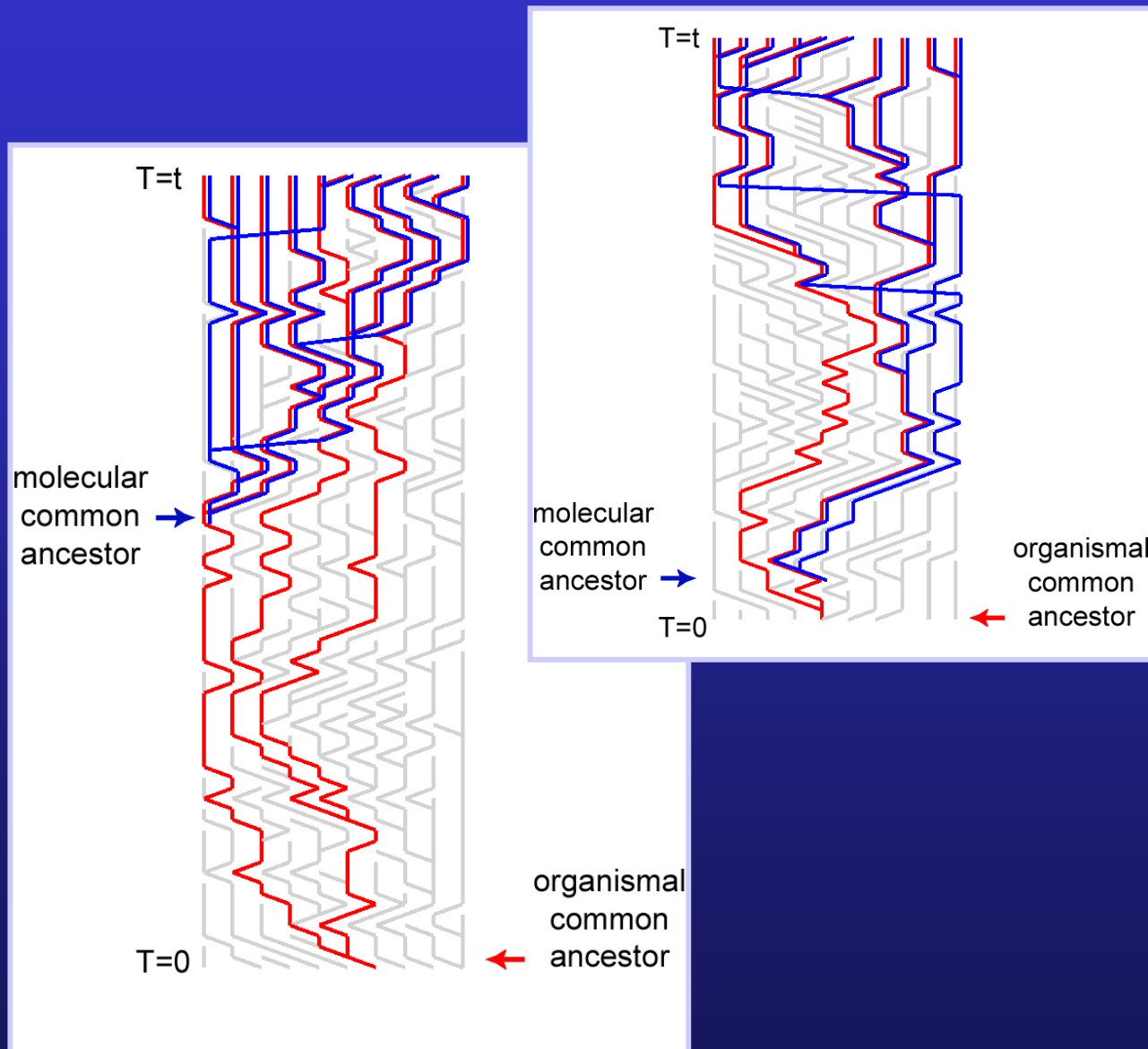
Coalescence as an Approach to Study Cladogenesis

Clade – (from the Greek “klados” meaning branch or twig) – a group of organisms that includes all of the descendants of an ancestral taxon. In a rooted phylogeny every node defines a clade as the lineages originating from this node, including those that arise in successive furcations.



Cladogenesis – the process of clade formation

Simulations of cladogenesis by coalescence



- One extinction and one speciation event per generation

- Horizontal transfer event once in 10 generations

RED: organismal lineages (no HGT)

BLUE: molecular lineages (with HGT)

GRAY: extinct lineages

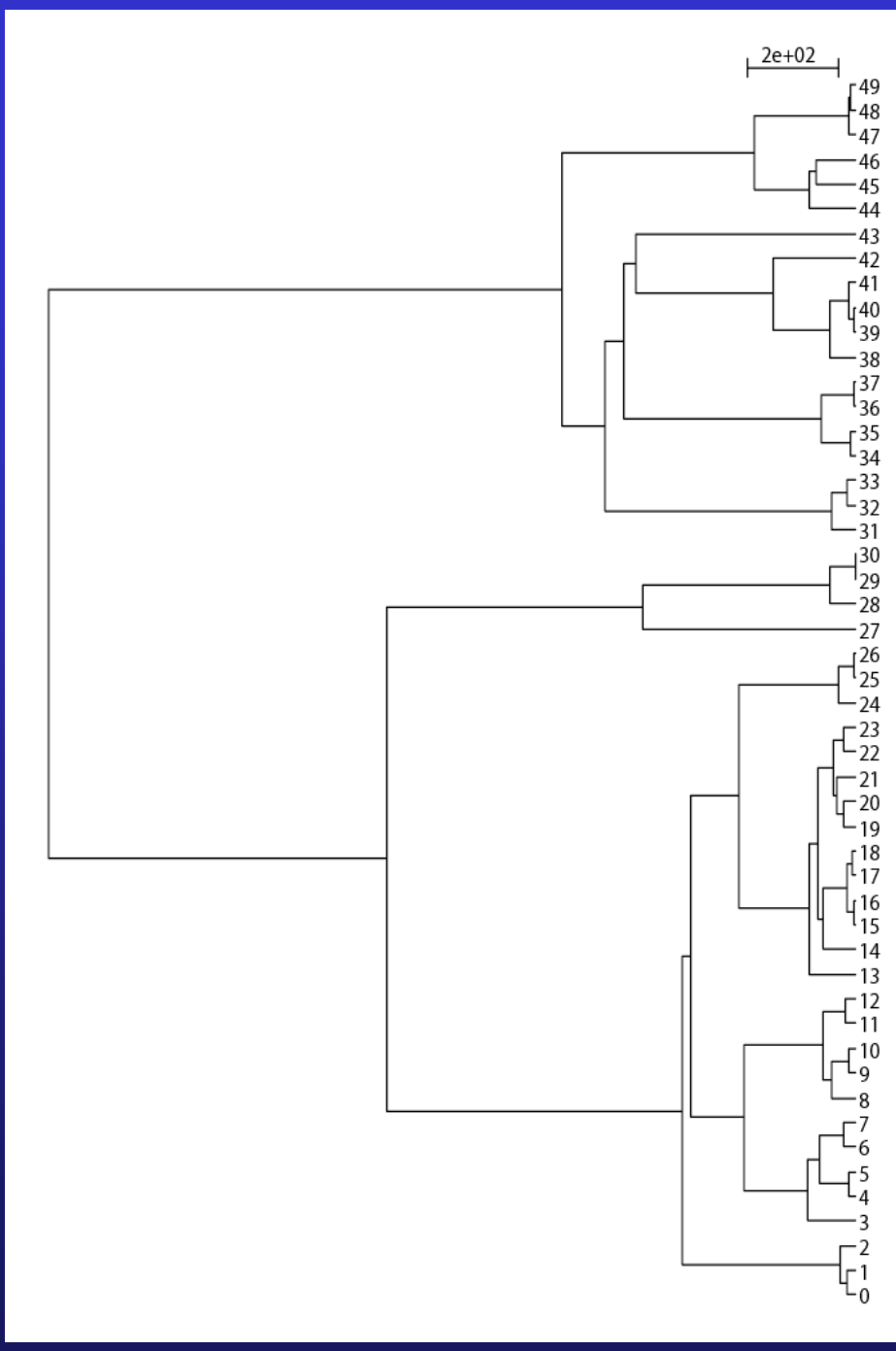
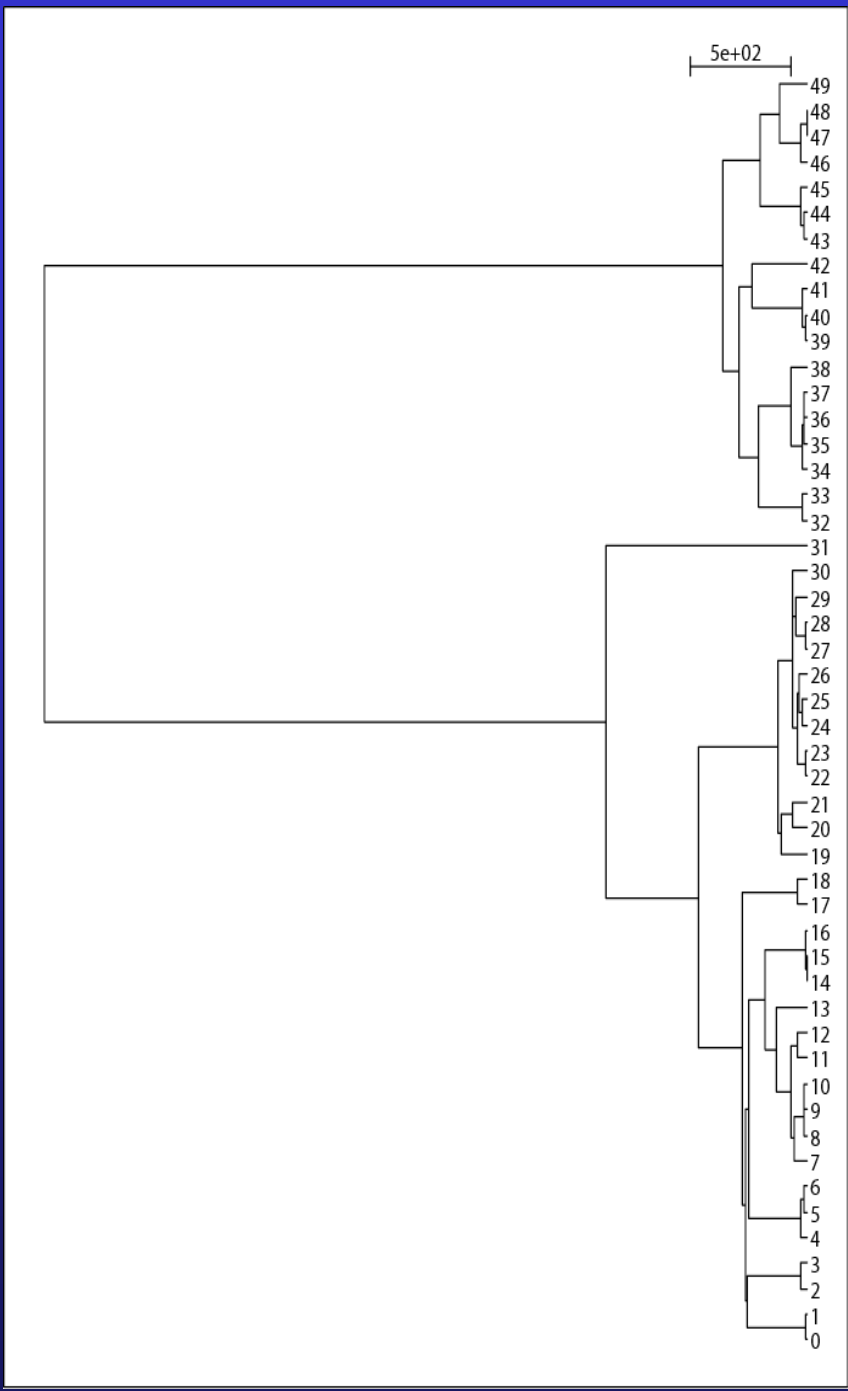
RESULTS:

- Most recent common ancestors are different for organismal and molecular phylogenies

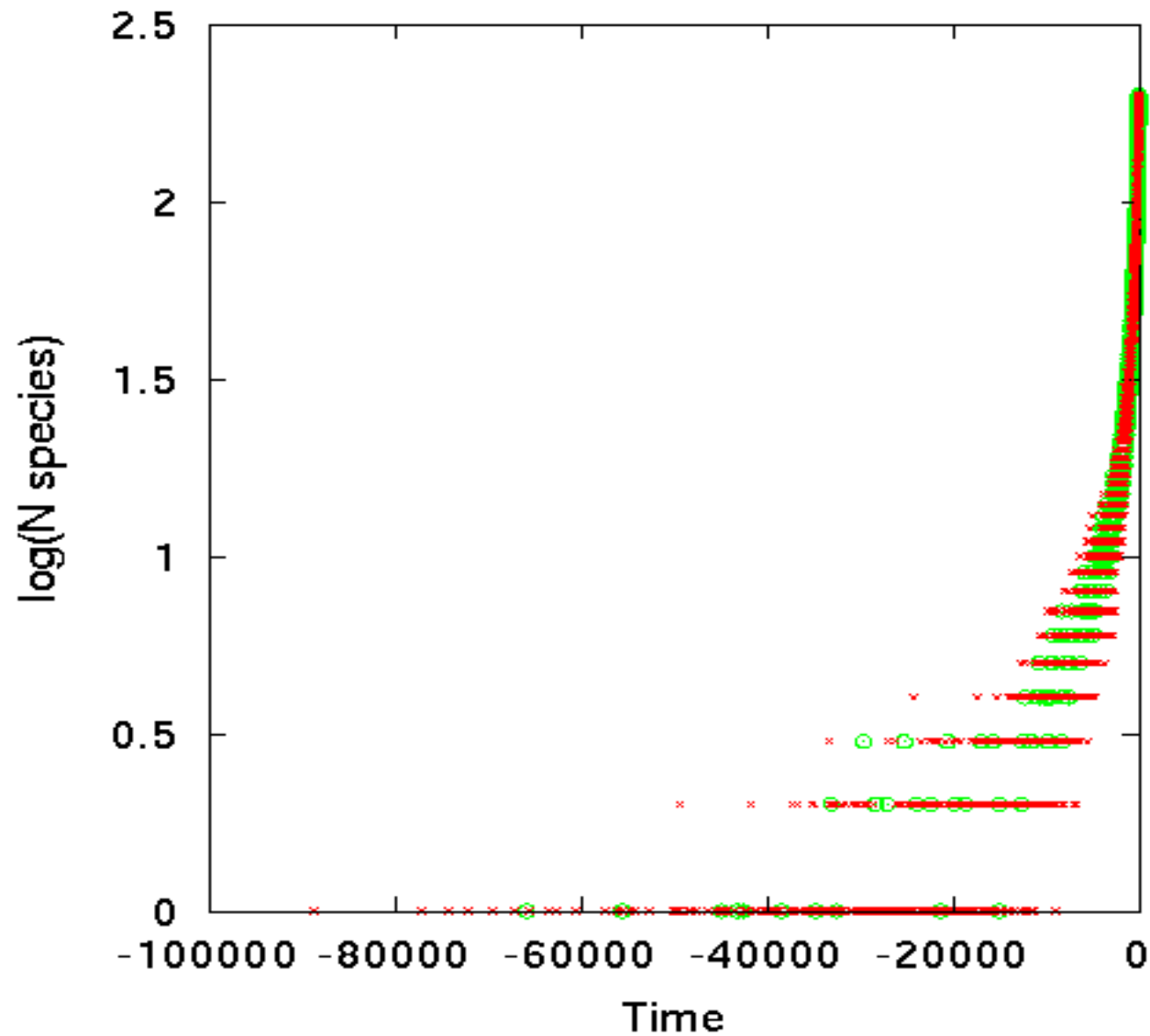
- Different coalescence times

- Long coalescence of the last two lineages

EXTANT LINEAGES FOR THE SIMULATIONS OF 50 LINEAGES



Number of extant lineages over time



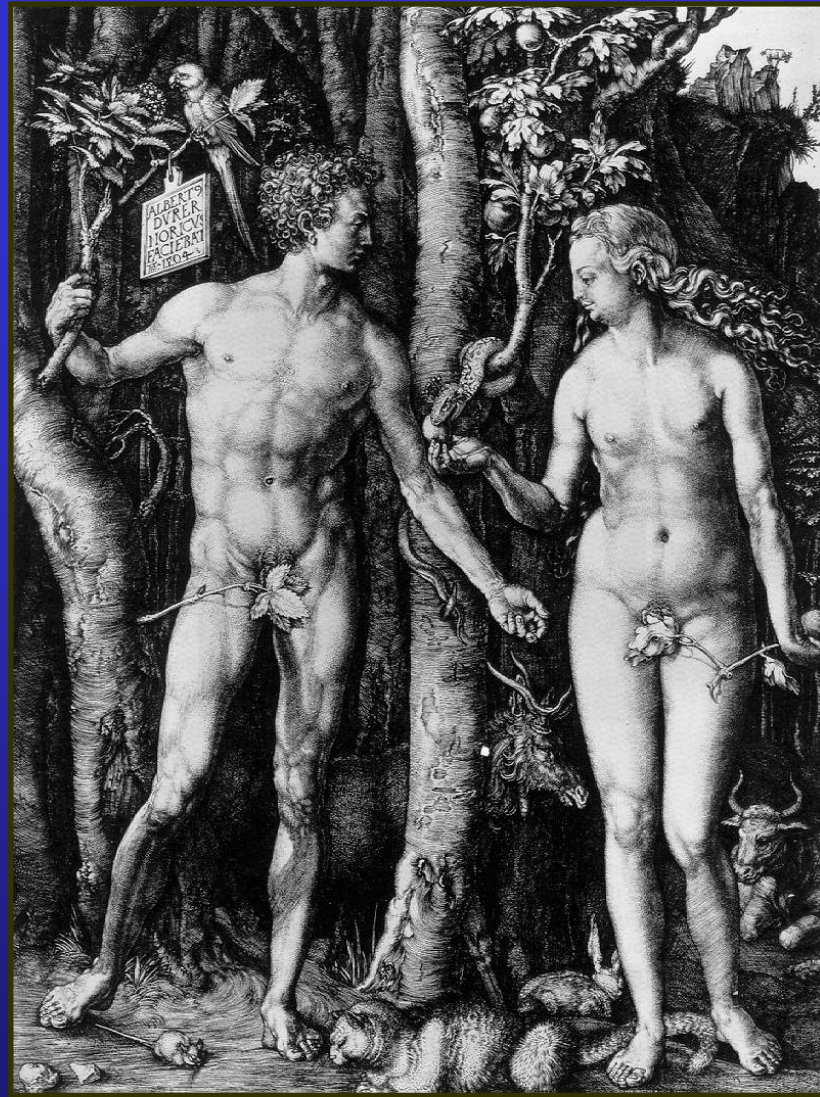
green: organismal lineages ;
red: molecular lineages (with gene transfer)

Y chromosome Adam

Lived
approximately
50,000 years ago

Thomson, R. *et al.* (2000)
Proc Natl Acad Sci U S A 97,
7360-5

Underhill, P.A. *et al.* (2000)
Nat Genet 26, 358-61



Albrecht Durer, *The Fall of Man*, 1504

Mitochondrial Eve

Lived
166,000-249,000
years ago

Cann, R.L. *et al.* (1987)
Nature 325, 31-6

Vigilant, L. *et al.* (1991)
Science 253, 1503-7

Adam and Eve never met ☹️

CONCLUSIONS

- Coalescence leads to long branches at the root.
- Using single genes as phylogenetic markers makes it difficult to trace organismal phylogeny in the presence of horizontal gene transfer.
- Each contemporary molecule has its own history and traces back to an individual molecular ancestor, but these molecular ancestors were likely to be present in different organisms at different times.
- The model alone already explains some features of the observed topology of the tree of life. Therefore, it does not appear warranted to invoke more complex hypotheses involving bottlenecks and extinction events to explain these features of the tree of life.

OUTLOOK

- Incorporate non-random Horizontal Gene Transfer into the model.
- Consider the model as a null hypothesis and look at deviations from it. E.g., the bacterial clade does not conform to the model's prediction. This deviation could be due to sudden radiation.
- Explore if the model can be used to infer parameters that describe the early evolution of life. E.g., number of species.