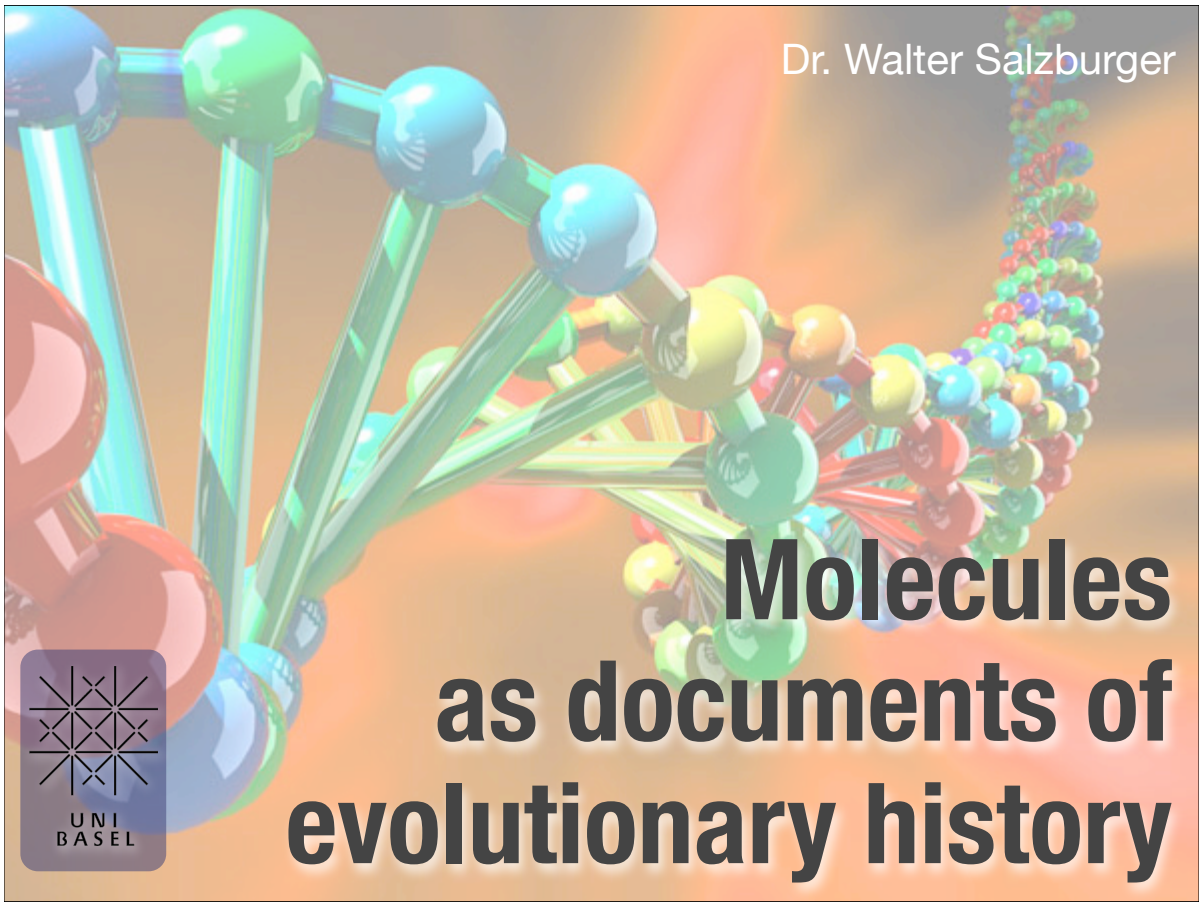
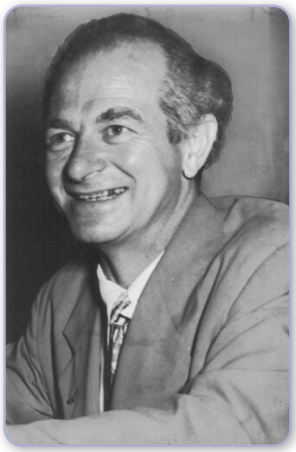


"The most rational, universal and informative molecular phylogeny will be built on **semantophoretic molecules** alone"

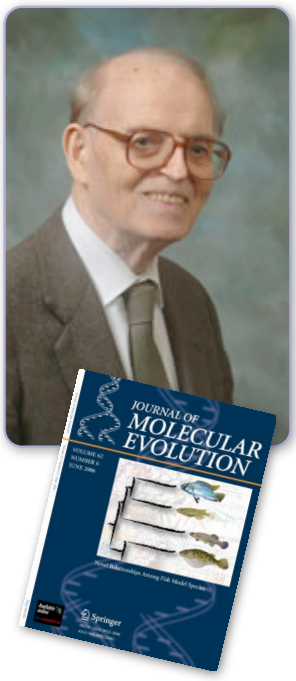
Zuckerkandl and Pauling (1965)

Linus Carl Pauling (1901-1994)



- quantum chemistry (USA)
- Nobel Prize (1954) for his work “on the nature of chemical bonds”
- Nobel Peace Price (1962) for his campaign against nuclear testing
- founder of molecular biology; influential in the fields of molecular evolution, molecular medicine, etc.

Emile Zuckerkandl (1922-)



- biologist (Austria, USA)
- protein chromatography and electrophoresis in Linus Pauling’s lab
- Zuckerkandl & Pauling (1962): concept of molecular clocks
- founder of molecular evolution; founding editor of the *Journal of Molecular Evolution*

- **Semantophoretic molecules**, **semantides** are molecules that carry information of genes of transcripts thereof: DNA, mRNA, polypeptides (proteins)
- **Episemantic molecules** are synthesized under the control of (tertiary) semantides but in the absence of a template.
- **Asemantic molecules** are not produced by the organism and do not express information that this organism contains (e.g. vitamins, phosphate ion).

> "It is plain that asemantic molecules are not worthy in inquiries about phylogenetic relationships."

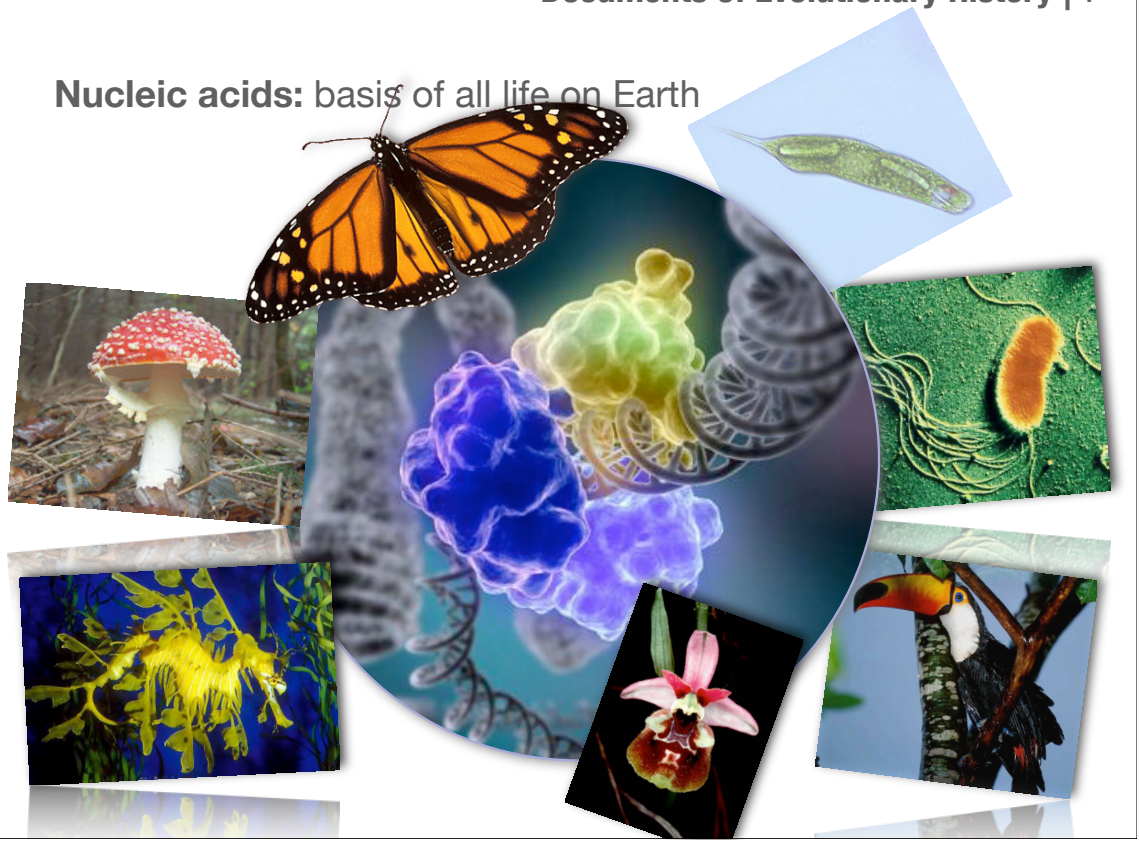
Zuckerkandl and Pauling (1965)

The comparison of homologous semantophoretic molecules yields threefold information:

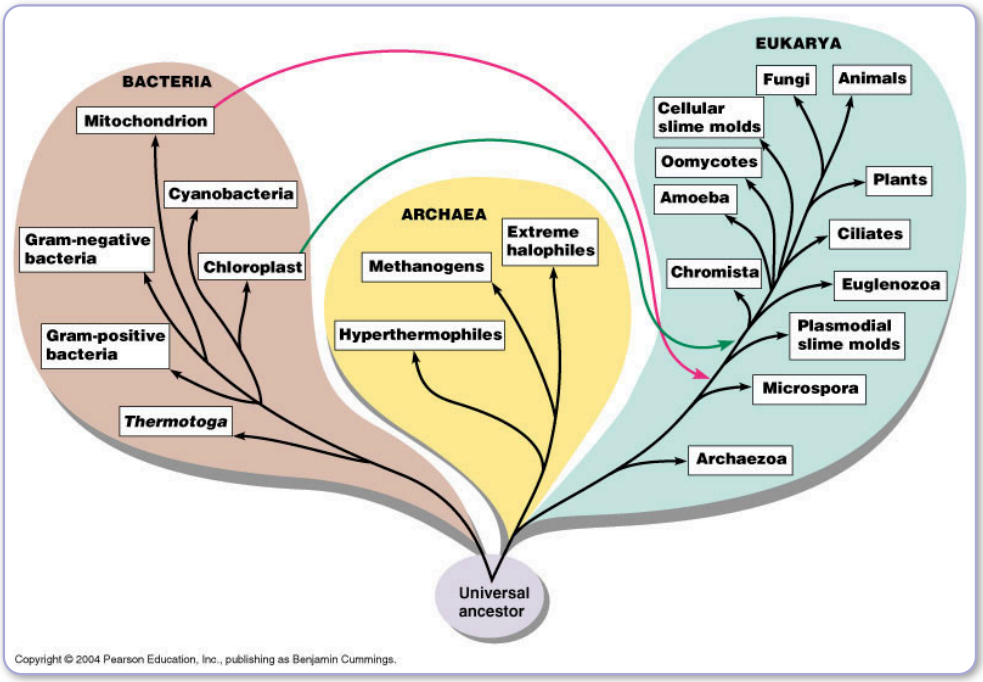
- **the approximate time of existence**
- **the probable amino-acid sequence of the ancestor**
- **the lines of descent along which changes occurred**

Zuckerkandl and Pauling (1965)

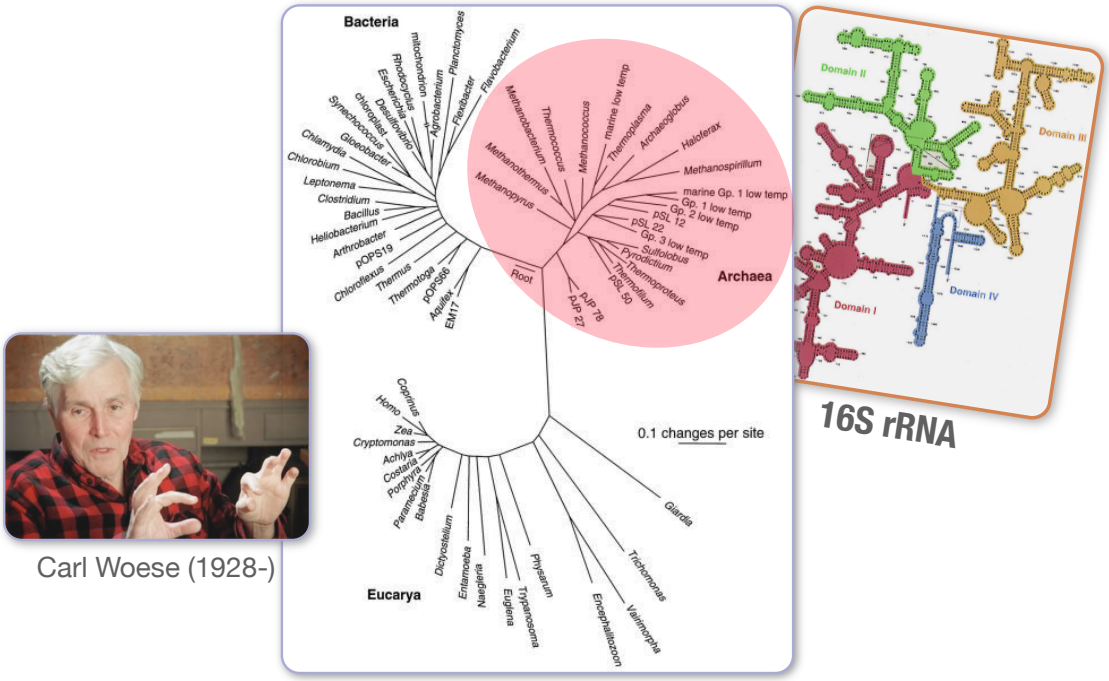
Nucleic acids: basis of all life on Earth



Three domains of life

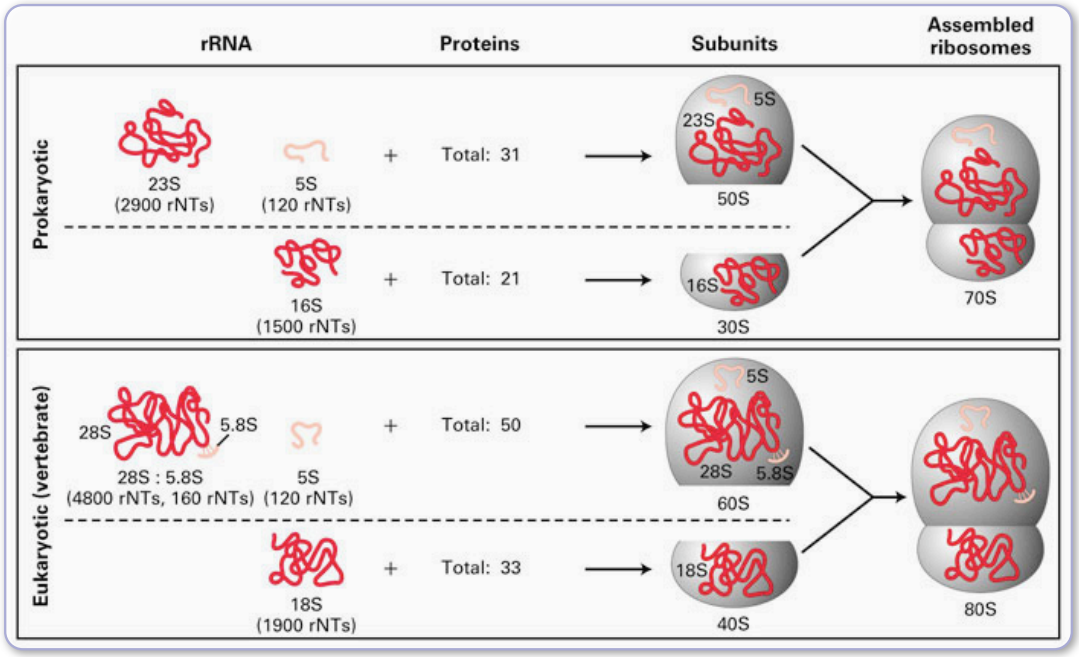


Three domains of life

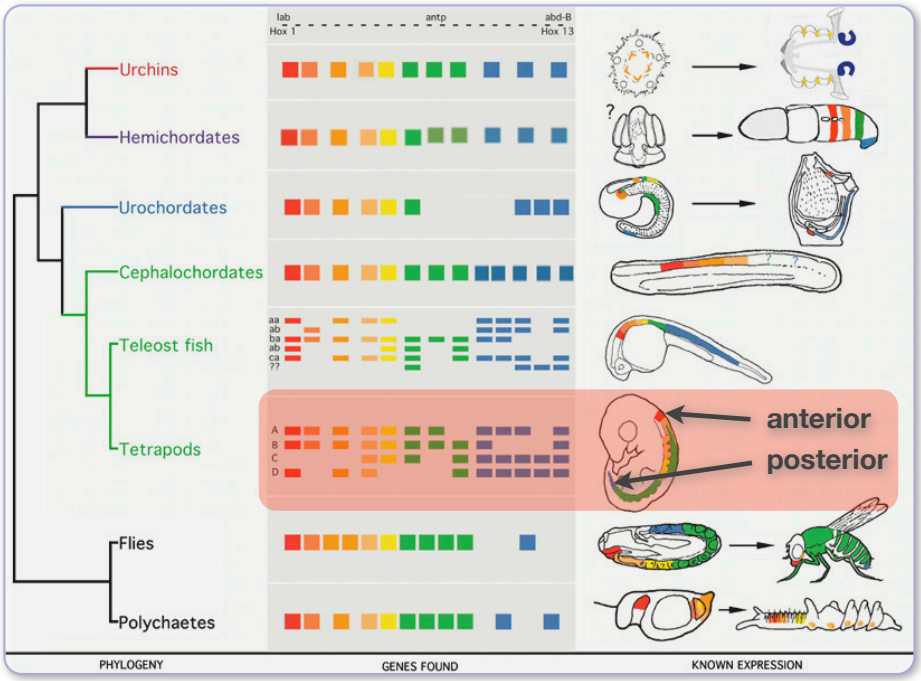


Carl Woese (1928-)

cellular processes: rRNA subunits

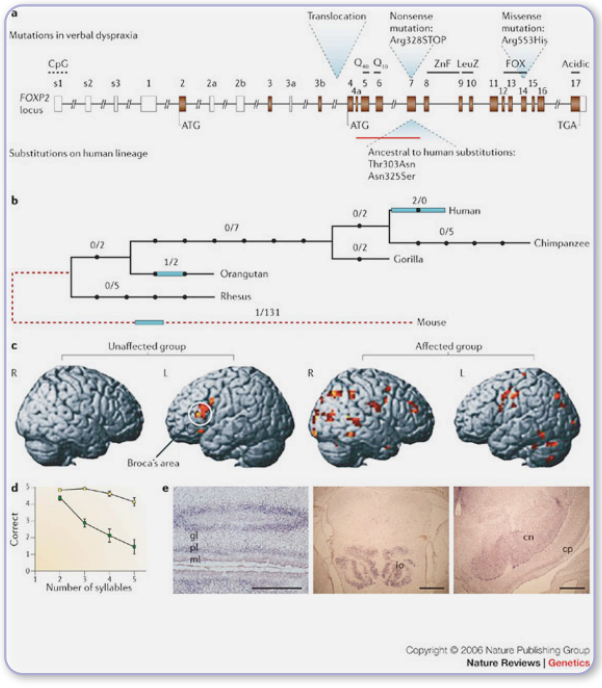


genomic architecture: *Hox* gene clusters



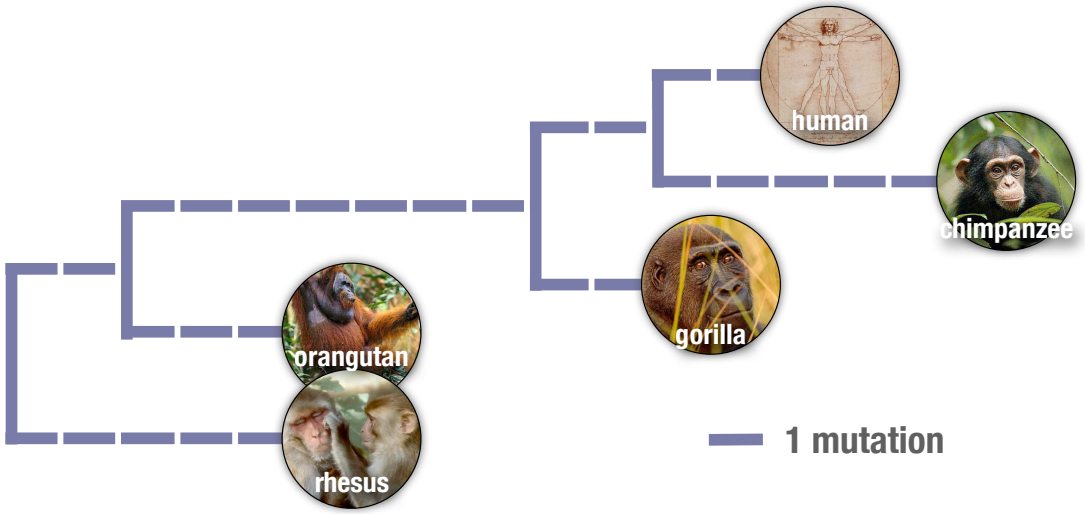
Swalla (2006)

mutational difference: *foxp2* in apes



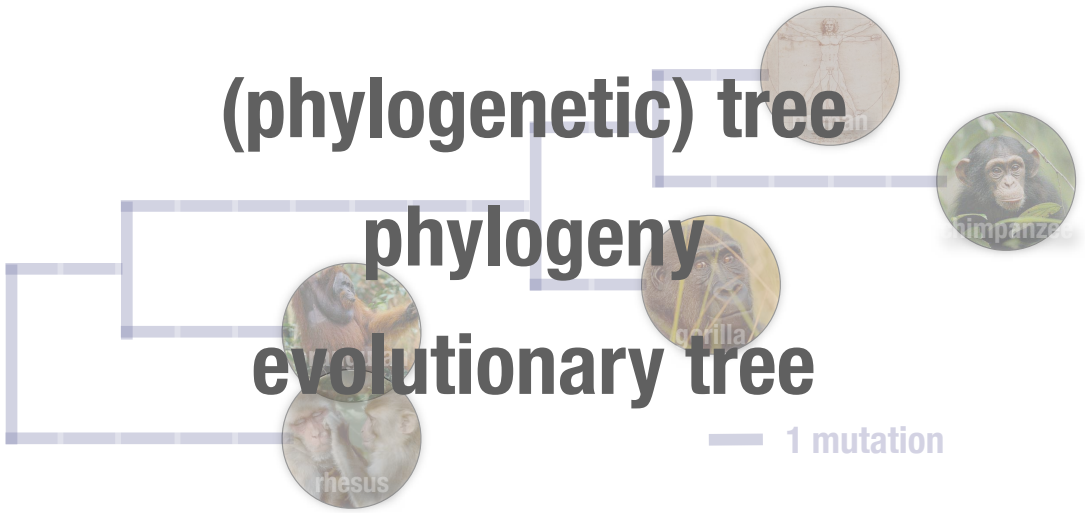
Fisher & Marcus (2006)

molecular evolution of foxp2 in apes



Enard et al. (2002)

diagram of evolutionary history

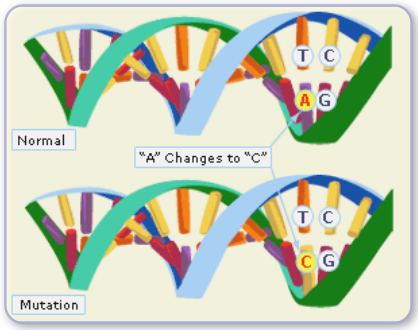


"The **stream of heredity** makes **phylogeny**: in a sense, it is phylogeny. Complete genetic analysis would provide the most priceless data for the mapping of this stream"

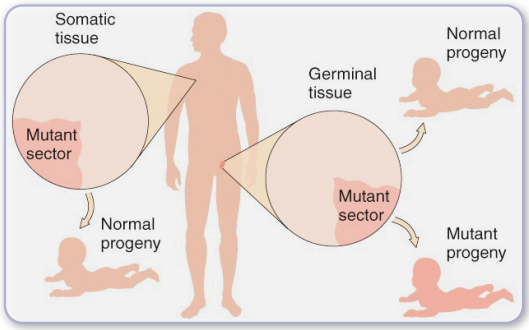
Simpson (1945)

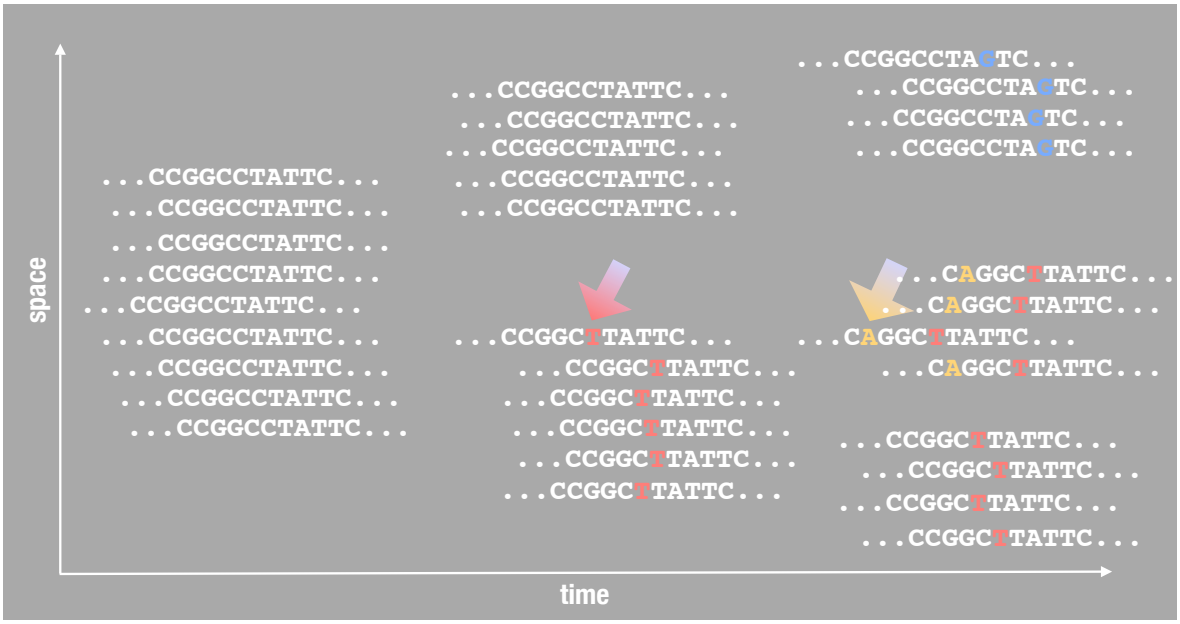
George G. Simpson (1902-1984)

mutational change



inheritance




space
time
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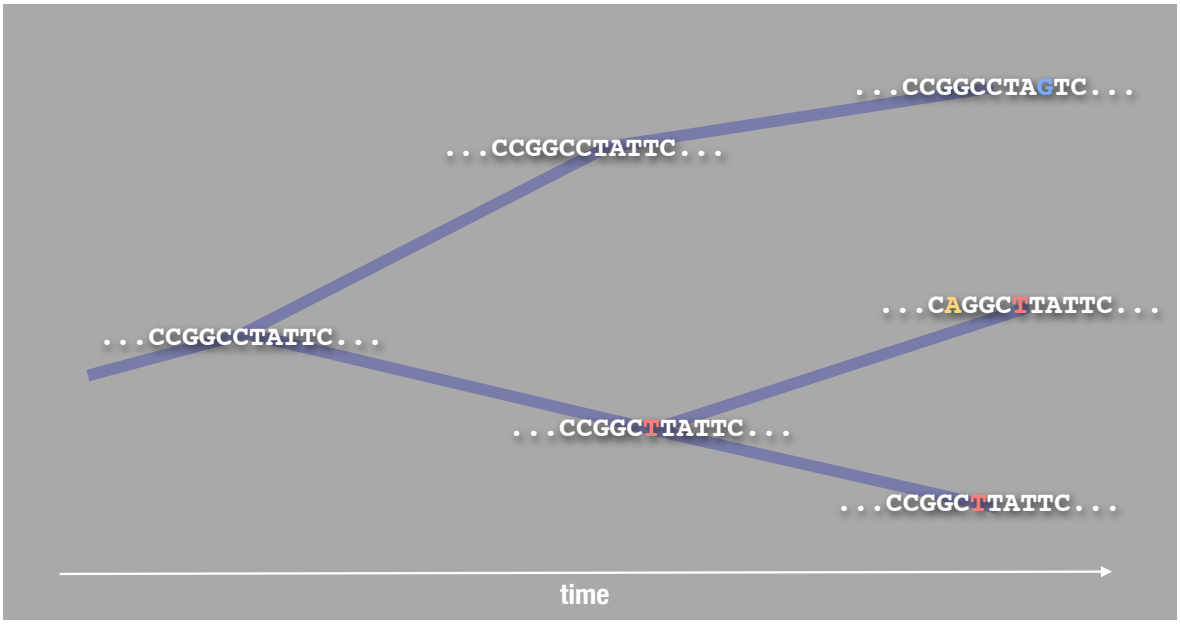
time
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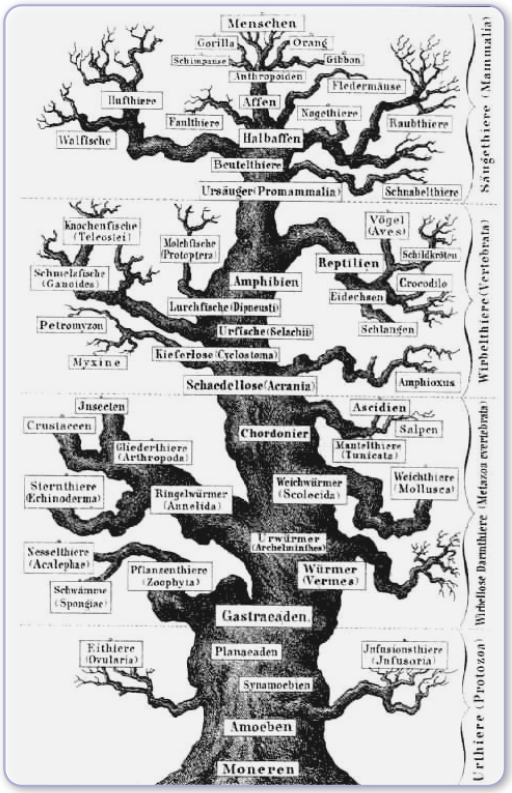
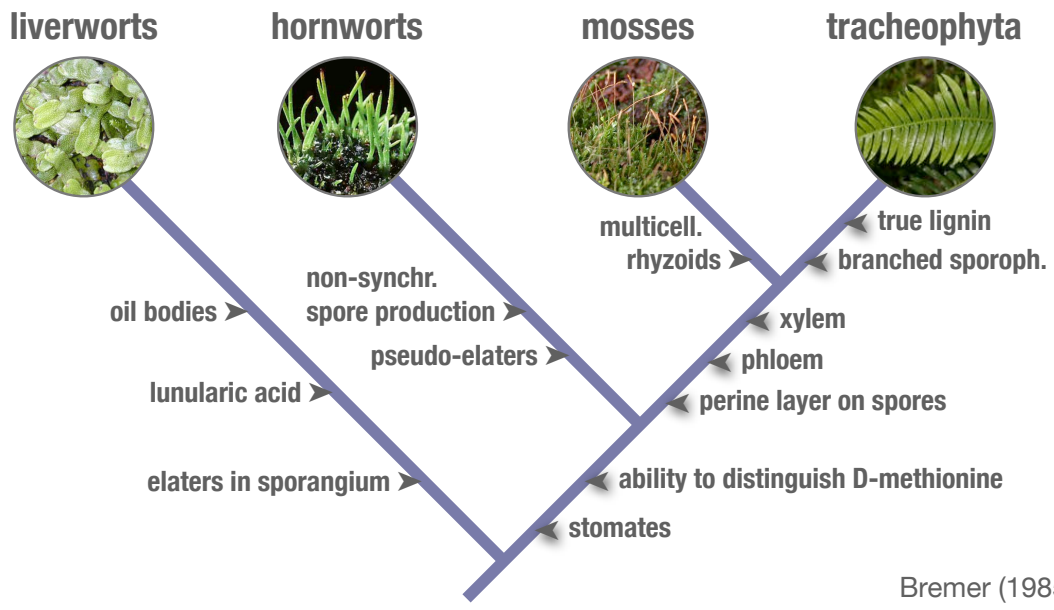
...CCGGCTTATTC...



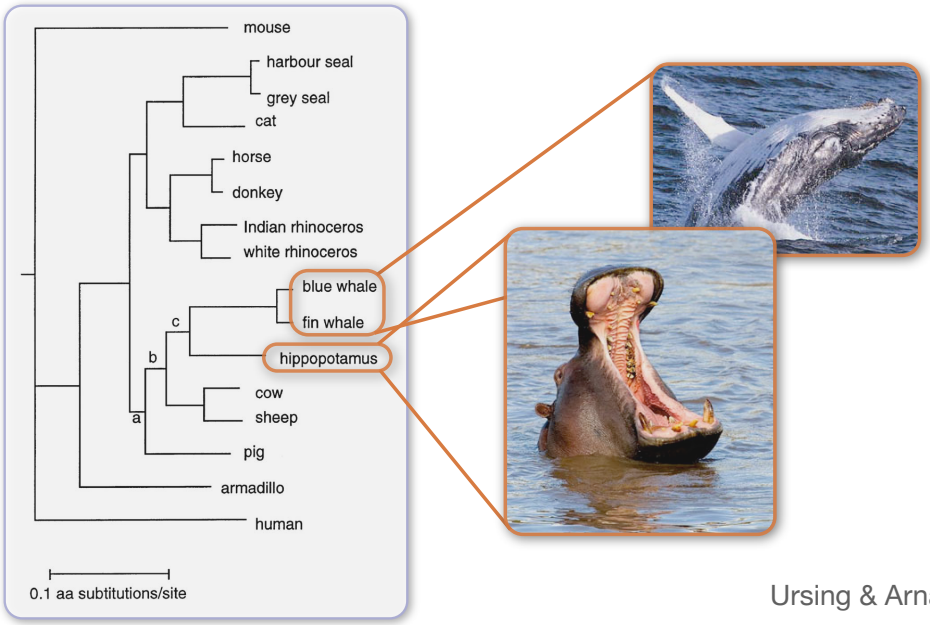
Ernst Haeckel
(1834-1919)

- Phylogeny of plants based on **morphological characters**



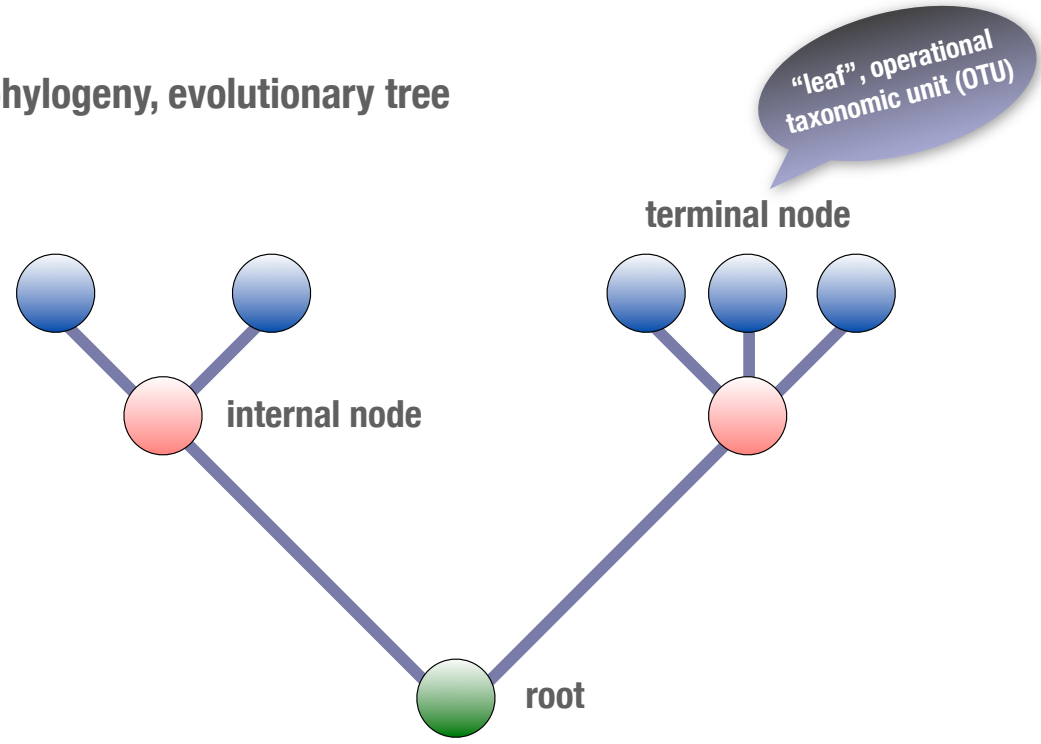
Bremer (1985)

Molecular phylogeny of Cetacea and Artiodactyla

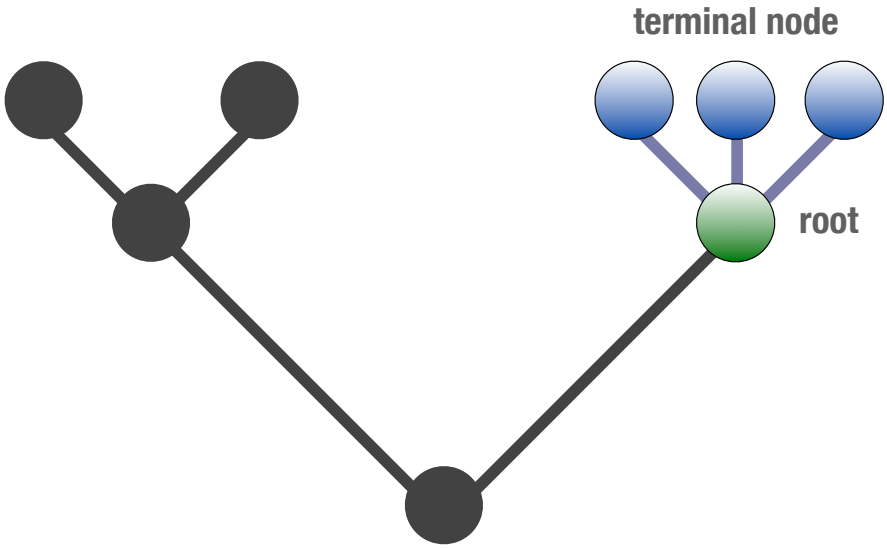


Ursing & Arnason (1998)

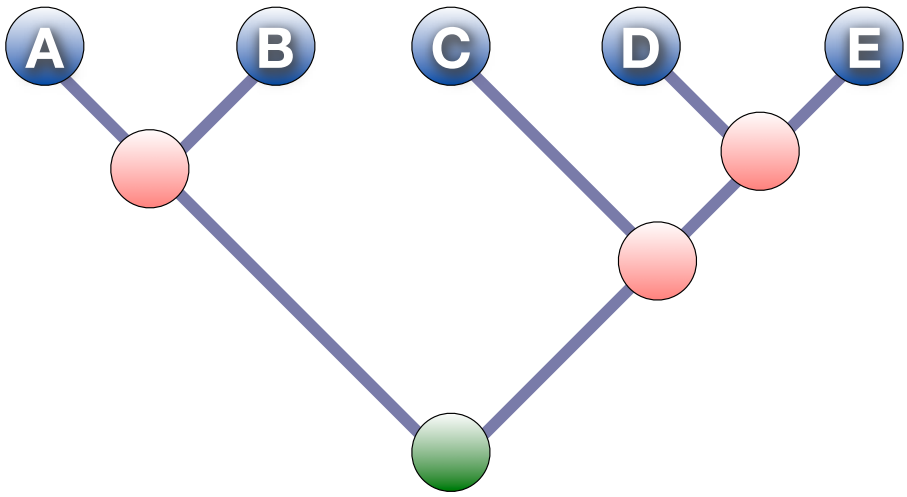
phylogeny, evolutionary tree



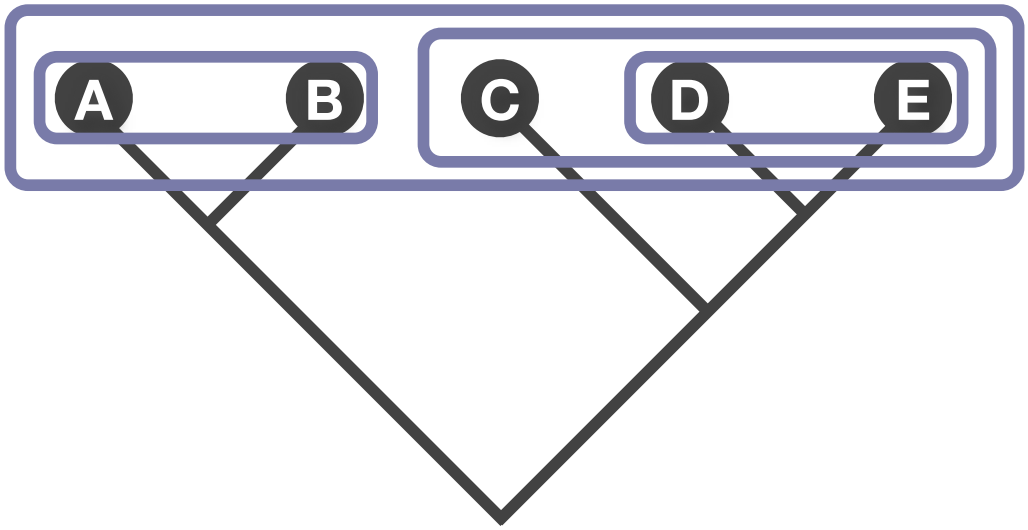
phylogeny, evolutionary tree



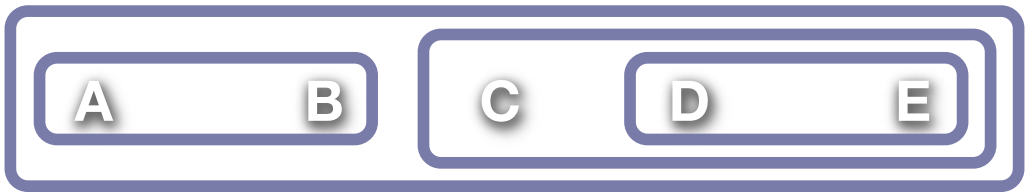
phylogeny, evolutionary tree



Venn diagram



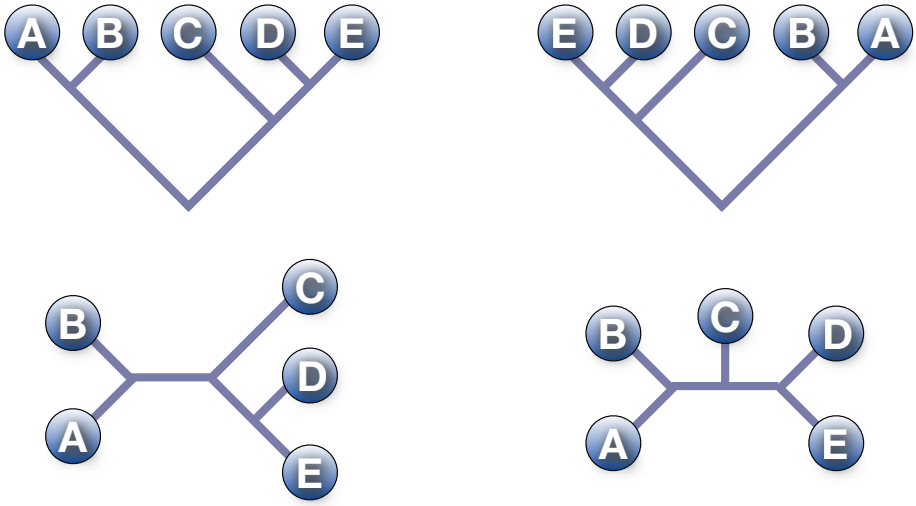
Venn diagram



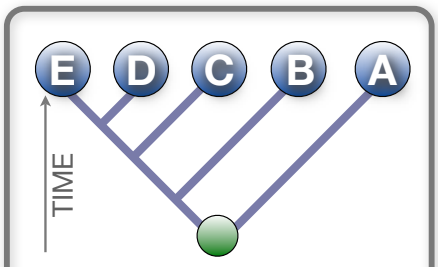
Nested parentheses

((A , B), (C, (D , E))

((A , B), (C, (D , E))

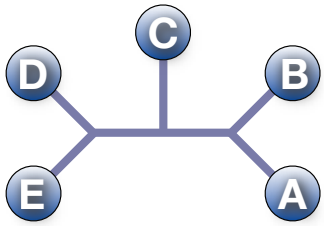


Rooted and unrooted trees



rooted tree

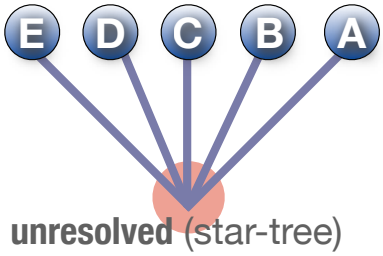
- has a defined “root”
- and therefore a defined direction



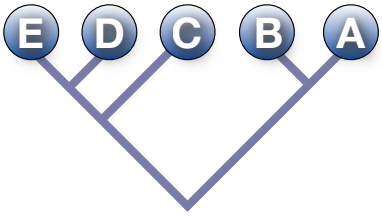
unrooted tree

- no defined direction
- no information about ancestry

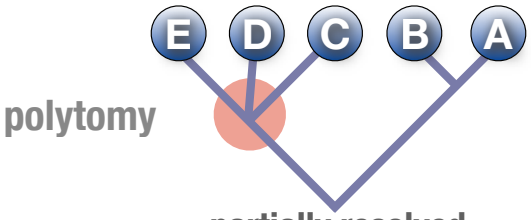
The resolution of trees



unresolved (star-tree)



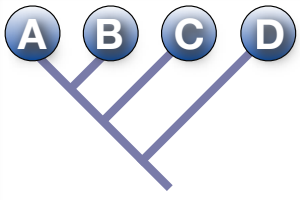
fully resolved



polytomy

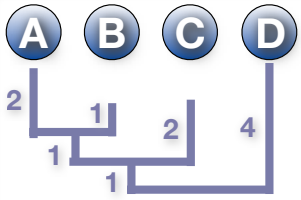
partially resolved

The basic kinds of threes



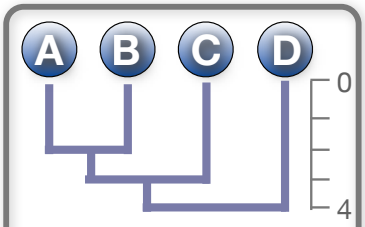
cladogram

shows relative recency of common ancestry



phylogram
("additive tree")

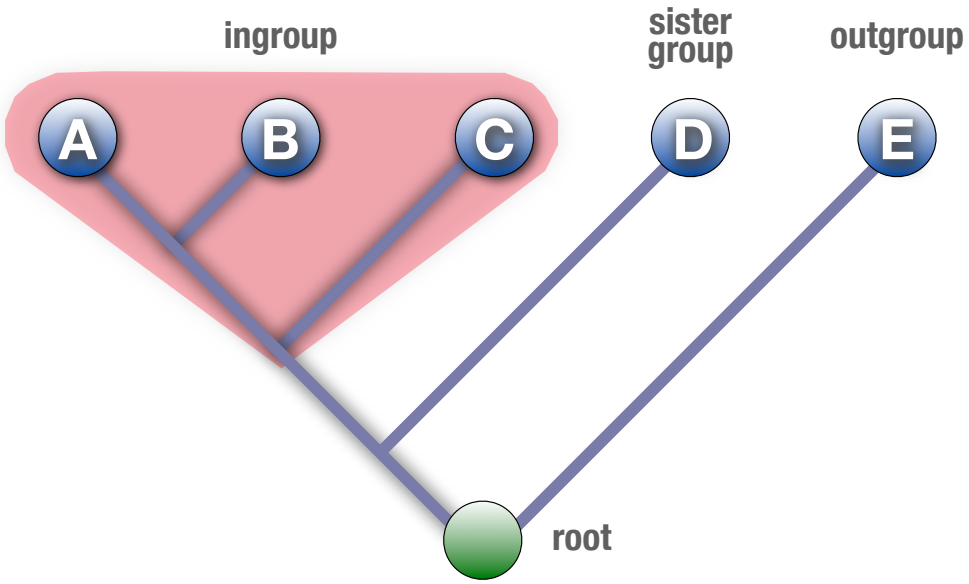
shows branch lengths/amount of evolutionary change



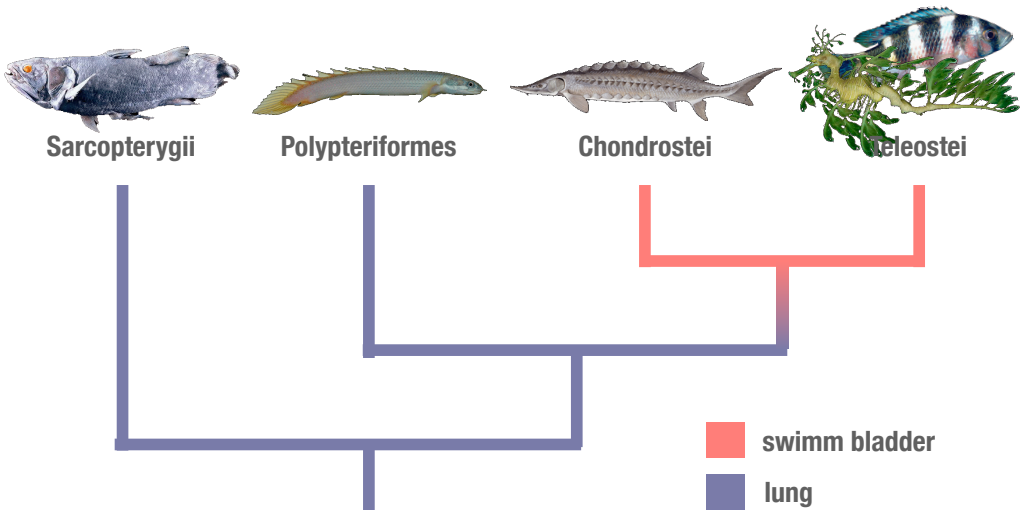
dendrogram
("ultrametric tree")

tips are aequidistant from the root, nodes reflect evoluionary time

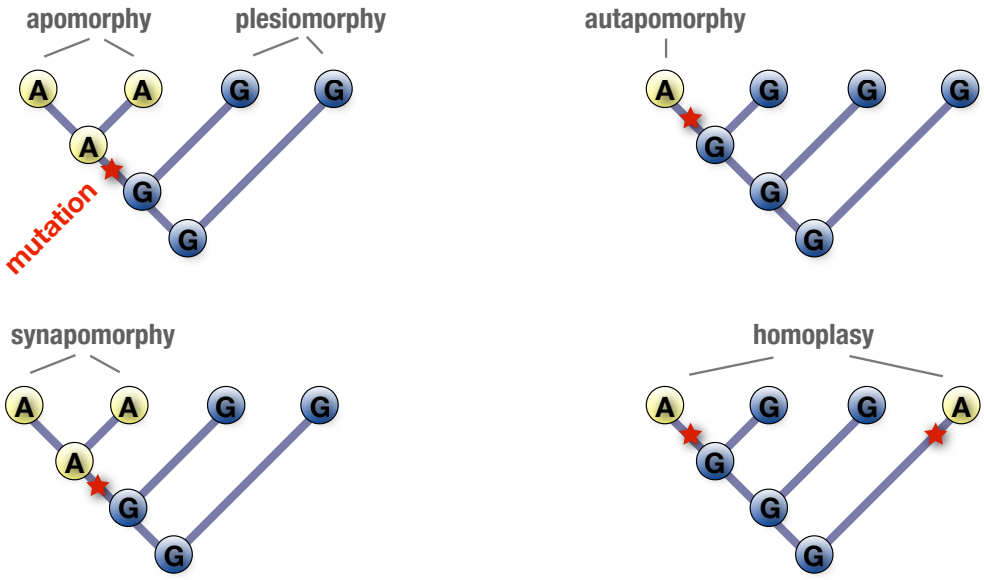
Tree terminology I: outgroup, ingroup and sistergroup



- A character can be - in relative terms - **ancestral** or **derived**. Ancestral character stages are referred to as **plesiomorphies**, derived ones as **apomorphies**.



Tree terminology II: ancestral/derived character states



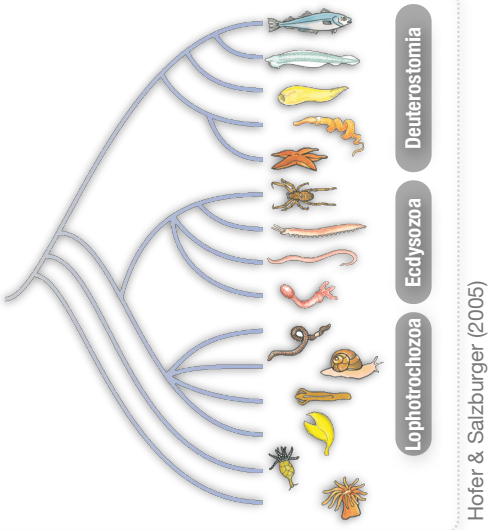
- A **monophyletic group** contains a common ancestor and all of its descendants

Deuterostomia et al.:

Monophyletic groups are natural. Looking at the animal phylogeny on the right, many of the major animal **clades*** are monophyletic, *e.g.*,:

- Deuterostomia
- Ecdysozoa
- Lophotrochozoa

*clade is in fact a synonym of monophyletic group

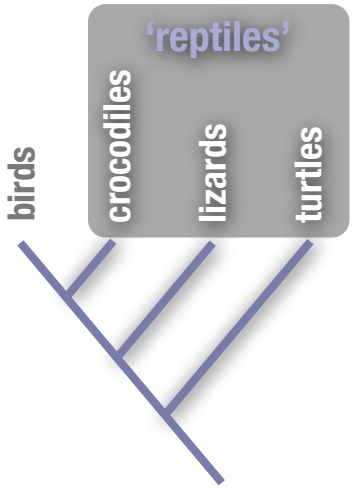


Hofer & Salzburger (2005)

- A **paraphyletic group** contains a common ancestor and some, but not all of its descendants

‘Reptilia’:

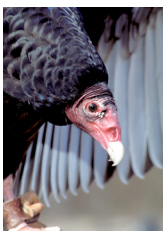
The ‘Reptilia’ are a paraphyletic group. The species included in the ‘Reptilia’ still resemble their ancestor morphologically. The birds, however, have evolved more rapidly and no longer resemble their ancestor but have evolved a variety of derived characters. Note that if a group is not monophyletic, its name is put in quotation marks.

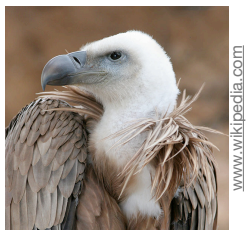


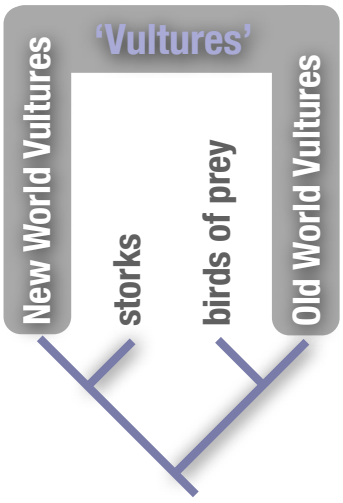
- A **polyphyletic group** is a set of taxa descended from more than one common ancestor

‘Vultures’:

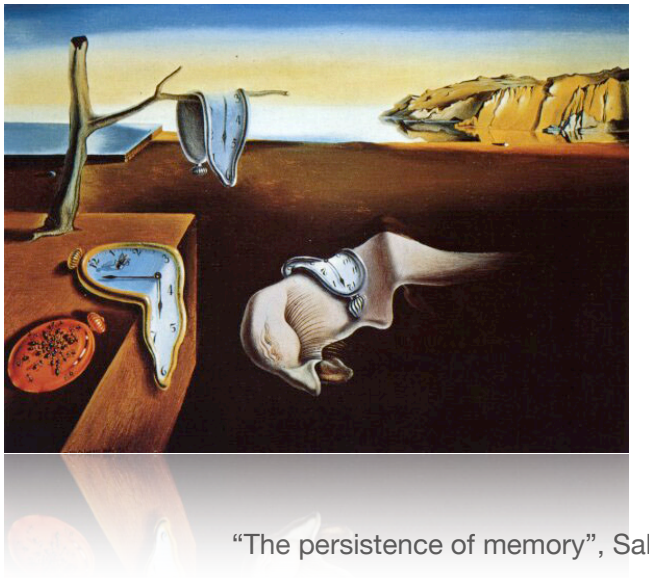
‘Vultures’ are a polyphyletic grouping comprised of birds that have independently evolved similar morphology and habits from different ancestors.


www.haveyouseenmybird.com


www.wikipedia.com



Molecular clocks



"The persistence of memory", Salvador Dalí (1931)

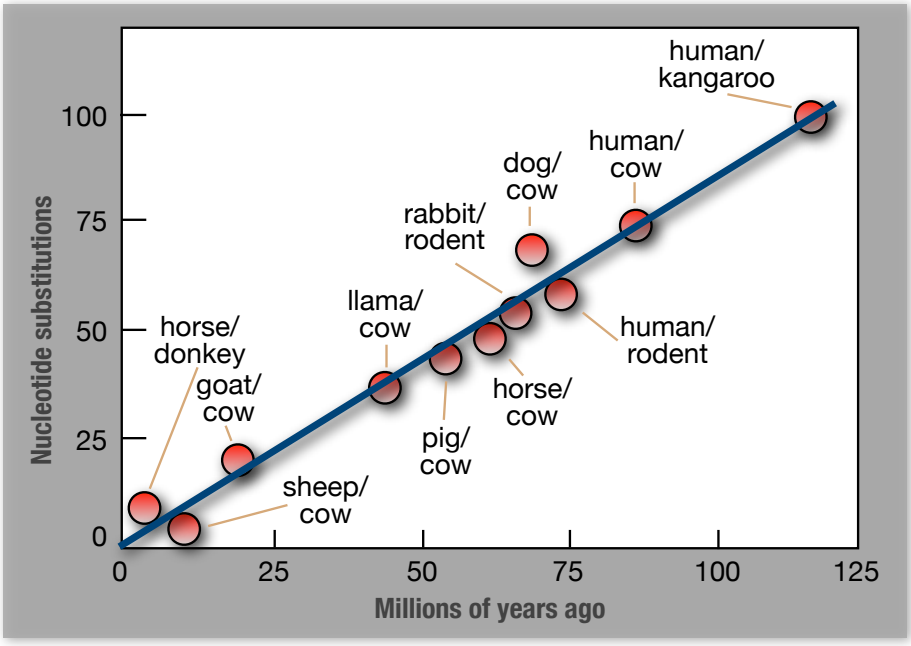
"Soft watches, biologically speaking, are the giant Dalinian DNA molecules which constitute the factors of eternity"

Dalí (~1961)

Salvador Dalí
(1904-1989)

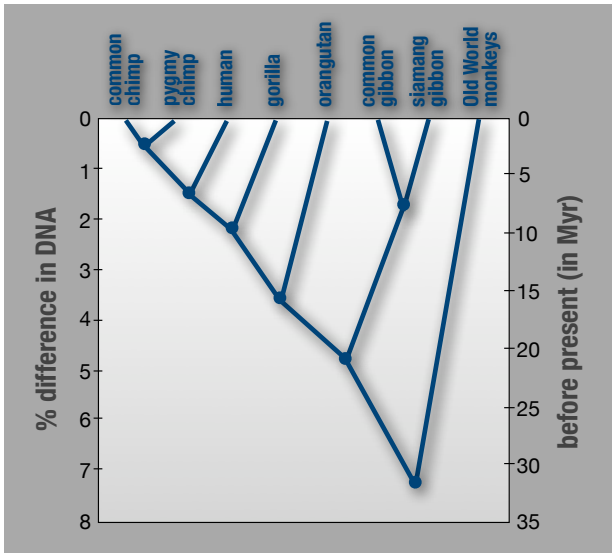
- **Molecular clock** is the theory that molecules evolve at an approximately constant rate
- The difference between the form of a molecule in two species is then proportional to the time since divergence from a common ancestor
- The molecular clock hypothesis is a testable prediction

molecular clock in hemoglobin



Kimura (1993)

molecular clock in hominoids as revealed by DNA hybridiation



Sibley & Ahlquist (1987)

Is there a universal molecular clock?

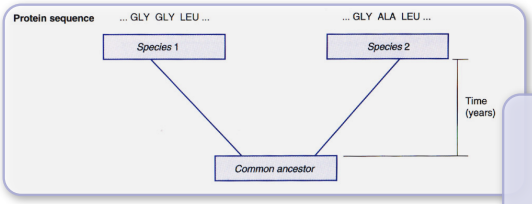
Gene	Rate of amino acid evolution	Rate of nucleotide evolution
Albumin	0.92	6.08
α-globin	0.56	4.92
β-globin	0.78	3.36
Immunoglobin V	1.1	5.87
Parathyroid hormone	1.0	4.57
Relaxin	2.59	8.98
Ribosomal S14	0.02	2.18
average (45 genes)	0.74	4.25

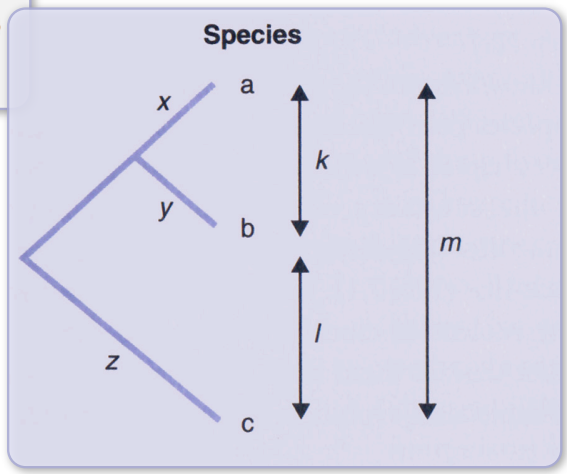
no!

in changes per 10^9 years for an average site

Li (1997), Ridley (2004)

Relative rate test: rate constancy in a molecule in two independent lineages?

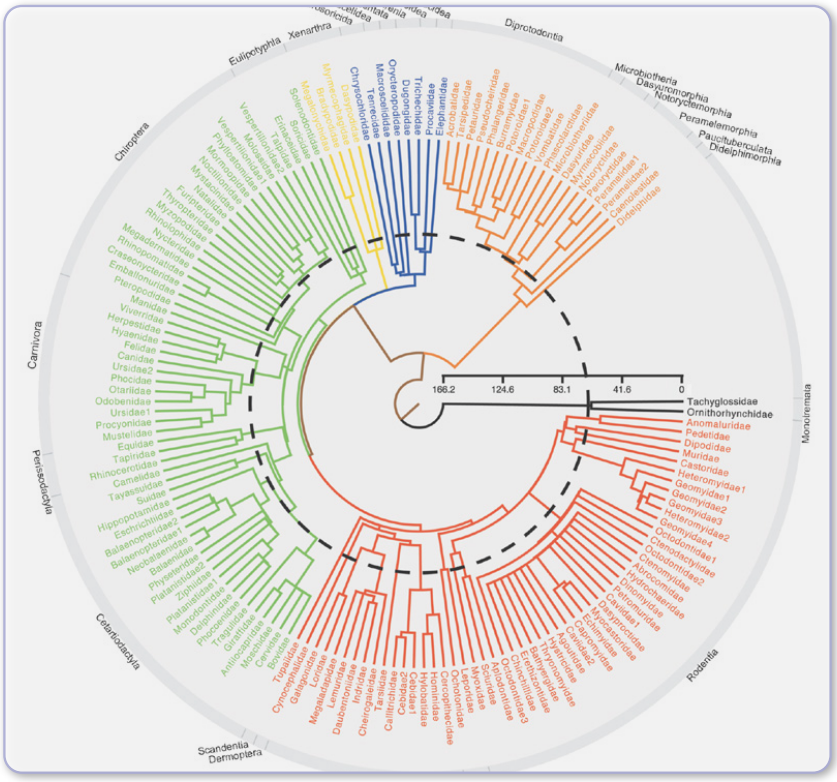




k=x+y
l=y+z
m=x+z

Sarich and Wilson (1977)

mammalian radiation and K/T boundary



Bininda-Emonds et al. (2007)