

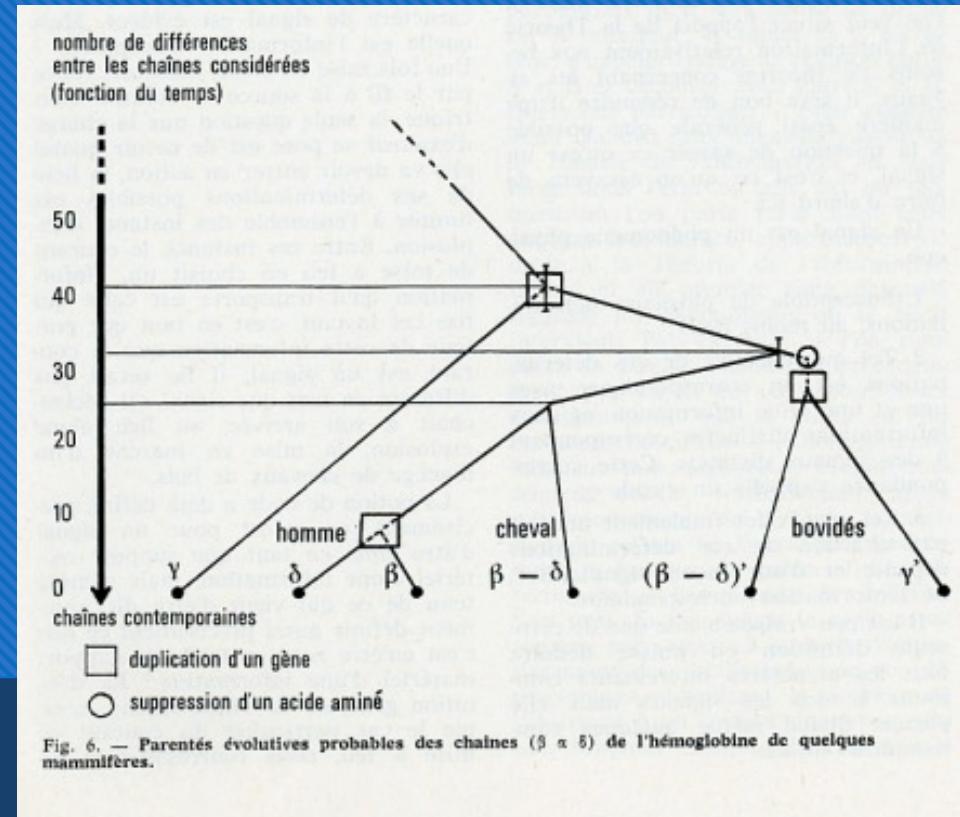
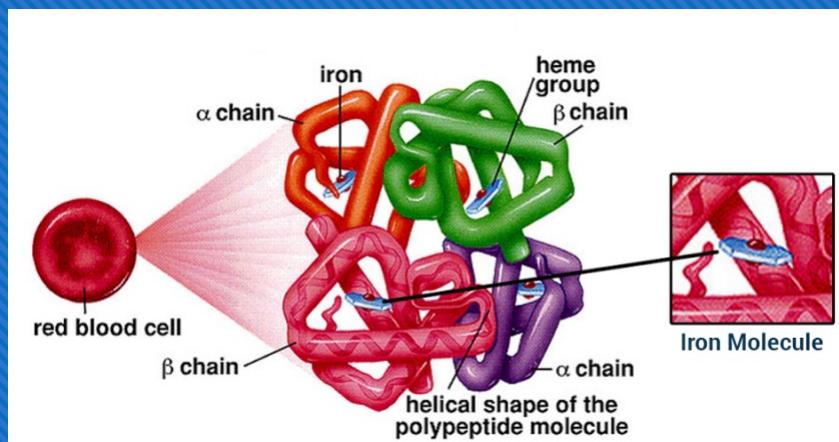


UH Systematics fall 2023: Molecular clocks



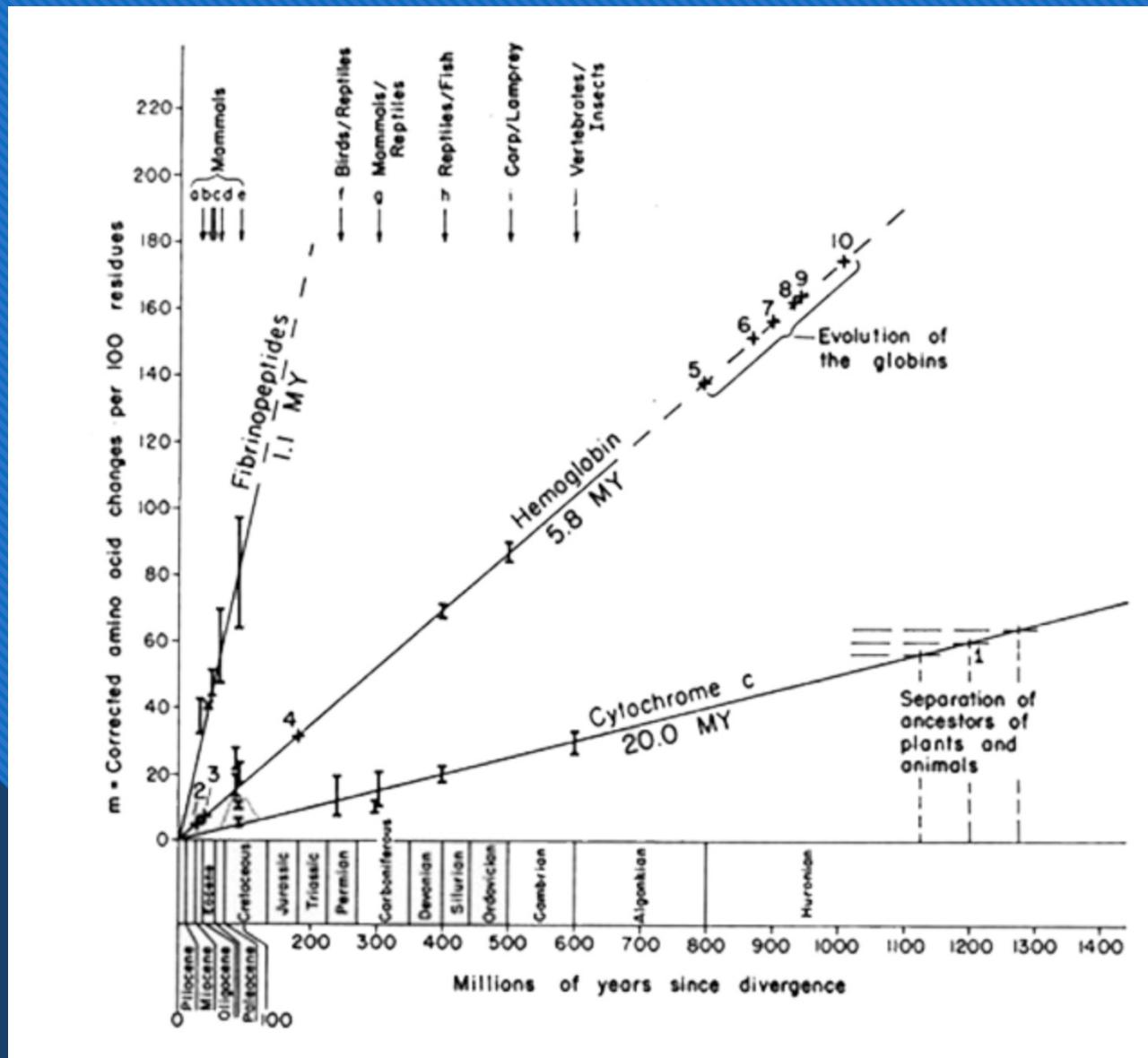
Camiel Doorenweerd
20231009

1965 Zuckerkandl & Pauling “Molecules as documents of Evolutionary history”

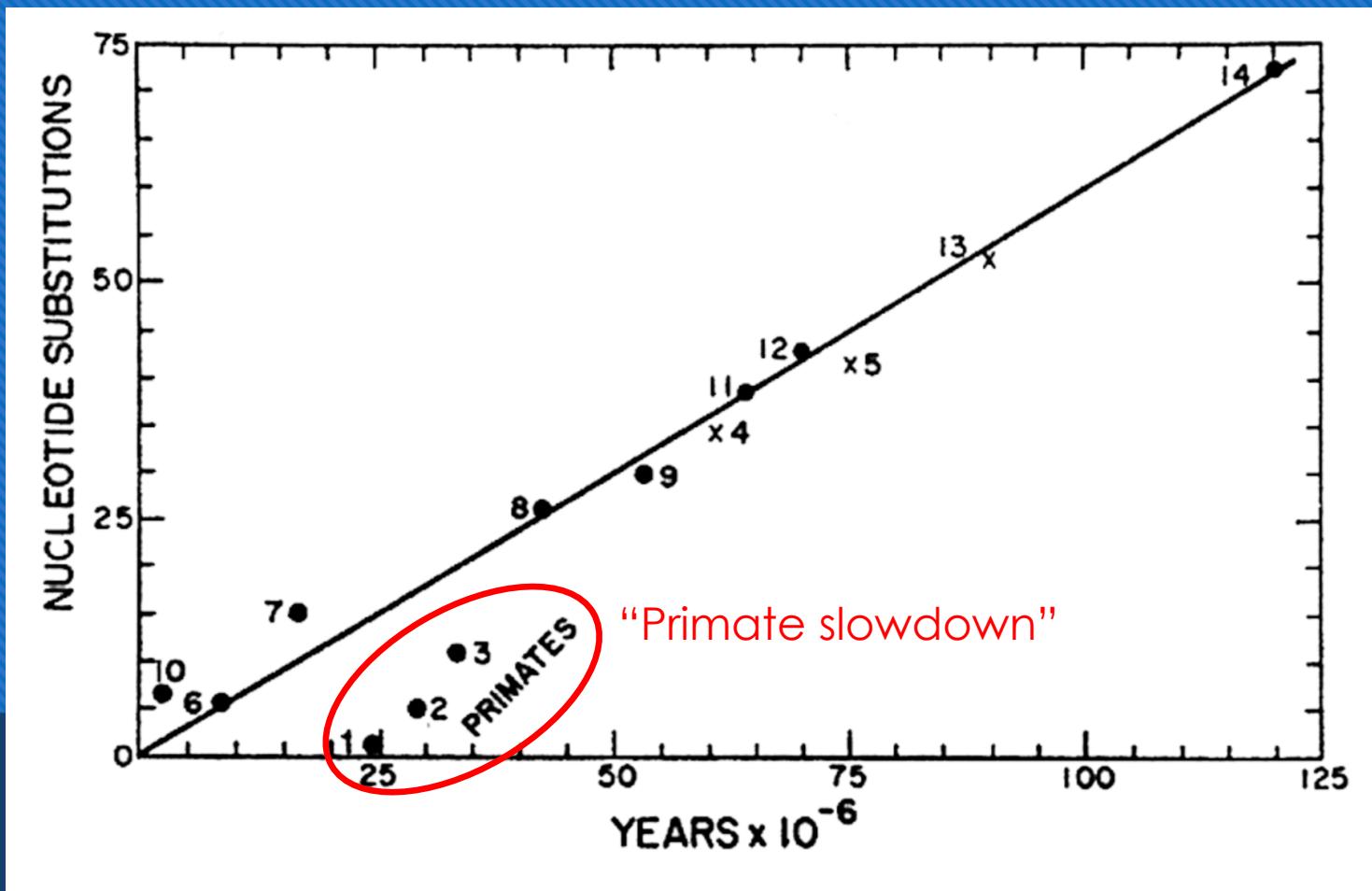


Substitutions accumulate as a function of time

Dickerson 1971: a linear representation

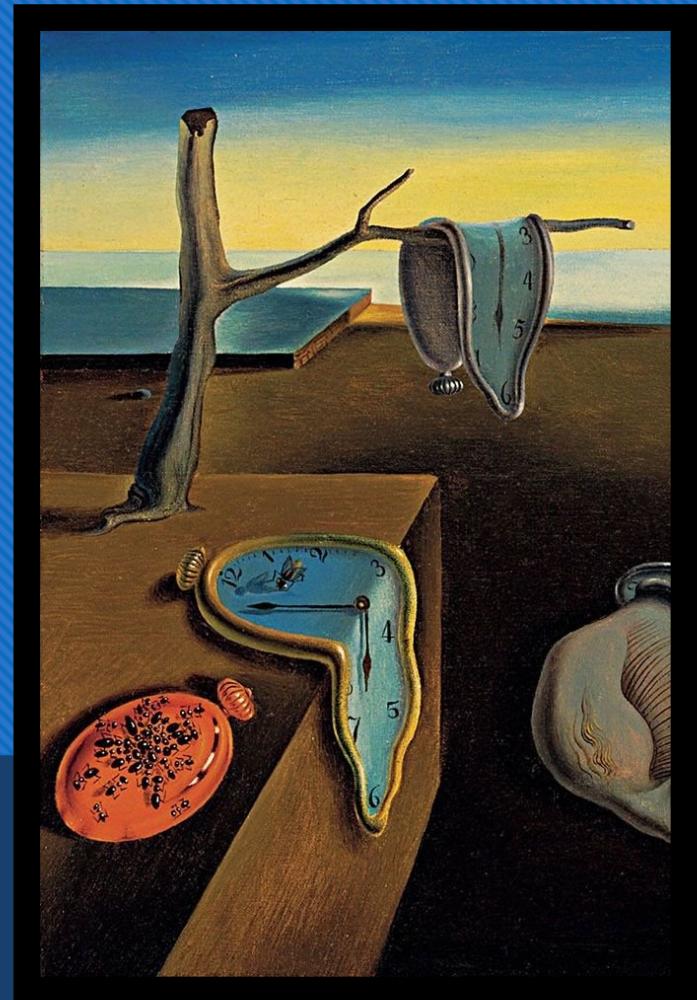


Langley and Fitch 1974



Strict clocks and relaxed clocks

- **Strict molecular clock model:** constant substitution rate across all branches
- **Uncorrelated relaxed clock model:** branch substitution rate is drawn independently from a common underlying distribution
- **Correlated (or autocorrelated) relaxed clock:** branch substitution rates depend on the rate of neighboring branches



Ultrametric trees

Example with tip dating: virus genomes on
nextstrain.org

Nextstrain: real-time tracking of pathogen evolution

James Hadfield , Colin Megill, Sidney M Bell, John Huddleston, Barney Potter, Charlton Callender, Pavel Sagulenko, Trevor Bedford, Richard A Neher [Author Notes](#)

Bioinformatics, Volume 34, Issue 23, 01 December 2018, Pages 4121–4123,

<https://doi.org/10.1093/bioinformatics/bty407>

Published: 22 May 2018 [Article history ▾](#)

Not every dated tree has to be ultrametric

Substitution rates versus calibration points



Setting calibration points:

- Crown or stem?
- Strict, normal or log-normal distribution?

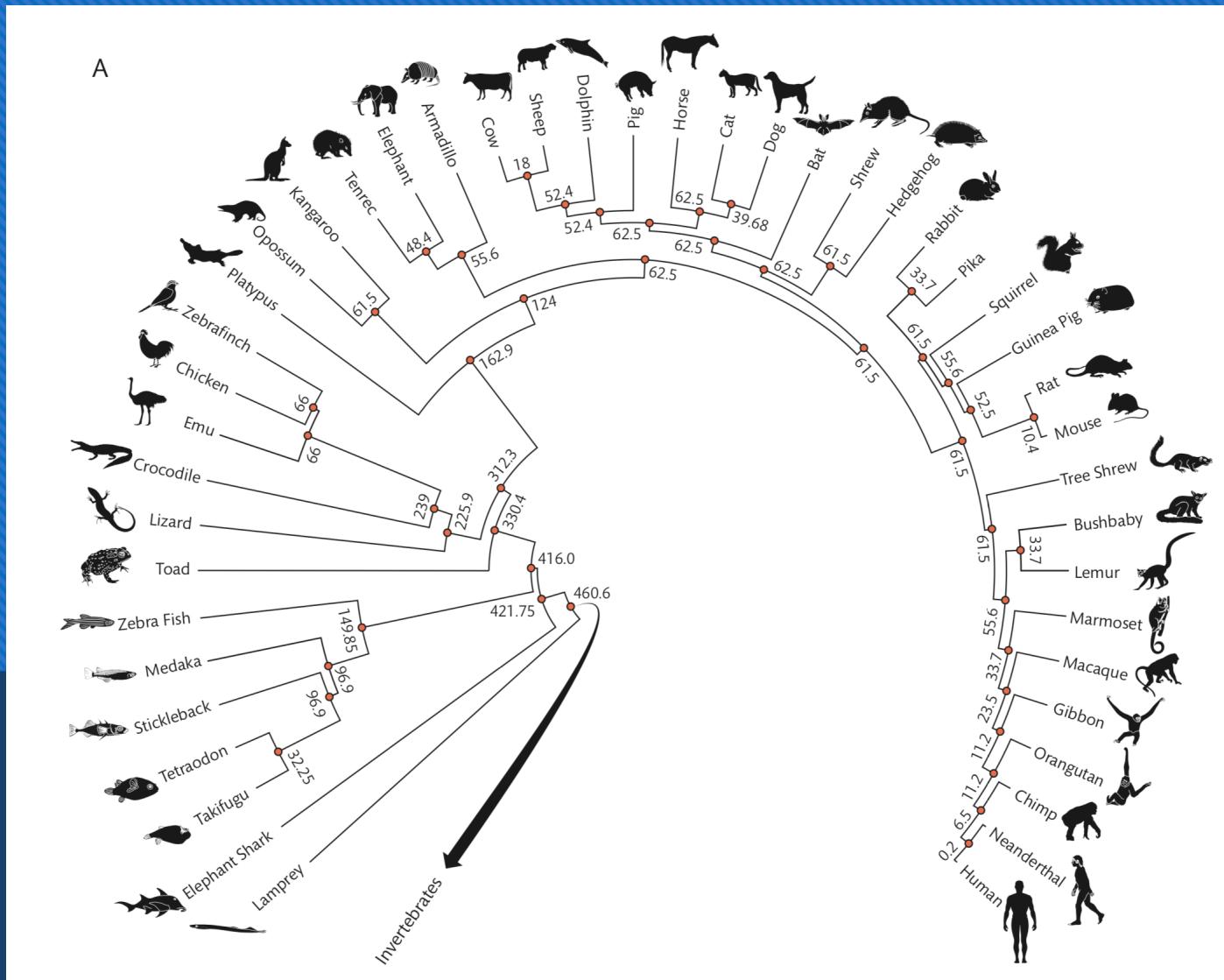


Software driven innovation

- 2021: IQ-Tree [Least-Square Dating] [C++]
- 2018: RevBayes [Bayesian] [R-like language]
- 2017: MCMCTree [likelihood approximation, Bayesian] [C++]
- 2017: BEAST 2 (& Beauti) [Java]
- 2016: TreeTime [python] used for nextstrain.org
- 2016: treedater [R] Gamma-Poisson mixture model
- 2016: Least-Square Dating (LSD) [C++]
- 2015: (beta): PhyTime. [C] Part of PhyML package
- 2003: r8s [C] [Poisson distribution of substitutions]



Timed supertrees: Timetree.org



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