

Molecular Phylogenetics

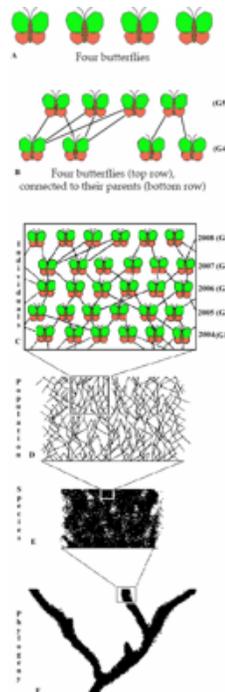
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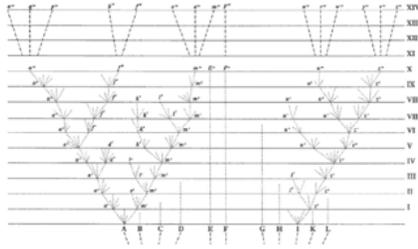
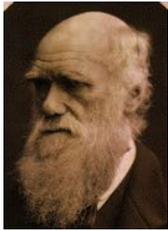
Phylogeny (from *phylum* – tribe, and *genesis* – origin)

- the term introduced by E. Haeckel in the second half of the XIX century and now has two somewhat different meanings.
- (1) Phylogeny in wide sense is a historical development of organisms
- (2) Phylogeny in narrow sense includes not all aspects of historic development, but only succession of branching of a genealogical (i.e. a phylogenetic) tree.
- Usually represented by a phylogenetic tree.

What is a phylogenetic tree?

- A tree is a mathematical structure which is used to model the actual evolutionary history of a group of sequences or organisms.
- The actual pattern of historical relationships is an evolutionary tree which we try to estimate



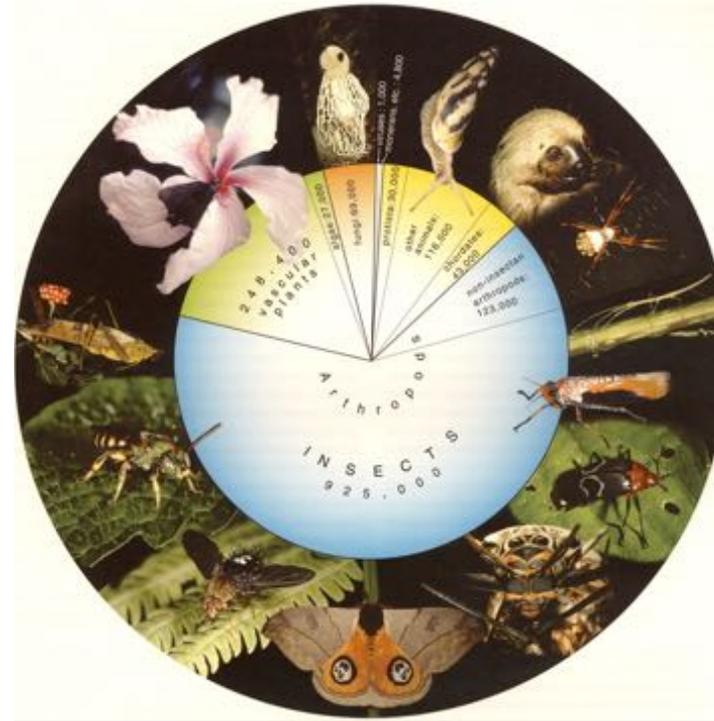


“The time will come I believe, though I shall not live to see it, when we shall have fairly true genealogical (phylogenetic) trees of each great kingdom of nature”

“... there is, after all, one true tree of life [...]. It exists. It is in principle knowable. We don't know it all yet. By 2050 we should –or if we do not, we shall have been defeated only at the terminal twigs, by the sheer number of species.”

Darwin's letter to Thomas Huxley (1857)

Dawkins (2003), *A Devil's Chaplain*

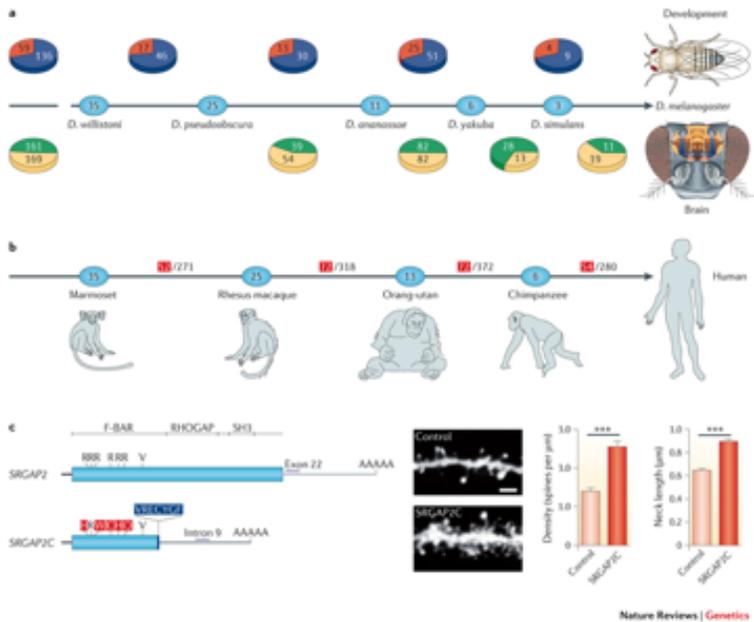


AToL
Assembling the Tree of Life

The AToL initiative (Assembling the Tree of Life) is a large research effort sponsored by the National Science Foundation. Its goal is to reconstruct the evolutionary origins of all living things.

Space, time, form: viewing the Tree of Life

Roderic D.M. Page



a | The phylogeny shows the distributions of new *Drosophila* spp. genes involved in development (above) and in the brain (below) in various evolutionary stages within the past 36 million years.

Why molecular phylogenetics?



- 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. **George G. Simpson, 1945**

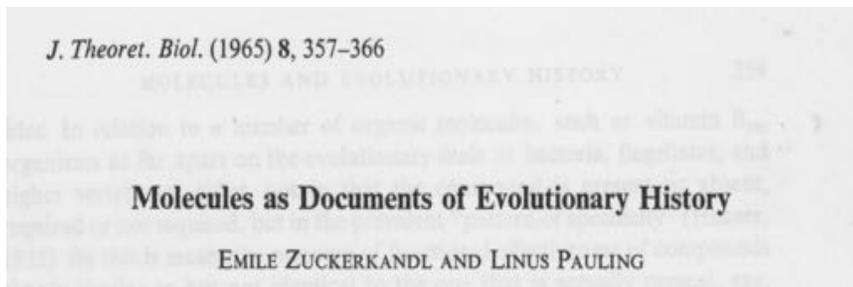
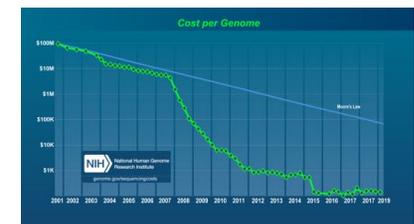
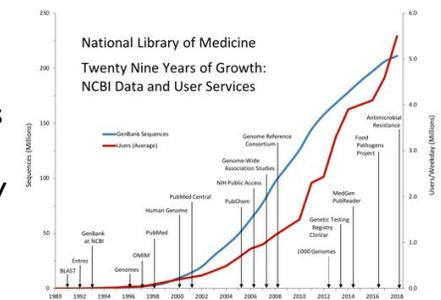


- “I do not fully understand why we are not proclaiming the message from the housetops ... We finally have a method that can sort homology from analogy.” **Stephen J. Gould, 1985**



Molecules as documents of evolutionary history

- “We may ask the question where in the now living systems the greatest amount of information of their past history has survived and how it can be extracted”
- “Best fit are the different types of macromolecules (sequences) which carry the genetic information”

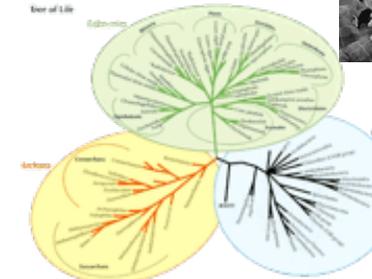


Applications of Phylogenetic Analysis

- Systematics and classification
- Discovering new life forms
- Phylogeography and speciation
- Molecular evolution
- Genomics
- Epidemiology and forensics
- Biotechnology
- Agriculture
- Conservation



Discovering new life forms



Proc. Natl. Acad. Sci. USA
Vol. 74, No. 11, pp. 3088-3090, November 1977
Evolution

Phylogenetic structure of the prokaryotic domain: The primary kingdoms

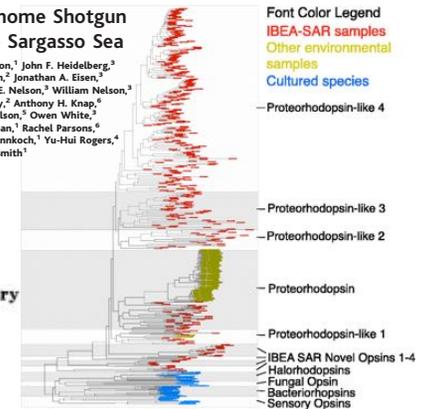
(archaebacteria/eubacteria/arkaryote/16S ribosomal RNA/molecular phylogeny)

CARL R. WOESE AND GEORGE E. FOX*

Department of Genetics and Development, University of Illinois, Urbana, Illinois 61801

Environmental Genome Shotgun Sequencing of the Sargasso Sea

J. Craig Venter,^{1*} Karin Remington,¹ John F. Heidelberg,² Aaron L. Halpern,² Doug Rusch,² Jonathan A. Eisen,² Dongying Wu,² Ian Paulsen,² Karen E. Nelson,² William Nelson,² Derrick E. Fouts,² Samuel Levy,² Anthony H. Knap,² Michael W. Lomas,² Ken Nealson,² Owen White,² Jeremy Peterson,² Jeff Hoffman,¹ Rachel Parsons,⁴ Holly Baden-Tillson,¹ Cynthia Pfannkoch,¹ Yu-Hui Rogers,⁴ Hamilton O. Smith¹



Disease Transmission and Medical Forensics

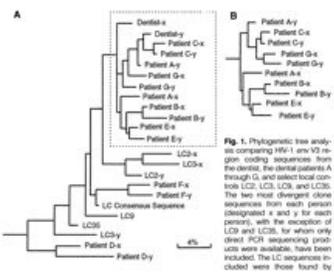
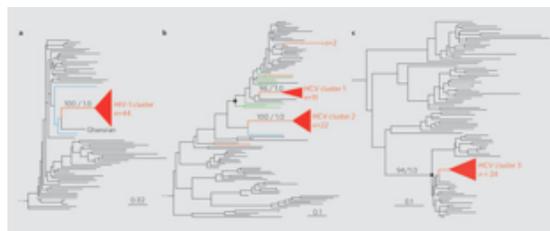


Fig. 1. Phylogenetic tree analysis comparing HIV-1 and HCV nucleotide coding sequences from the dental patients A through G, and select local controls LC2, LC3, LC4, and LC5. The two most divergent clone sequences from each person (designated x and y for each person), with the exception of LC3 and LC5, for whom only direct PCR sequencing products were available, have been included. The LC sequences included were those found by



Brief Communications

Nature 444, 838-837 (14 December 2006) | doi:10.1038/444838a | Received 4 November 2006; Accepted 24 November 2006; Published online 6 December 2006

Molecular Epidemiology: HIV-1 and HCV sequences from Libyan outbreak

Tullo de Oliveira¹, Oliver G. Pybus¹, Andrew Rambaut¹, Marco Salemi¹, Sharon Casso¹, Massimo Ciccozzi², Giovanni Rezza³, Guido Castelli Gattinara⁴, Roberta D'Arrigo⁵, Massimo Amicoant⁶, Luc Perrin⁷, Vittorio Colizzi⁸, Carlo Federico Perno⁹ and Benghazi Study Group¹⁰

In 1998, outbreaks of human immunodeficiency virus type 1 (HIV-1) and hepatitis C virus (HCV) infection were reported in children attending Al-Fateh Hospital in Benghazi, Libya. Here we use molecular phylogenetic techniques to analyse new virus sequences from these outbreaks. We find that the HIV-1 and HCV strains were already circulating and prevalent in this hospital and its environs before the arrival in March 1998 of the foreign medical staff (five Bulgarian nurses and a Palestinian doctor) who stand accused of transmitting the HIV strain to the children.

Molecular Epidemiology of HIV Transmission in a Dental Practice

Chin-Yih Ou, Carol A. Ciesielski, Gerald Myers, Claudia I. Bandea, Chi-Cheng Luo, Bettie T. M. Korber, James I. Mullins, Gerald Schochetman, Ruth L. Berkelman, A. Nikki Economou, John J. Witte, Lawrence J. Furman, Glen A. Satten, Kersti A. MacIntyre, James W. Curran, Harold W. Jaffe, Laboratory Investigation Group,* Epidemiologic Investigation Group†

Ou et al. 1992

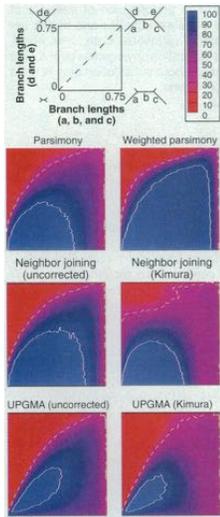
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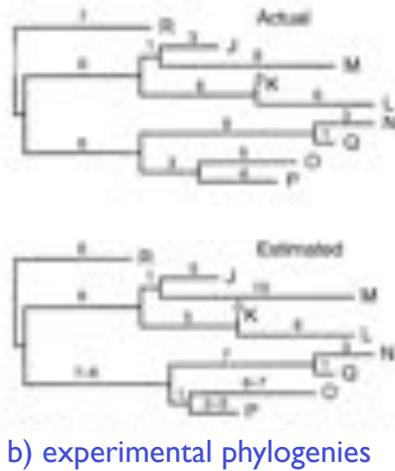
“Simple identification via phylogenetic classification of organisms has, to date, yielded more patent filings than any other use of phylogeny in industry.”
Bader et al. (2001)



How do we know that phylogenetics work?



a) simulations



b) experimental phylogenies

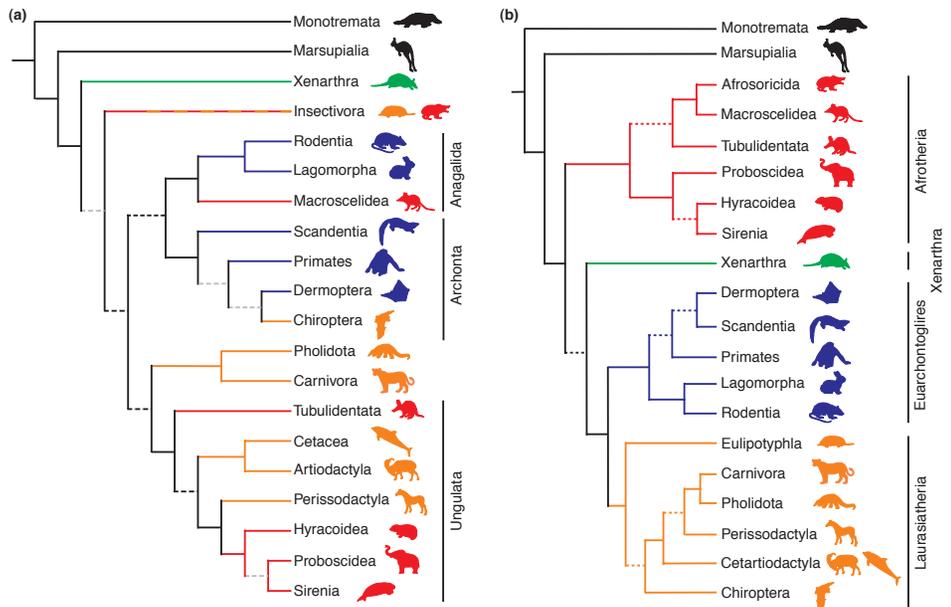
ARTICLE
Application and Accuracy of Molecular Phylogenies
 David M. Hillis, John P. Huelsenbeck, Clifford W. Cunningham

Niche	Placental Mammals	Australian Marsupials
Burrower	Mole	Marsupial mole
Anteater	Anteater	Numbat (anteater)
Mouse	Mouse	Marsupial mouse
Glider	Flying squirrel	Spotted quoll
Cat	Bibaco	Tasmanian "tiger cat"
Wall	Wall	Tasmanian wall

Convergence is widespread!



Springer et al. 2004



TRENDS in Ecology & Evolution
 Springer et al. 2004

Type filter query here...

Genomic epidemiology of novel coronavirus - Global subsampling

Maintained by the Nextstrain team. Enabled by data from GISAID

Showing 3899 of 3899 genomes sampled between Dec 2019 and Jan 2021.

Tree Options

Layout: RECTANGULAR, RADIAL, UNROOTED, CLOCK

Branch Length: TIME, DIVERGENCE

Branch Labels: none

Tip Labels: Sample Name

Second Tree: Select...

Frequency Options: Normalize frequencies

Animation Options

Nextstrain

Real-time tracking of pathogen evolution

Nextstrain is an open-source project to harness the scientific and public health potential of pathogen genome data. We provide a continually updated view of publicly available data alongside powerful analytic and visualization tools for use by the community. Our goal is to aid epidemiological understanding and improve outbreak response. If you have any questions, or simply want to say hi, please give us a shout at hello@nextstrain.org.

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