Pipeline

Raw reads (fastq)

BMGE

Genome/ transcriptome assembly

DNA alignments

DNA sequences of new species

BLAST

New dataset

MAFFT

BMGE

Dataset assembly

Filtered gene alignments

Concatenated supermatrix

Phylogenetic analysis

IQTREE

MRBAYES

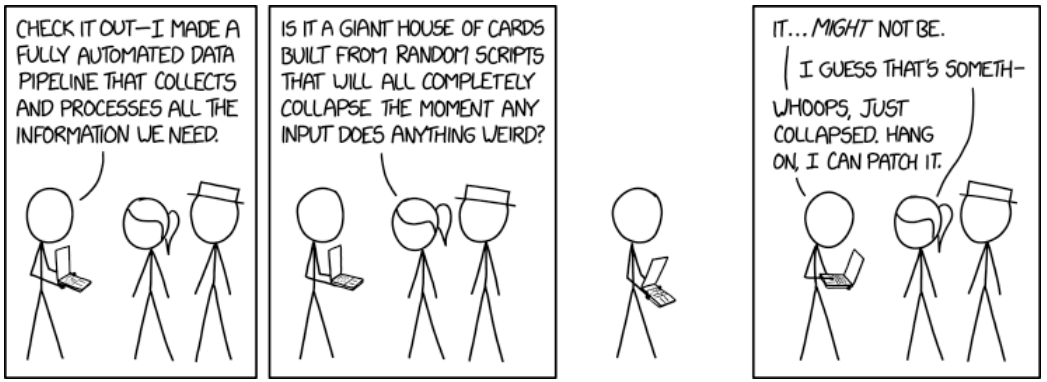
ML tree

Bayesian tree

Tracer

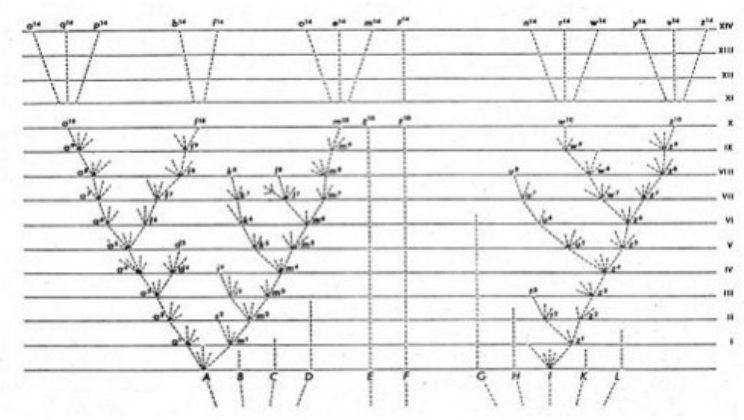
Convergence analysis

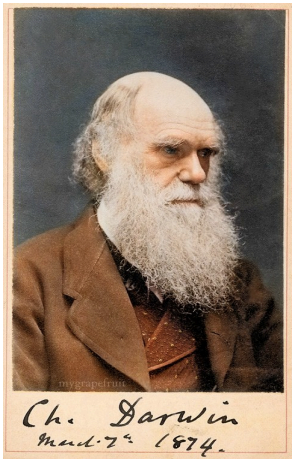
FigTree, iTOL



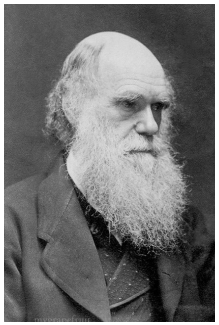
"I am fully convinced that species are not immutable; but that those belonging to what are called the same genera are lineal descendants of some other and generally extinct species, in the same manner as the acknowledged varieties of any one species are the descendants of that species. Furthermore, I am convinced that natural selection has been the most important, but not the exclusive, means of modification."

— Charles Darwin,
On the Origin of Species 1859

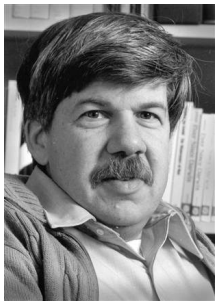




- Ancestor-descent relationships imply we can use trees to express evolutionary relationships



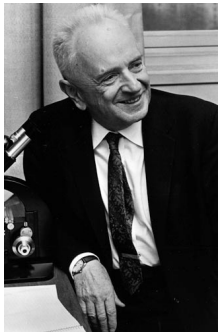
- Evolution is an historical science (contingency)



- Evolution is a population process

"Nothing in biology makes sense, except in the light of evolution. Without that light it becomes a pile of sundry facts - some of them interesting or curious but making no meaningful picture as a whole"

– Theodosius Dobzhansky



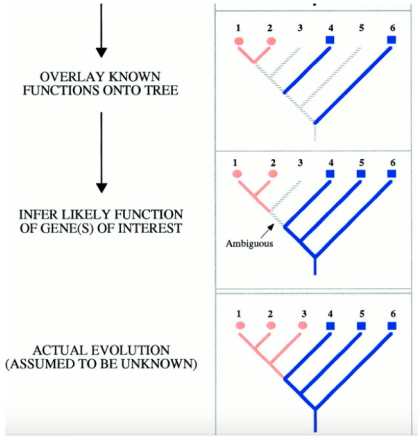
Definitions

Phylogenomics: Improving Functional Predictions for Uncharacterized Genes by Evolutionary Analysis

Jonathan A. Eisen[1]

Department of Biological Sciences, Stanford University, Stanford, California 94305-5020 USA

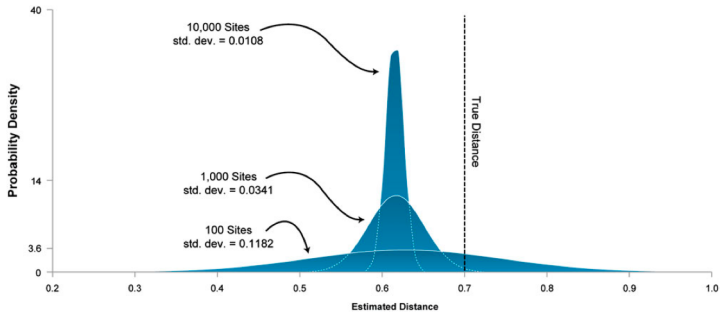
Eisen 1998 Genome Res



Phylogenomics

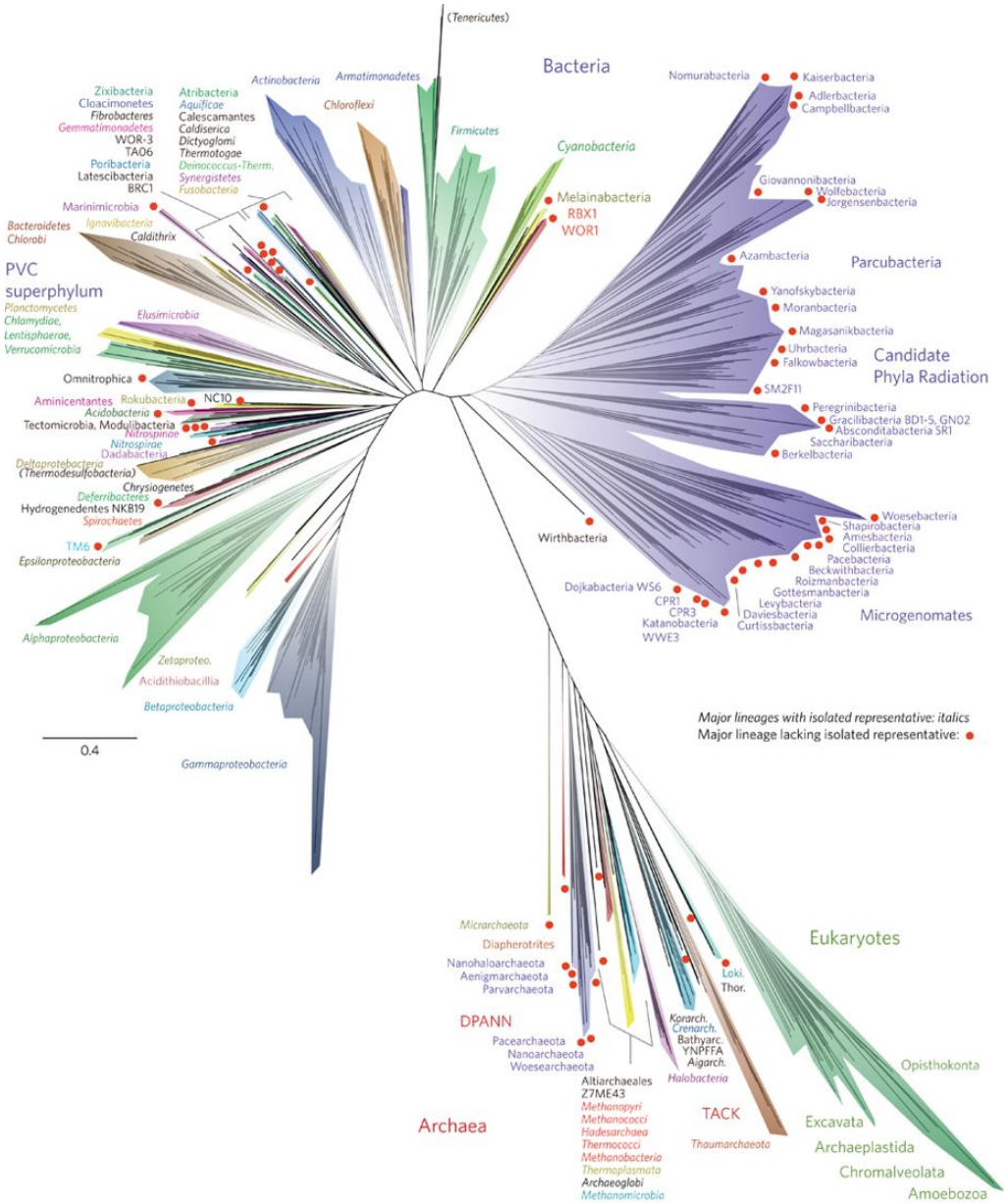
From Wikipedia, the free encyclopedia

Phylogenomics is the intersection of the fields of evolution and genomics.[1] The term has been used in multiple ways to refer to analysis that involves genome data and evolutionary reconstructions. It is a group of techniques within the larger fields of phylogenetics and genomics. Phylogenomics draws information by comparing entire genomes, or at least large portions of genomes.[2] Phylogenetics compares and analyzes the sequences of single genes, or a small number of genes, as well as many other types of data.



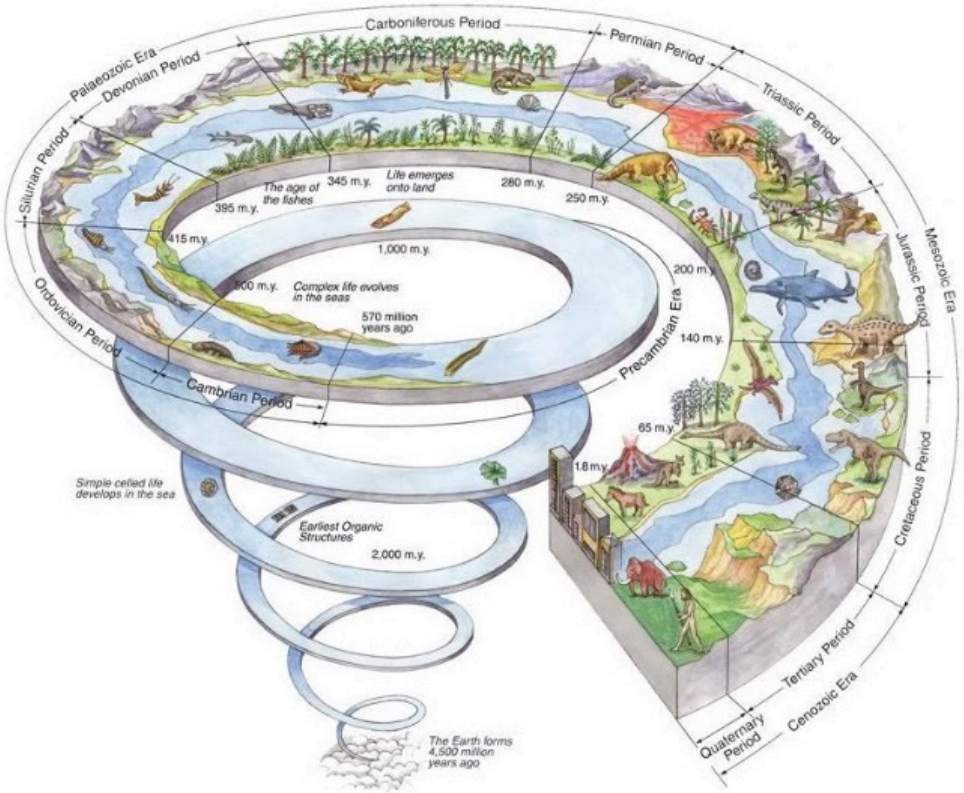
Kumar et al. 2012 Mol Biol Evol

Tree of Life



Hug et al. 2016 Nat Microbiol

Phylogenomics: “molecular archaeology”



Understand evolution of traits: morphology, behaviour, etc.

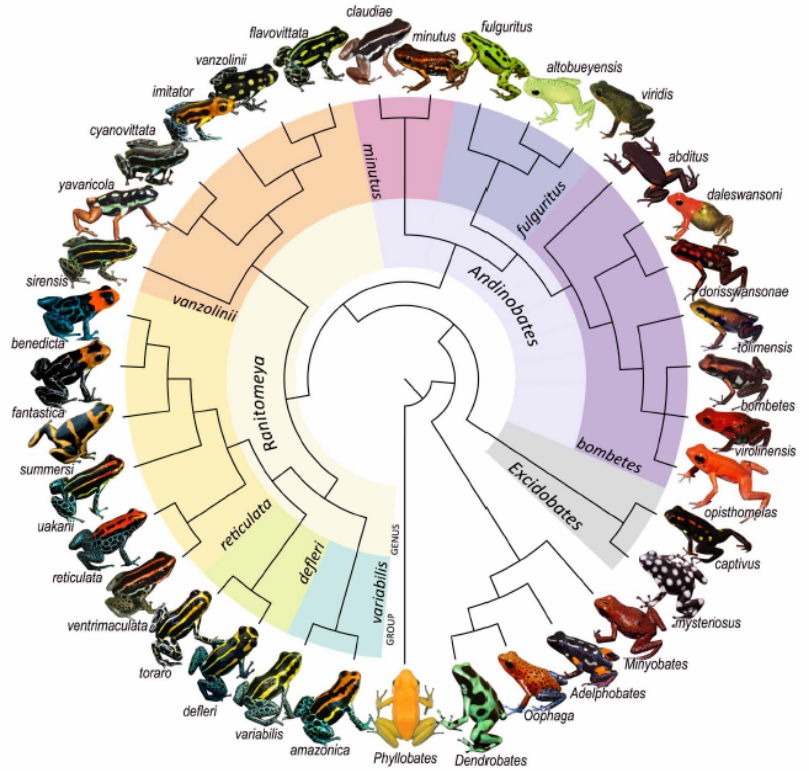
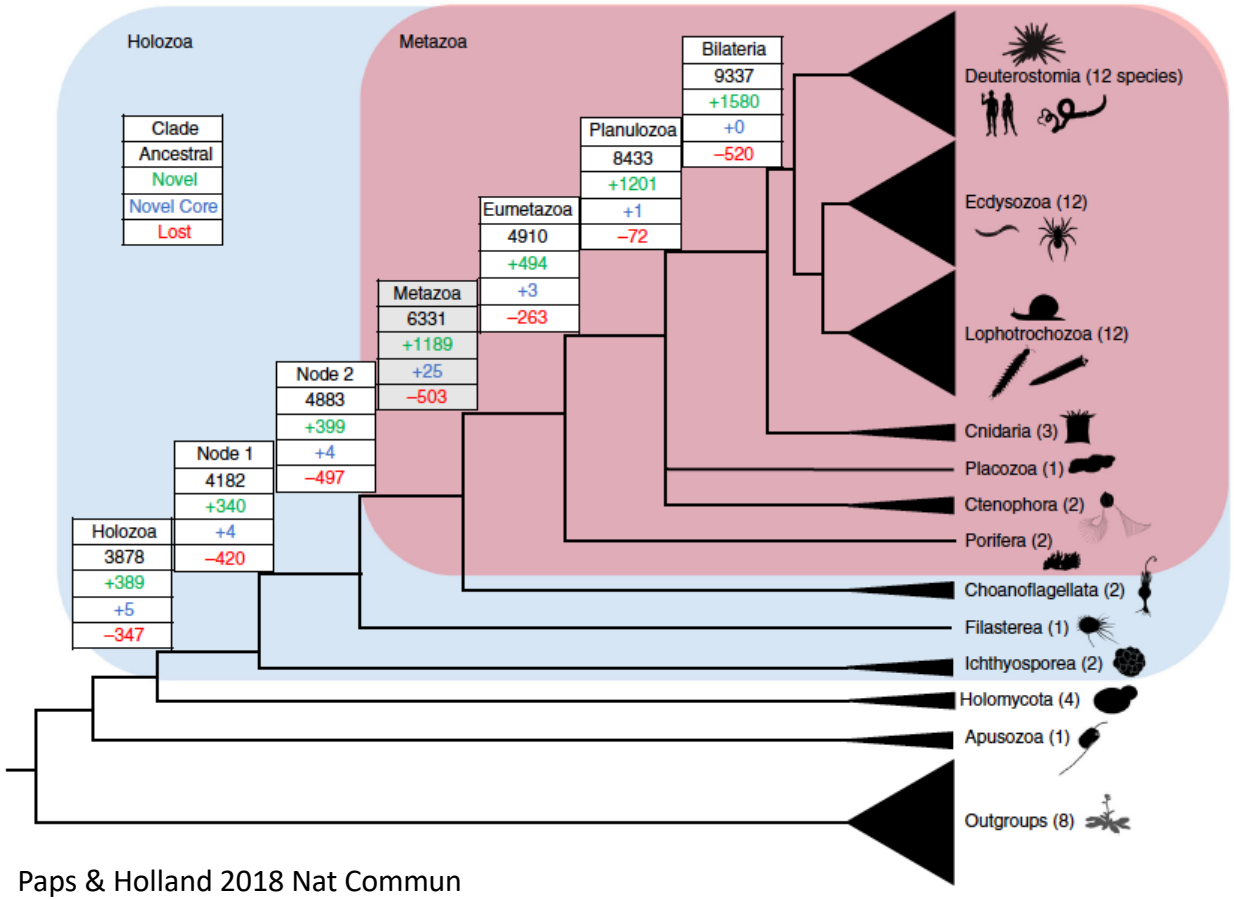


Figure 1. Mimetic forms of *Ranitomeya imitator* and its Müllerian co-mimics.
Top row, the mimic *Ranitomeya imitator*: left, "Varadero" blotched morph; right, striped morph. Bottom row, the models: left, the aptly named *R. fantastica*; right, *R. variabilis*. Photos courtesy of Evan Twomey.

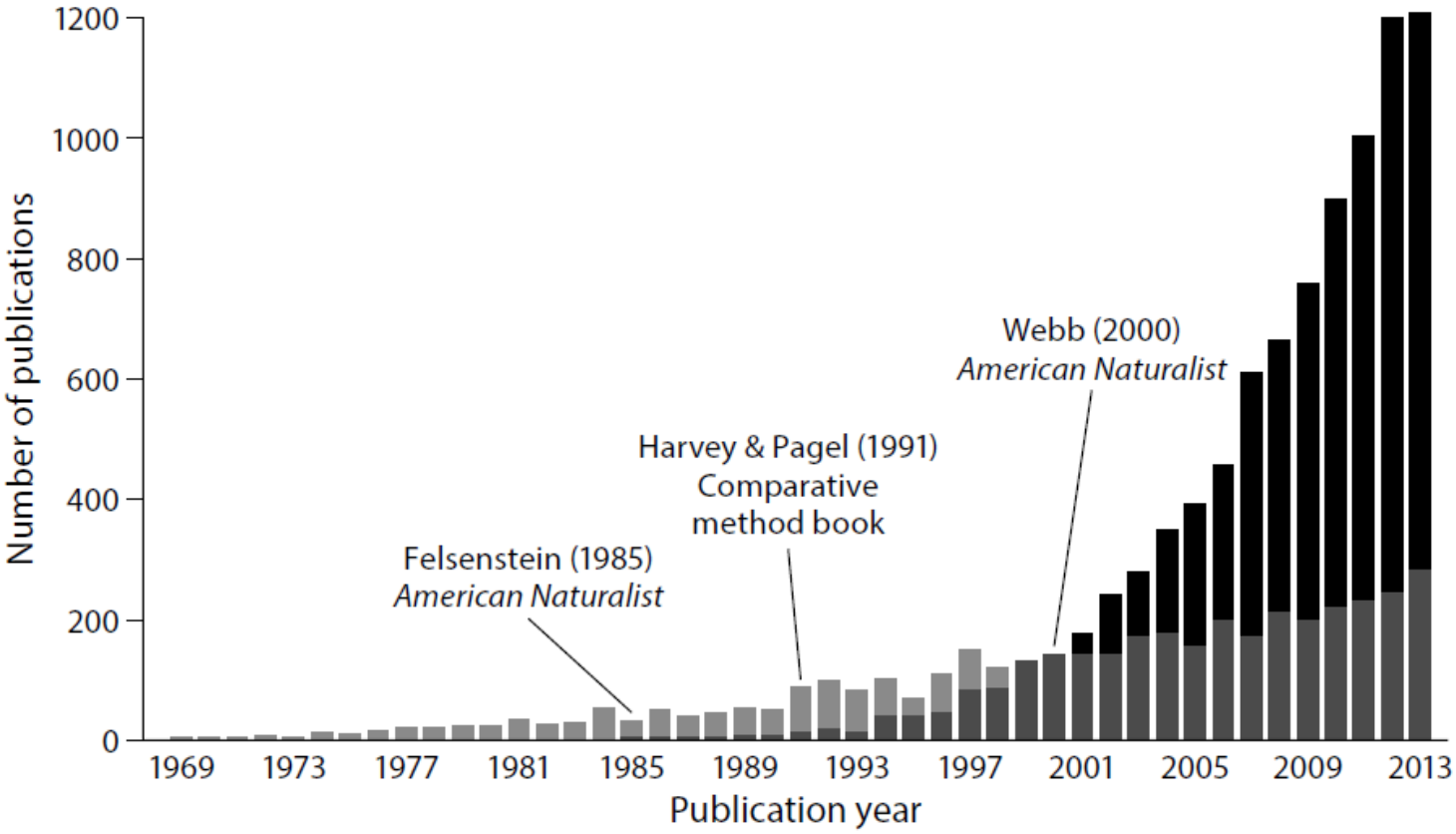
Mallet 2014 Curr Biol
Brown et al. 2011 Zootaxa

Evolution of genomes and gene families



Paps & Holland 2018 Nat Commun

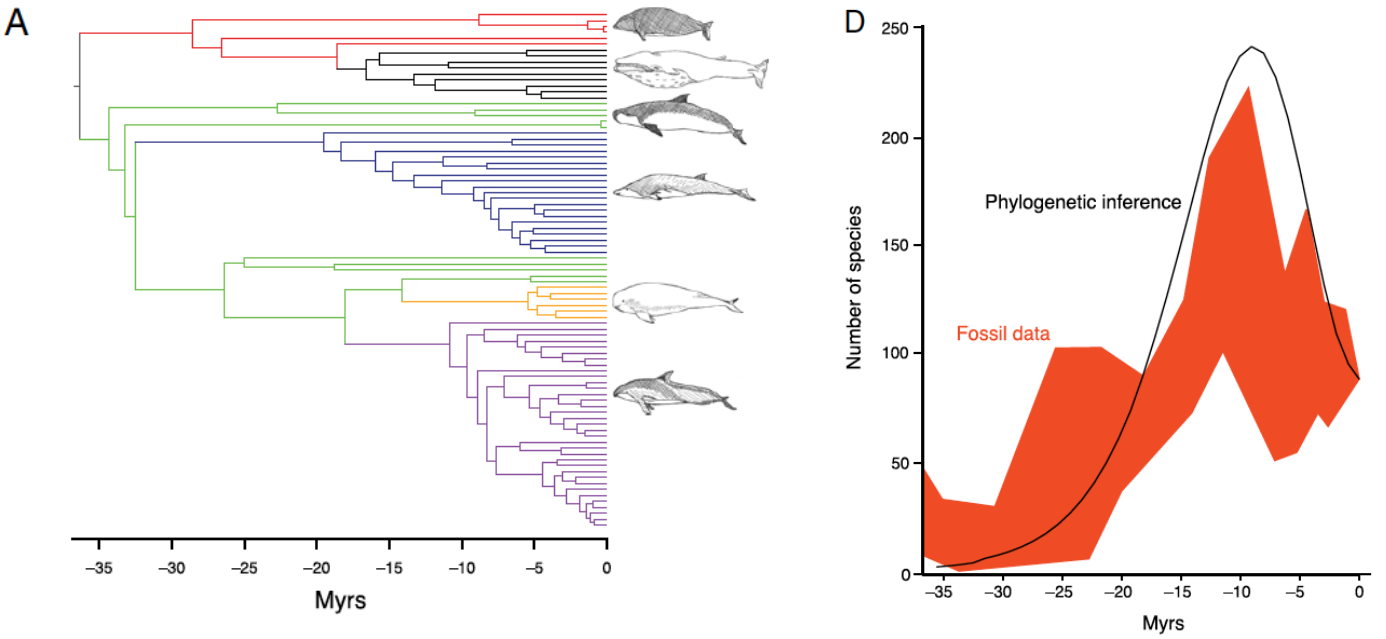
Testing hypothesis in Ecology with phylogenies



Cadotte & Davies (2016) Phylogenies in ecology

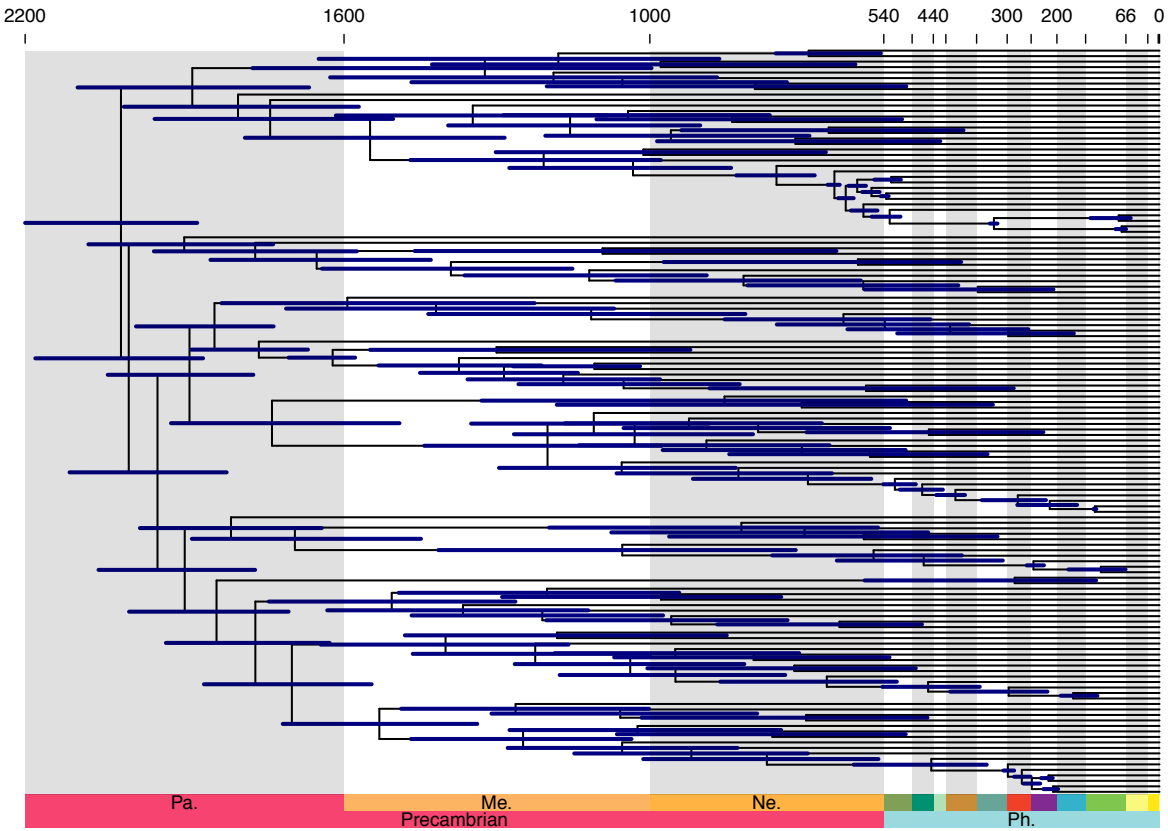
C. Bleidorn

Testing hypothesis: Macroevolution



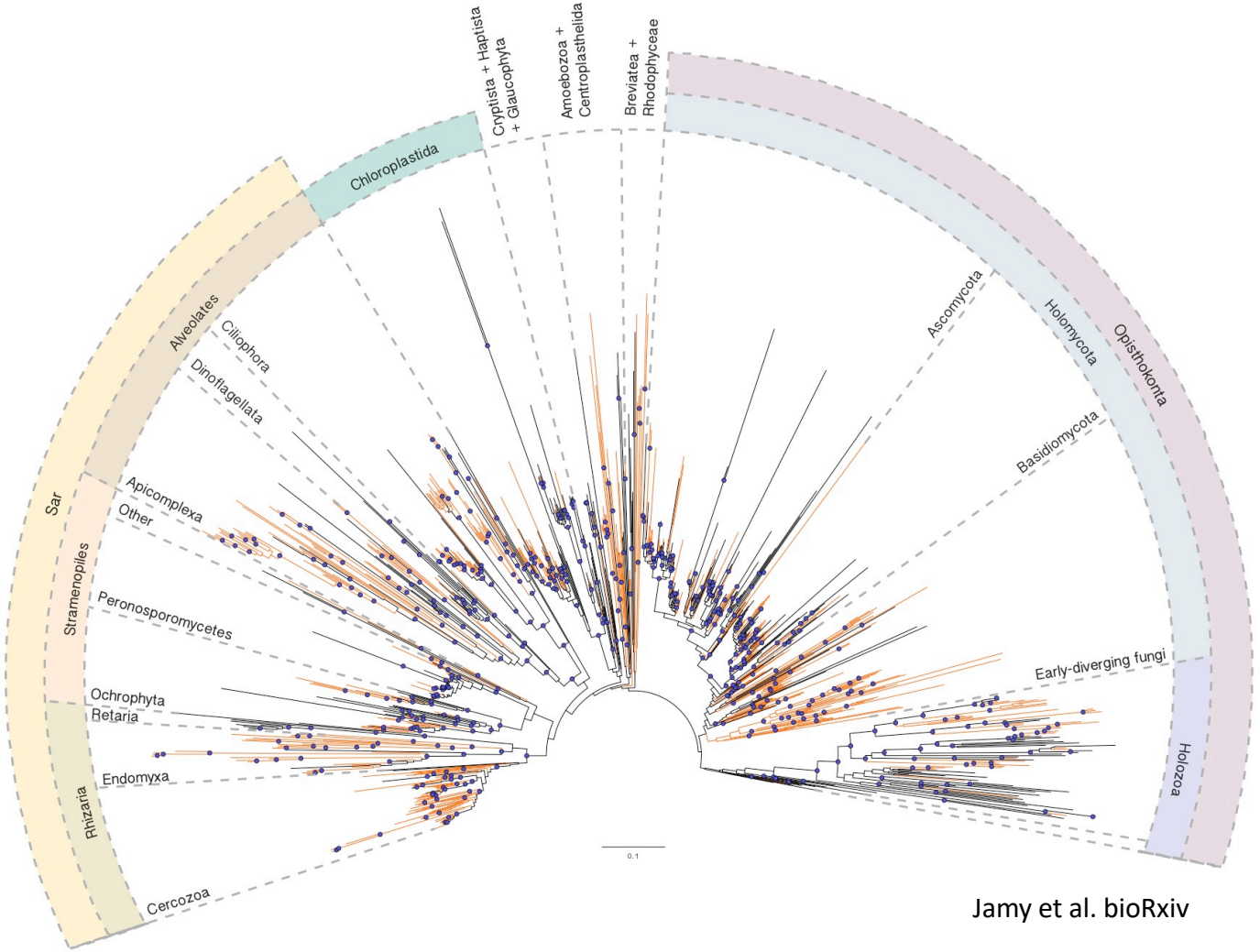
Morlon et al. 2011 PNAS

Molecular clock



Strassert et al.

Classification, metagenomics



Jamy et al. bioRxiv