

Challenges in constructing very large evolutionary trees

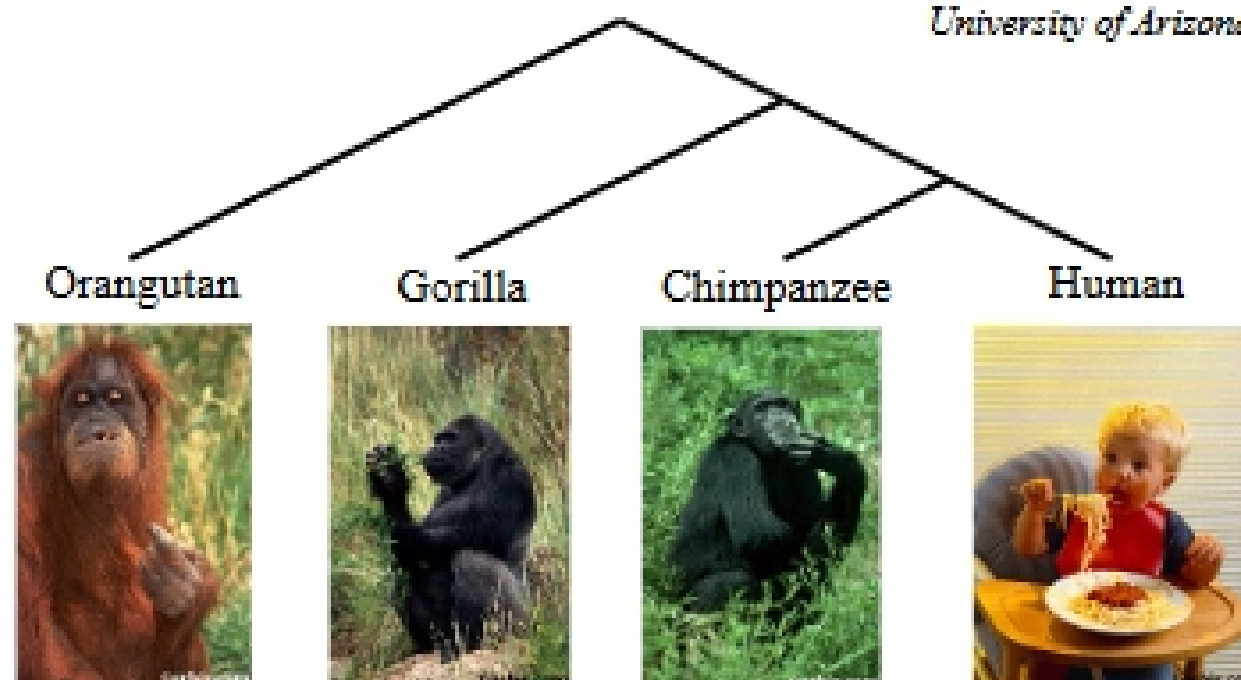
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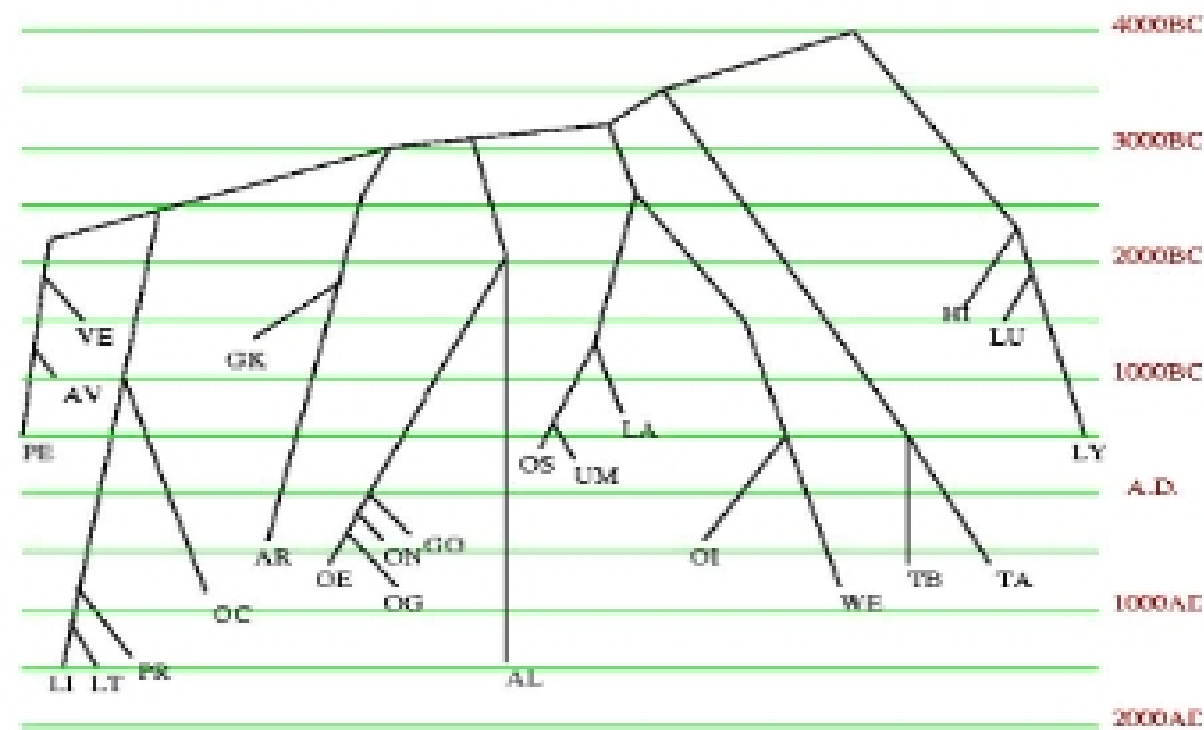
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Phylogeny

*From the Tree of the Life Website,
University of Arizona*



Ringe-Warnow Phylogenetic Tree of Indo-European



Major methods for phylogeny reconstruction

- Biology: Polynomial time methods (good enough for small datasets), and local search heuristics for NP-hard optimization problems
- Linguistics: exact algorithms for NP-hard optimization problems

Evolution informs about everything in biology

- Big genome sequencing projects just produce data -- so what?
- Evolutionary history relates all organisms and genes, and helps us understand and predict
 - interactions between genes (genetic networks)
 - drug design
 - predicting functions of genes
 - influenza vaccine development
 - origins and spread of disease
 - origins and migrations of humans

Main research foci

- Solving maximum parsimony and maximum likelihood more effectively
- “Fast converging methods”
- Gene order and content phylogeny
- Reticulate evolution
- Phylogenetic multiple sequence alignment