

TECHNIQUES

Distance
Parsimony
Maximum Likelihood
Bayesian Inference

DISTANCE

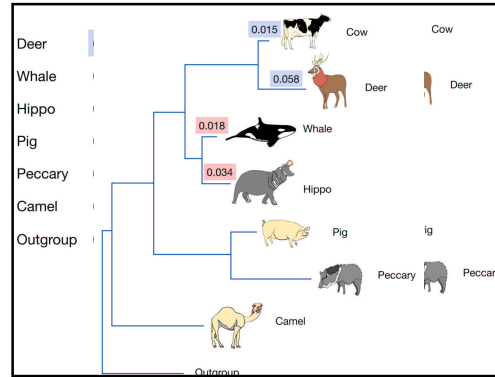
Sokal, R. R. & P. H. A. Sneath. 1963.
Principles of Numerical Taxonomy.
Freeman, San Francisco.

e.g., UPGMA

“if it looks like a duck, then it is a duck”

UPGMA ALGORITHM

construct distance matrix
 find i, j such that d_{ij} is a minimum
 define branching depth $l_{ij} = d_{ij} / 2$
 if i and j comprise final 2 clusters, then end
 otherwise, create new cluster u
 define $d_{uk} = (T_i d_{ki} + T_j d_{kj}) / 2$
 repeat previous 5 steps



PARSIMONY

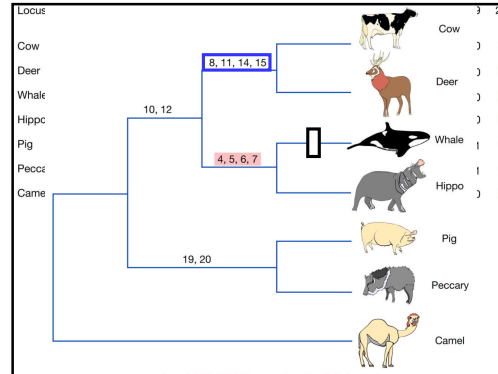
Hennig, W. 1966. *Phylogenetic Systematics*.
 University of Illinois Press, Urbana .

e.g., cladistics

“if it looks and quacks like a duck, then it is a duck”

CLADISTIC ALGORITHM

- construct taxon-character state matrix
- identify 'apomorphic' character states
- consider 'synapomorphic' character states
- create clades
- consider 'homoplasous' character states
- consider 'autapomorphic' character states



MAXIMUM LIKELIHOOD

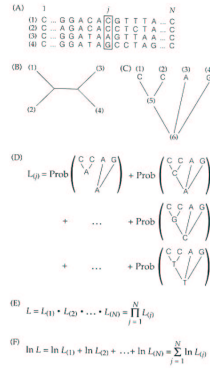
Cavalli-Sforza, L. L. and A. W. F. Edwards.
1967. Phylogenetic analysis: models
and estimation procedures. *Evolution*
32:550-570.

e.g., $P(\text{data} \mid \text{hypothesis})$

“if its sequence resembles that in a duck,
then it most-likely is a duck”

ML ALGORITHM

construct aligned-sequence matrix
 define $P(d | c)$ for a particular c
 if time reversible, then can use rooted c
 calculate $L_{(j)}$ by considering possibilities
 calculate L by taking product over $L_{(j)}$
 use Log-L for convenience



BAYESIAN INFERENCE

Larget, B. and D. L. Simon. 1999. Markov chain Monte Carlo algorithms for the Bayesian analysis of phylogenetic trees. *Molecular Biology and Evolution* 16:750-759.

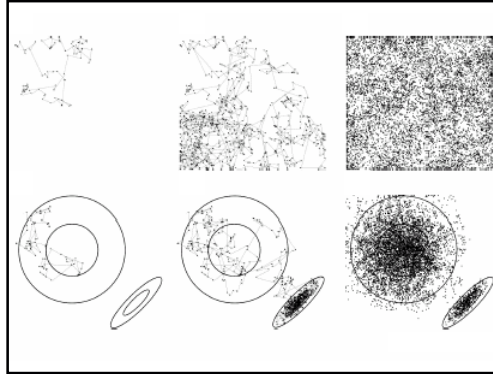
e.g., Bayesian inference

“if it looks like a duck, then it probably is a duck”

MCMC ALGORITHM

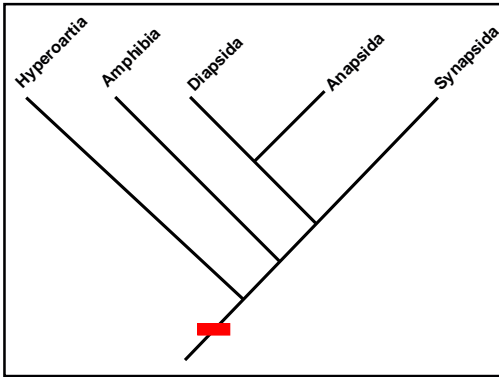
$$P(H | d) = P(d | H) P(H) / P(d)$$

consider a cladogram T_i
consider a neighbour cladogram T_j
calculate likelihood ratio for T_i, T_j
define $R = P(T_j|d) / P(T_i|d)$
if $R > 1$, accept new cladogram
if $R < 1$, select number r between 0 and 1
if $r < R$, accept new cladogram
otherwise, reject new cladogram
return to second step

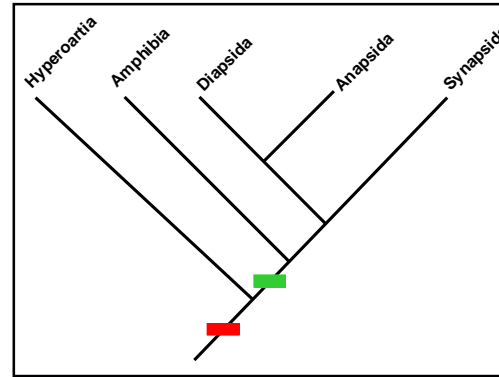


CLADISTICS

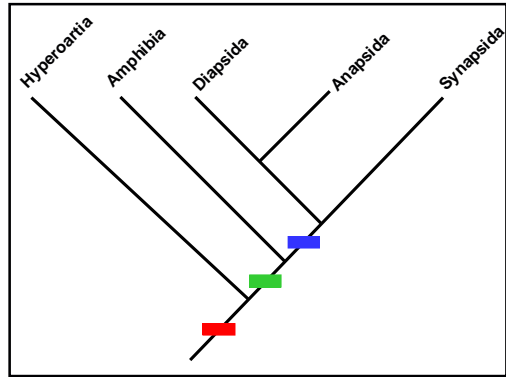
Urochordata	CGTACGTAC
Cephalochordata	CGTACGTAC
Hyperoartia	AGTAAGTAC
Amphibia	ACTACCTAC
Diapsida	ACGTCGGAC
Anapsida	ACGTCGTTC
Synapsida	ACGACGTAA



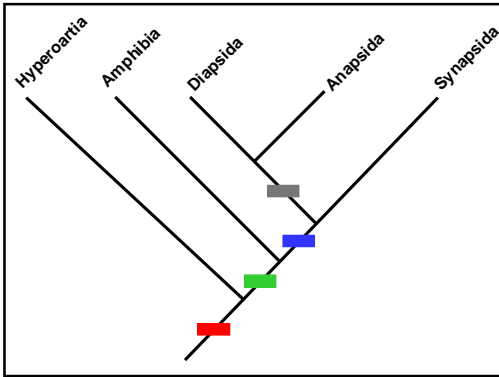
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