#### Tracing phylogenetic signal in datasets

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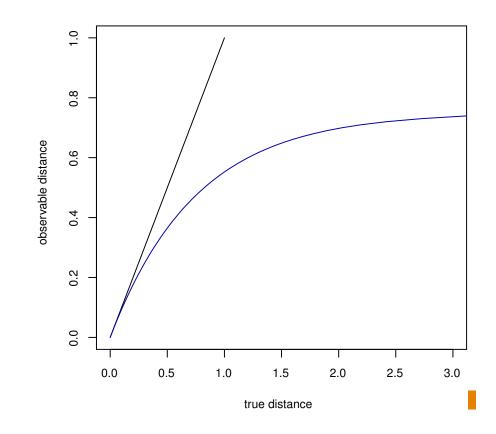
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### **Phylogenetic Information**

The information about the true tree, might be obscured or unextractable from an alignment due to

- too similar sequences (no differences  $\rightarrow$  no information)
- sequences are to divergent (saturated sequences → information drowned in noise)

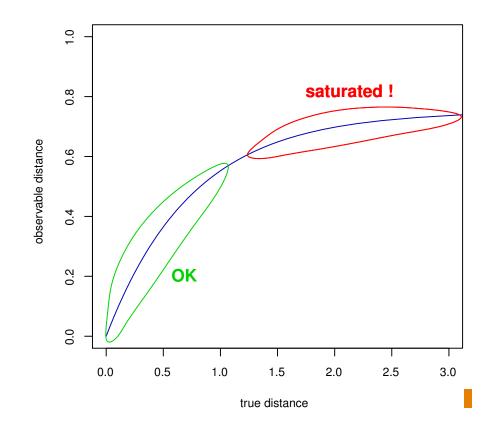
Is there a way to check for this?



### **Plotting Mutation Values**

- Take every pair of sequences
- Count the number of observable differences (e.g., transitions, transversions)
- Compute the distances of the sequence pair:.
- and plot the distance (x-axis) against the observable differences (y-axis)

# **Plotting Mutation Values (2)**



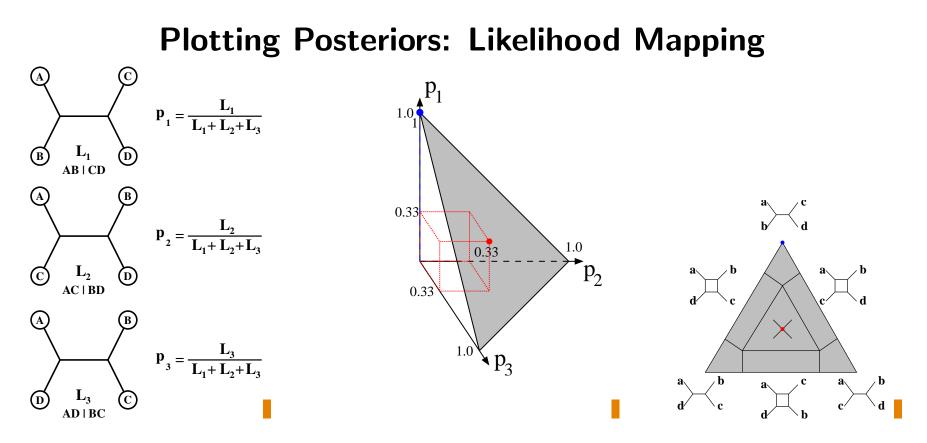
#### **Posterior Probabilities and Empirical Bayes**

- We can now reconstruct ML trees, but how comparable are the likelihoods, how reliable the groupings?
- Branch reliability can be checked, support values computed using:
  - Bootstrapping, Jackknifing alignment columns + consensus.
  - Randomizing input orders in stepwise insertions (TREE-PUZZLE).

#### **Posterior Probabilities and Empirical Bayes**

- We have learnt to reconstruct ML trees and heard that one can compare their posterior probabilities. . .
- Problem: How different are likelihoods? Just from the value of likelihoods one often cannot tell whether they are significantly different.
- Nomalization: Posterior probabilities are computed:

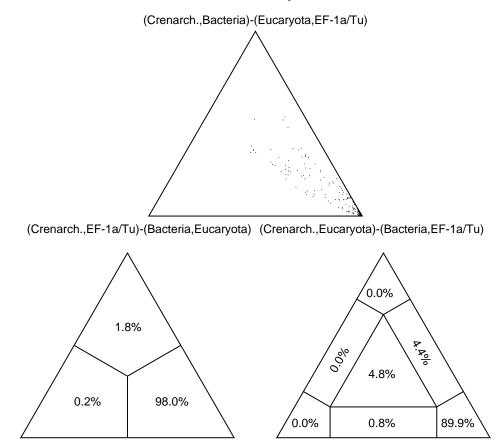
$$p_i = \frac{L_1}{\sum_n L_n}$$



Since  $p_1 + p_2 + p_3 = 1$ , 3D points  $(p_1, p_2, p_3)$  fall into a triangular (simplex).

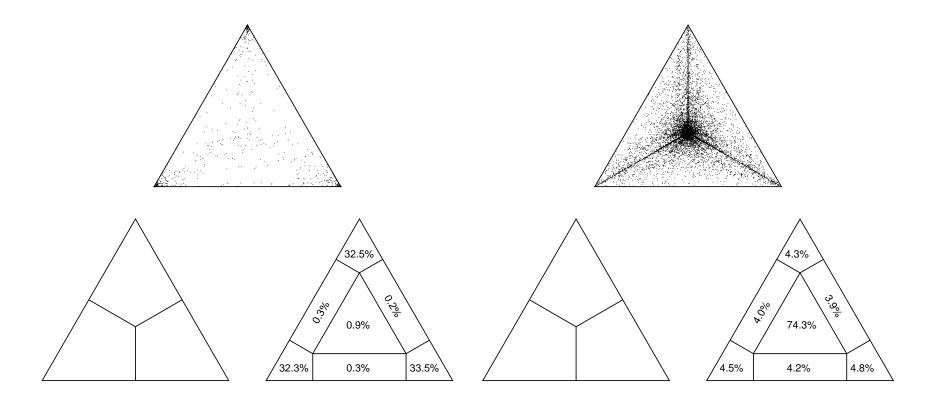
If we repeat this for all quartets (or a large random subset) in a dataset we can assess the amount of phylogenetic signal in the dataset.

## Likelihood Mapping (Cluster Analysis)



The Simplex Plot can visualize the relationship among clusters.

## Likelihood Mapping (Information Content)



The Simplex Plot can also visualize the information content in an alignment.