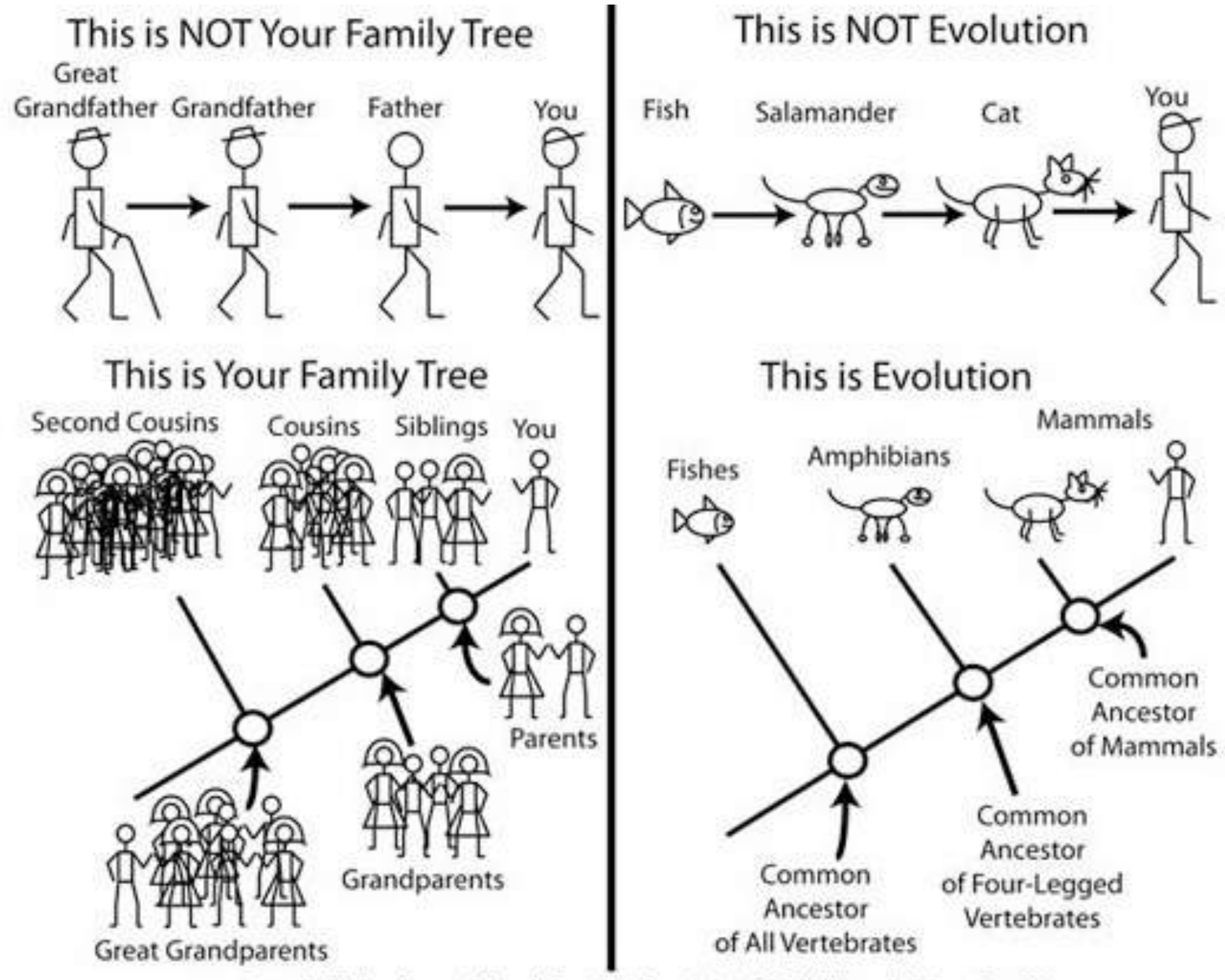
Algorithmic issues in (co)phylogenetic analysis

blerina sinaimeri

evolution



Cartoon by Matthew Bonnan of Macomb, IL, with kind permission of Florida Citizens for Science, Sept. 2010

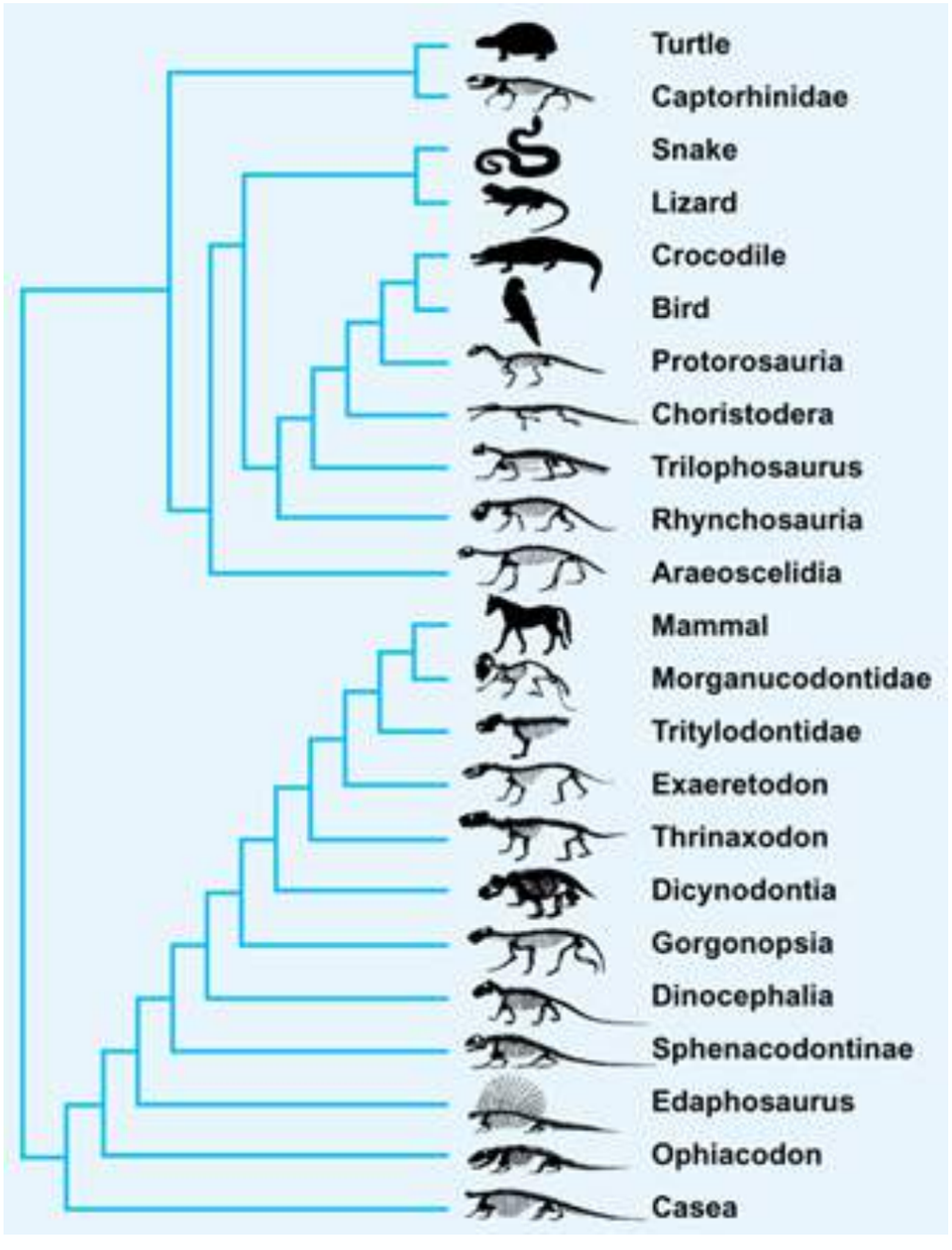
Phylogenetic tree

Phylogenetic Tree

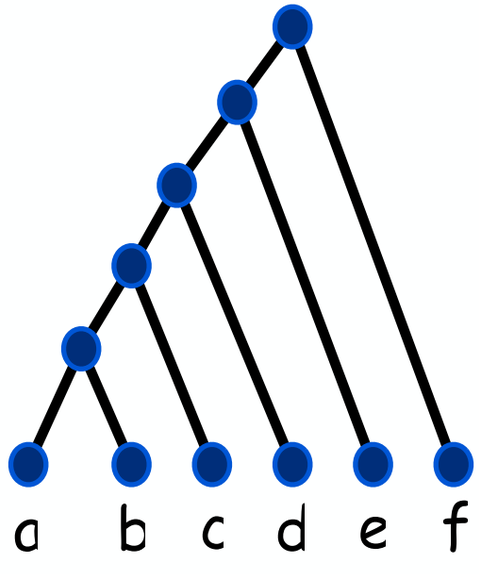
Phylogenetic tree

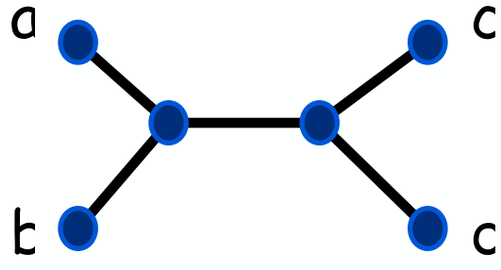
Phylogenetic Tree

Phylogenetic Trees



- rooted / unrooted
- binary / k-ary
- labeled from a set / labeled from a multiset
- unweighted / weighted (branch lengths)
- unordered / ordered





Phylogenetic Trees

- Maximum Parsimony
- Maximum Likelihood method

Maximum Parsimony

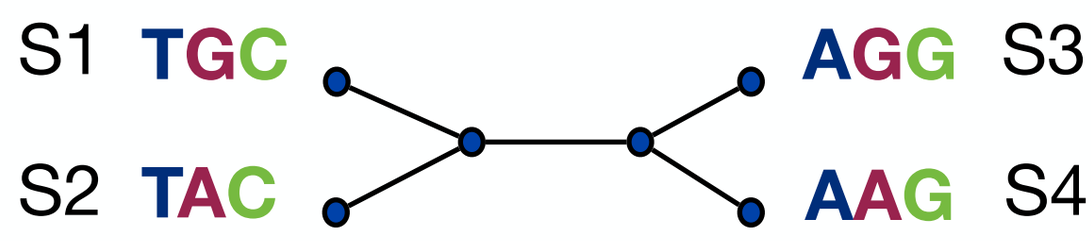
Sequence 1 **TGC**

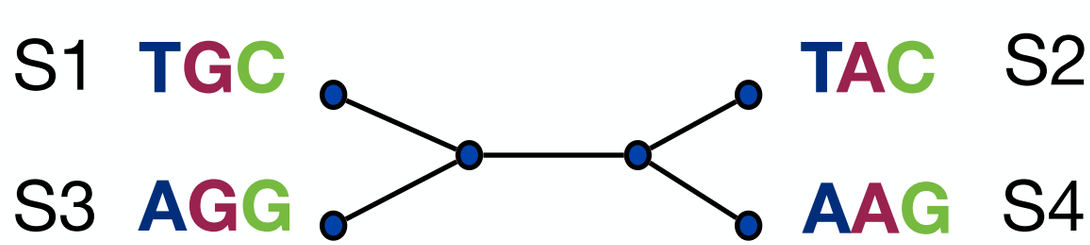
Sequence 2 **TAC**

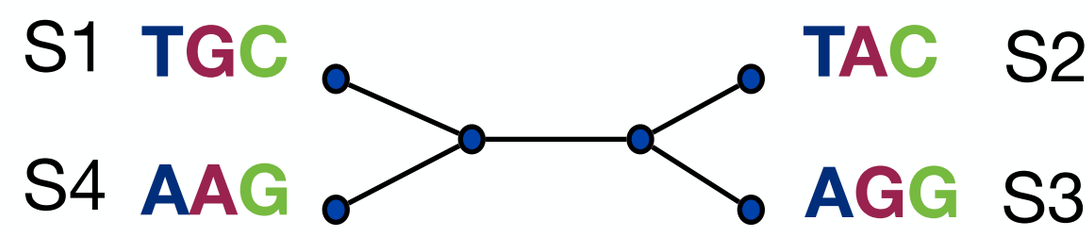
Sequence 3 **AGG**

Sequence 4 **AAG**

Find the “**best**” tree...but what does “best” mean?







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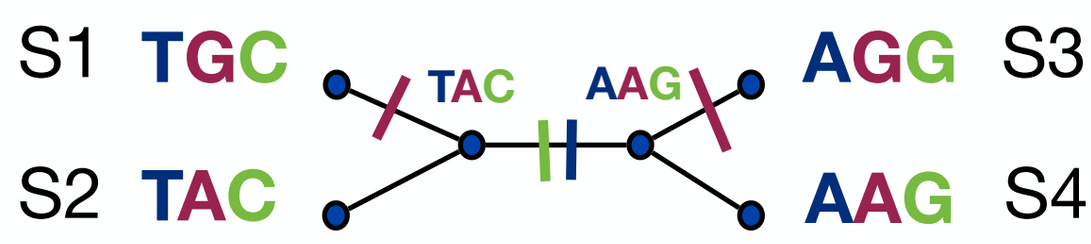
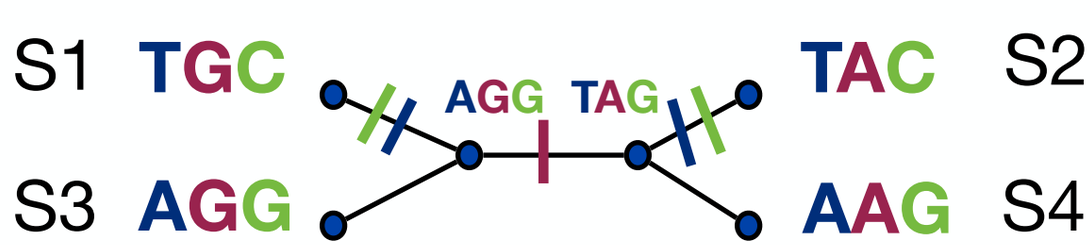
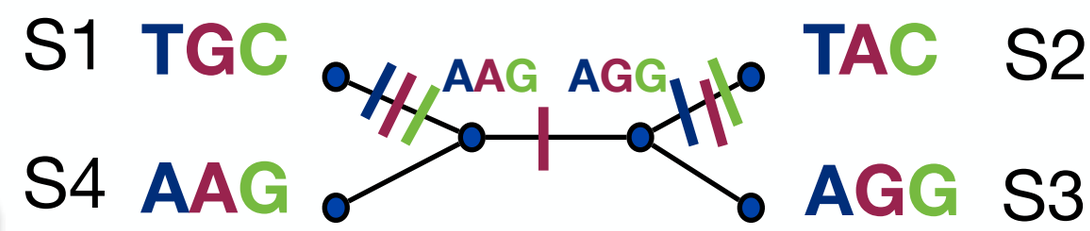




Find the "**best**" tree...but what does "best" mean?



In Maximum Parsimony: Minimize the number of mutations across the edges

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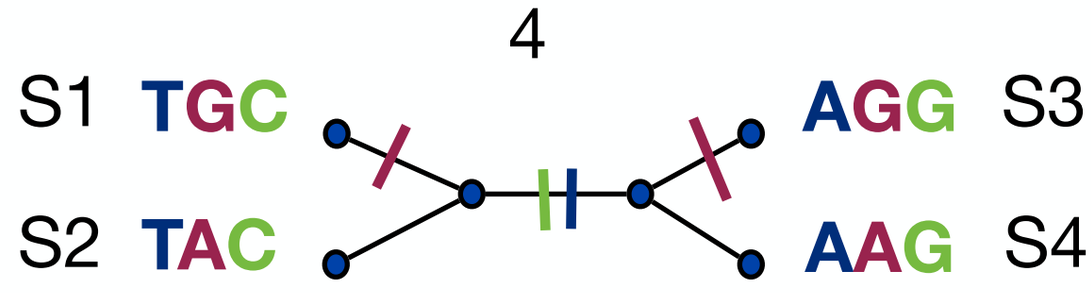

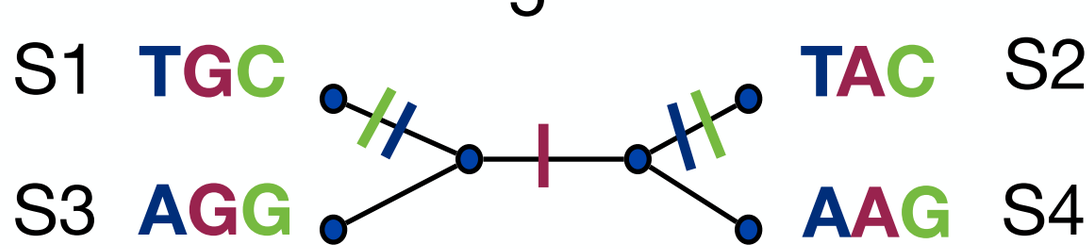

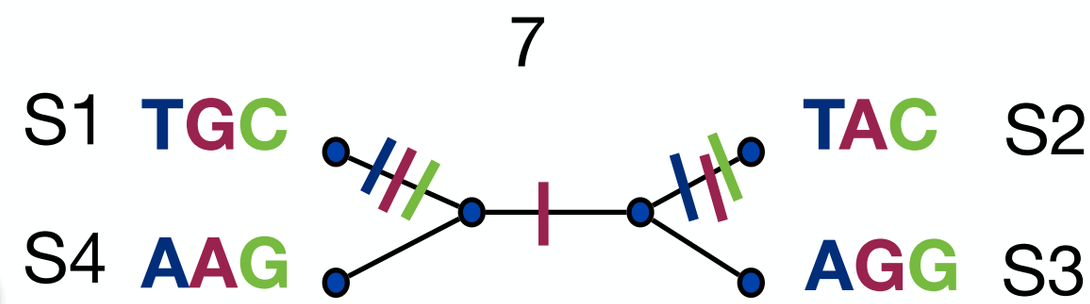

Maximum Parsimony

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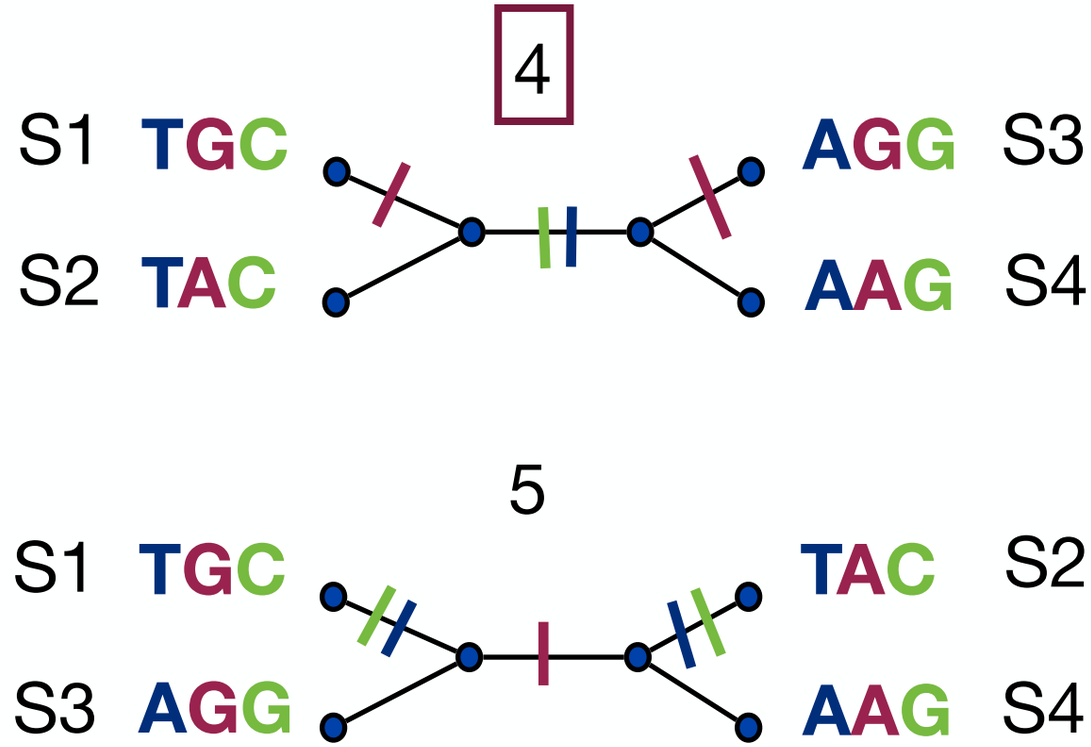


Maximum Parsimony

The problem

- Input : **n** DNA sequences
- Goal: Find the tree that minimizes the number of mutations along the edges.

Check for every tree?

Possible unrooted trees $\frac{(2n-5)!}{2^{n-3}\,(n-3)!}$

Maximum Parsimony

The problem

- Input : **n** DNA sequences
- Goal: Find the tree that minimizes the number of mutations along the edges.

Finding one optimal tree is NP-hard!

Maximum Likelihood

- Given certain rules about how sequences change over time, the best tree should reflect the most likely sequence of evolutionary events.

- maximize the probability that a given tree could have produced the observed data (i.e., the likelihood)

Differences with the parsimonious method

- Use of an explicit evolutionary model

- Allows variable substitution rates for each branch

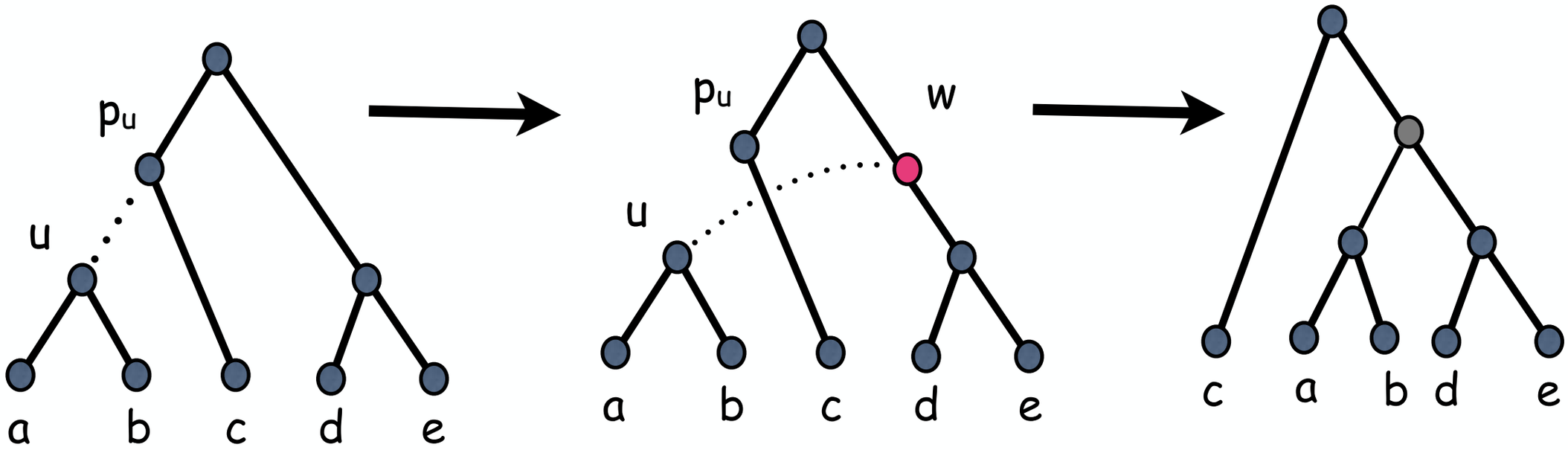
Comparing Trees

How similar two phylogenetic trees are?

- Robinson-Foulds
- Triplet distance
- Maximum agreement subtree
- Edit distances (SPR, TBR, NNI)
- …

Tree Metrics

SPR (Subtree Prune and Regraft)



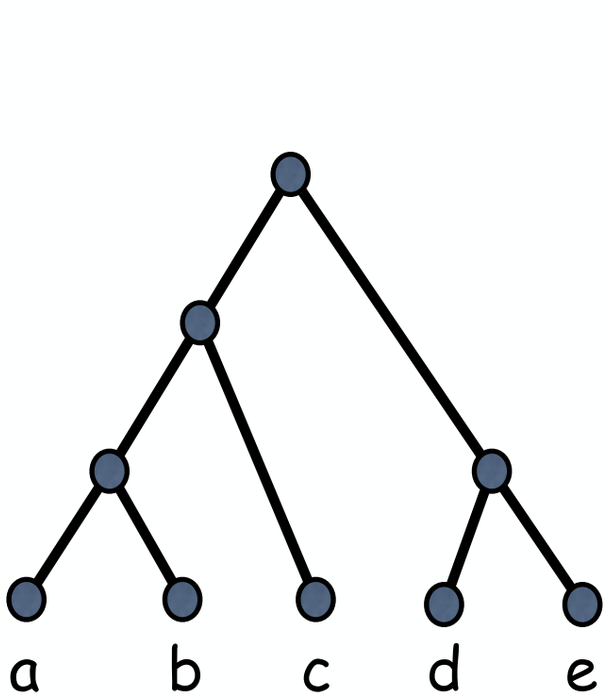
The SPR distance (d_{SPR}) is the minimal number of moves that transforms one tree into the other.

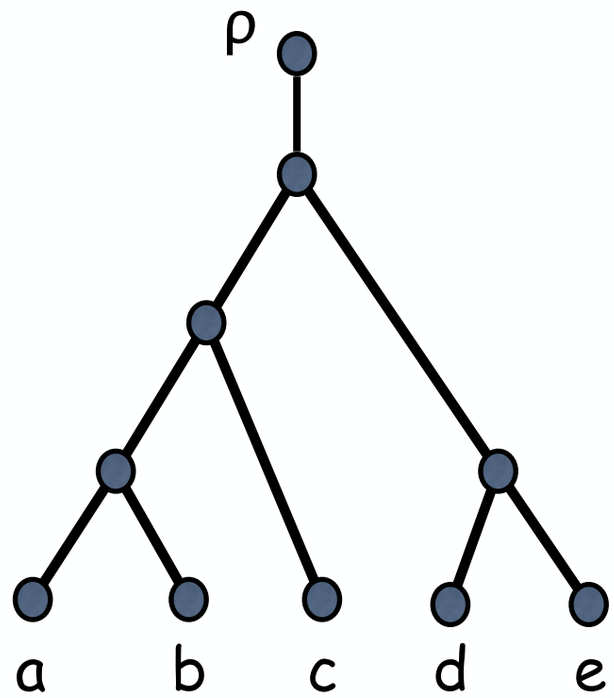
NP-hard

3-approximation algorithm

Maximum Agreement Forest

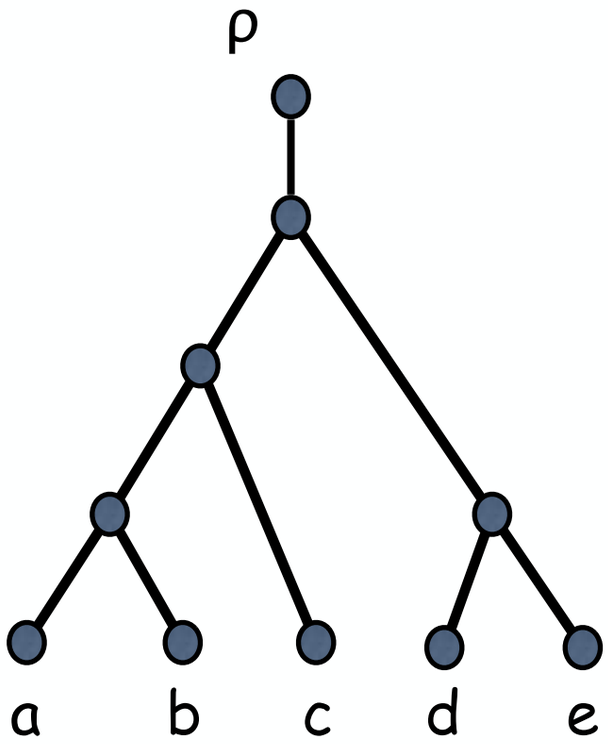
Technical detail

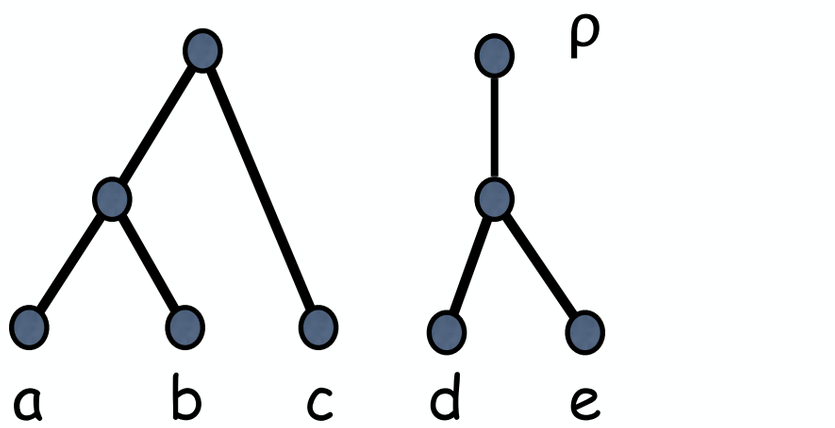


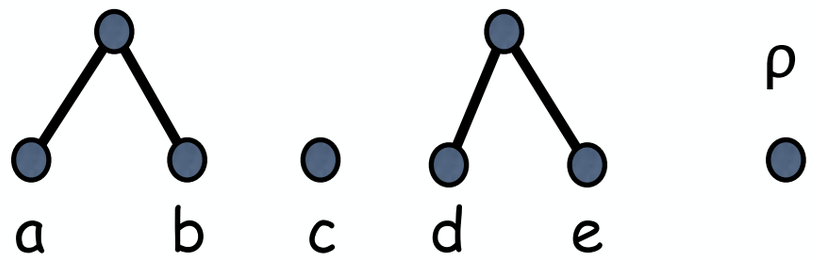


Maximum Agreement Forest

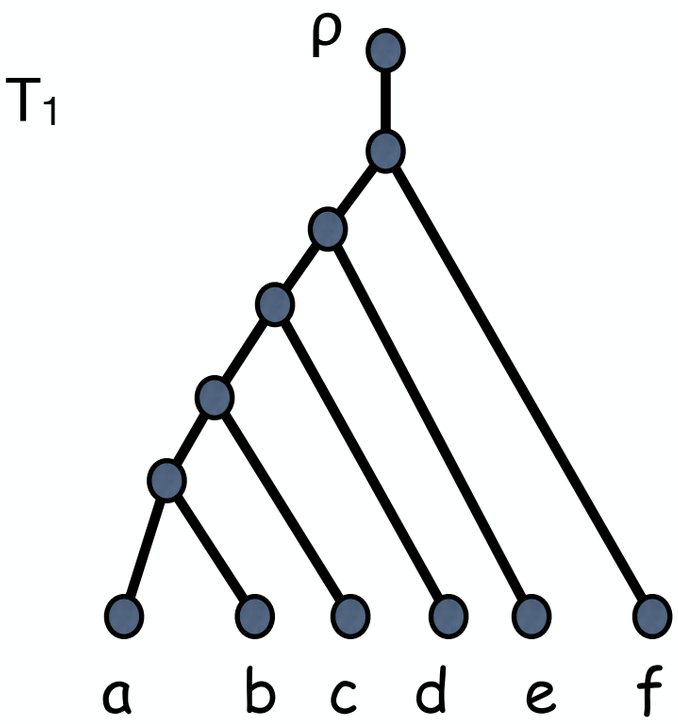
A Forest of T is a disjoint collection of phylogenetic subtrees whose union of leaf sets is X∪ρ.

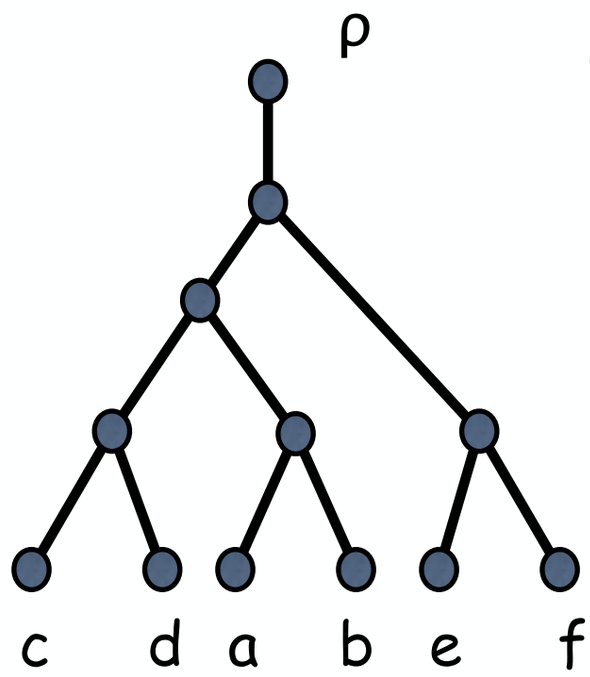






Maximum Agreement Forest





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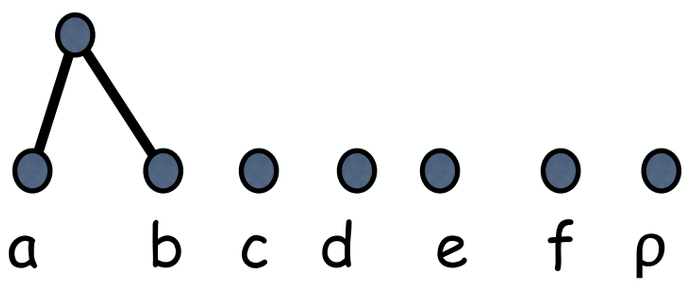
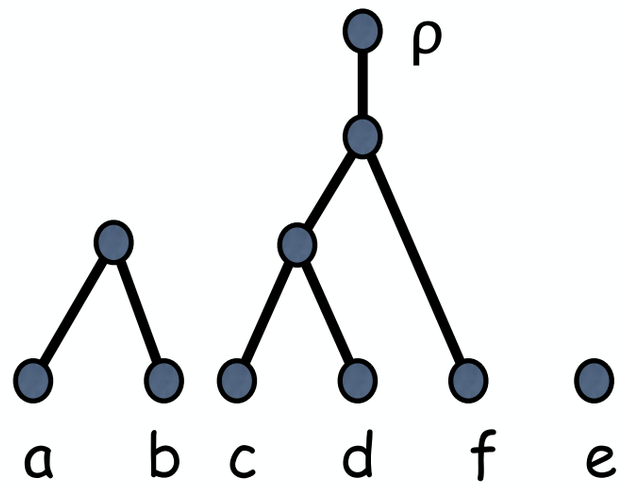


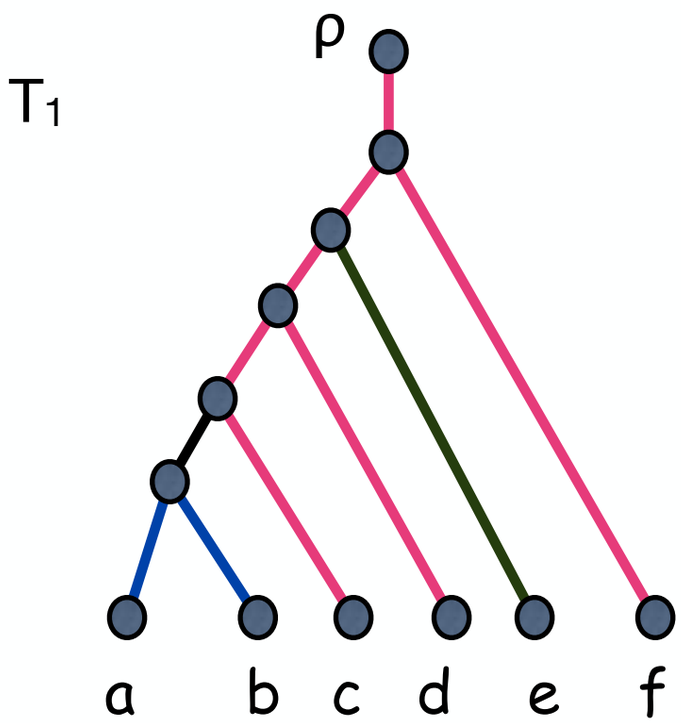
7 components

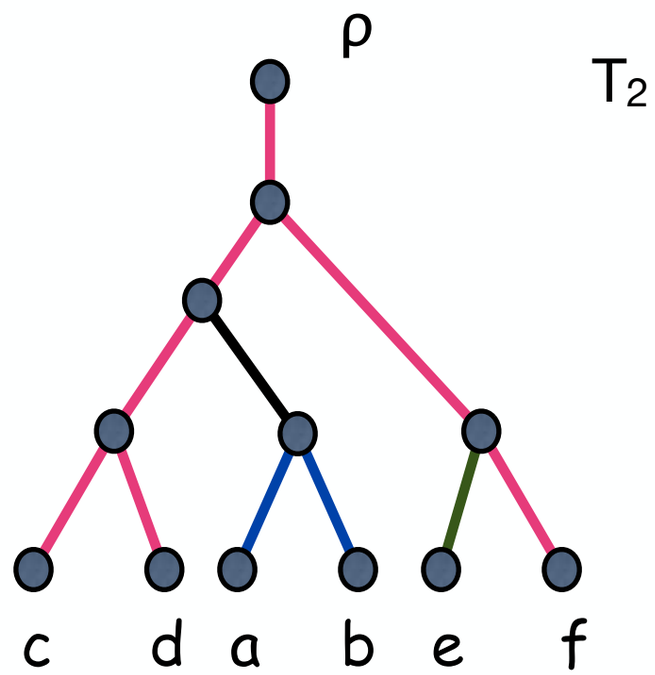
MAF



3 components

Maximum Agreement Forest





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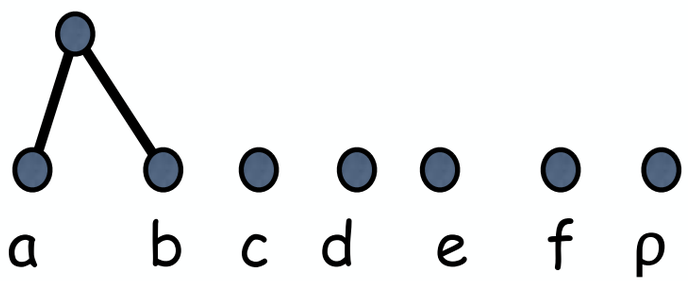

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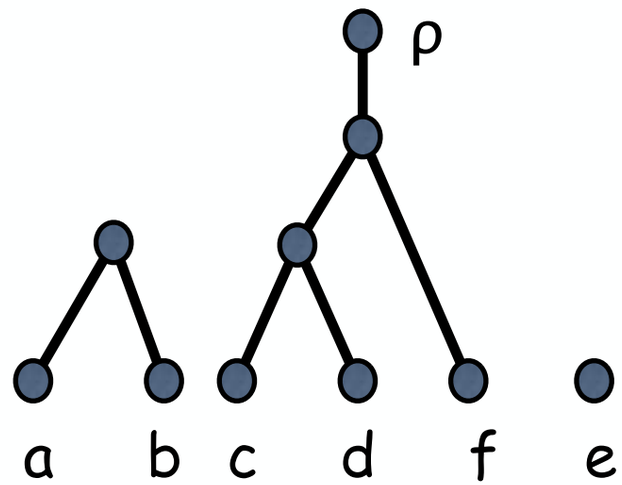
MAF



3 components

Maximum Agreement Forest

$m(T_1,T_2)$= size of maximum agreement forest

Theorem. (BS04)

Let T_1 and T_2 be two binary phylogenetic X-trees. Then

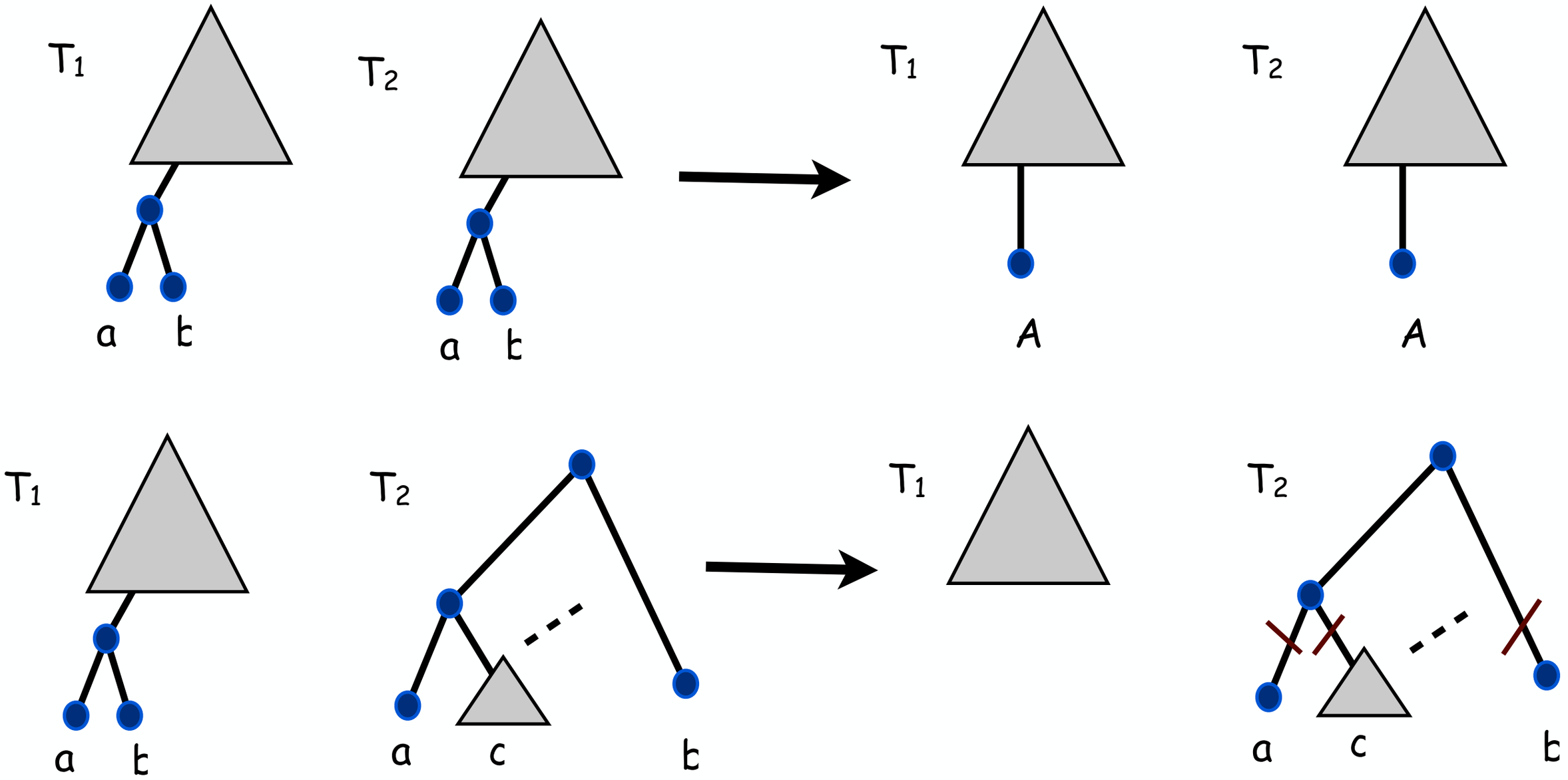
$$d_{SPR}(T_1,T_2)= m(T_1,T_2)-1$$

Exercise 1

- Explain the role of ρ in the relation between SPR and MAF. Does the theorem hold without introducing ρ?

Maximum Agreement Forest

3-approximation algorithm for MAF



coevolution

Symbiosis

Mutualism

Human Microbiota

Parasitism

Gopher

Lice

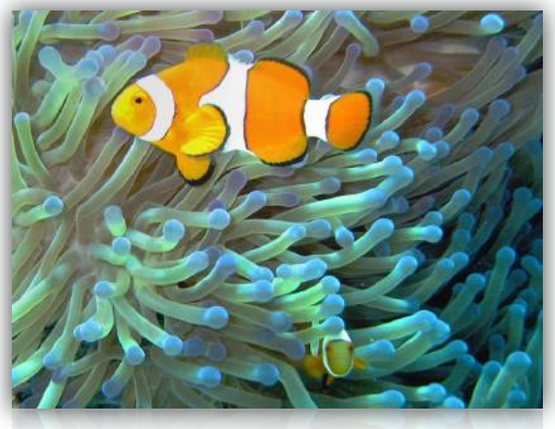
Interspecific interaction

Plant diversity

Mimicry

Human Microbiota

Parasitism



Mutualism