Character-based phylogenies

Lecture 6.3

by Marina Barsky

Recap: Parsimony

- *Parsimony* is preference for the least complex explanation.
- Under maximum parsimony, **the preferred phylogenetic tree** is the tree **that requires the smallest number of evolutionary changes**.

Character-based phylogeny problem with parsimony score

- Input:
  - a set of *N* species
  - a set of *M* characters for each species
  - The input is generally presented as an *NxM* matrix ***C***, where each entry $\boldsymbol{C}_{ij}$ represents the value of character *j* for species *i*

  In addition, the weight matrix may be supplied to weigh the score of transition between different characters

The *parsimony score* of the tree: Intuition

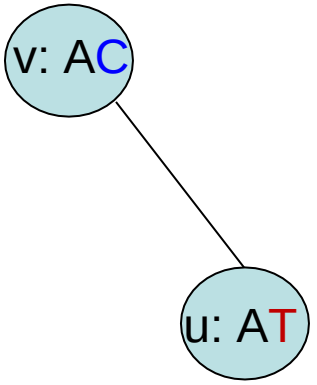
- Let the score L [tree *length*] be the total number of times the value of some character changed along some edge
- The most parsimonous explanation of a given phylogeny would be the tree with an overall minimum length (the smallest possible number of changes along its branches)

The *parsimony score* of the tree: Definition

- Let V(T) be a set of vertices and E(T) be a set of edges of a given phylogenetic tree, and let the value of a character j in vertex v be vj.

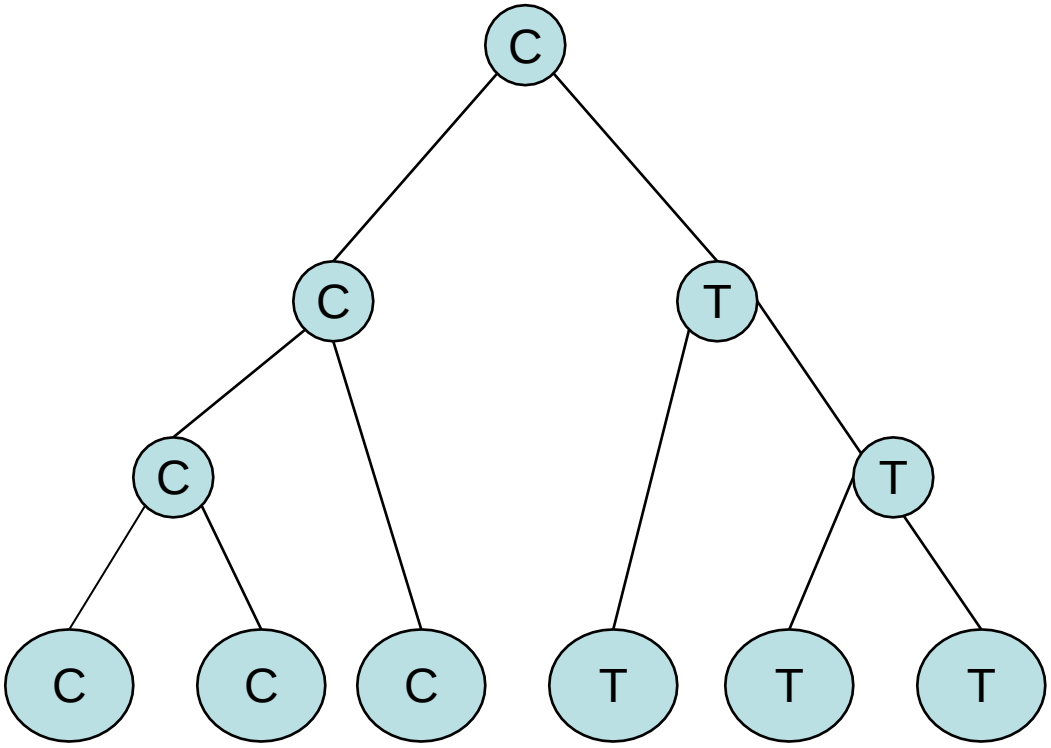
$$L(T)=\Sigma_{(\text{for each } v,u \in E(T))} |\{j: vj \neq uj\}|$$

At the same position j



For this edge, we would add 1 to the total parsimony score of the tree

What is P-score of this tree?



Assumptions

- The character changes are *mutually independent*
- After 2 species diverged, they continue to evolve separately
- Each character split is a 2-way split – bifurcating (*binary*) tree

Parsimony problems

- **Small parsimony problem**: given a topology of a rooted phylogenetic tree **and** the character matrix C, find a labeling of ancestral sequences which implies the minimum parsimony score

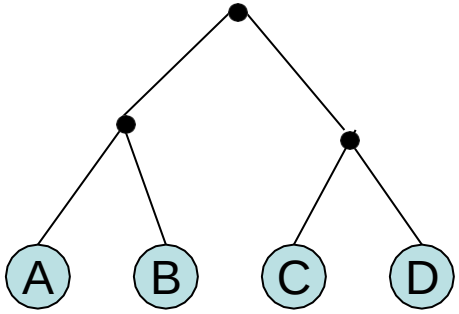
- **Large parsimony problem**: given the character matrix C, build the tree with the minimum parsimony score (minimum number of character changes along its edges) – NP-hard

Small parsimony problem

Matrix C

	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t

Tree T



Small parsimony problem

Input:

matrix C (multiple alignment)

tree T

Output:

Labeling of ancestral nodes which minimizes the parsimony score of the tree

The Fitch algorithm for evaluating the tree given the multiple alignment

Phase 1: Generate candidate labels.

Perform DFS (postorder) for each character position and label each parent node by an intersection of its children. If this intersection is empty, label parent by the union of its children.

Phase 2: Select labels from candidates.

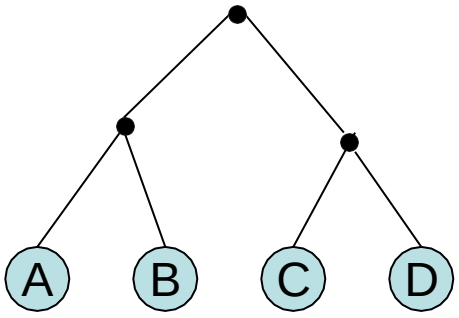
Perform DFS (preorder), label each node with a character from a candidate set. If parent contains child character, label this child with this character. If not, label with any character from the parent set.

The Fitch algorithm. Phase I

	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t

Goal: Compute the sets of all possible character states for each internal node, based on the states of its children

Each leaf node contains only 1 state for each character, and is initially marked with this character



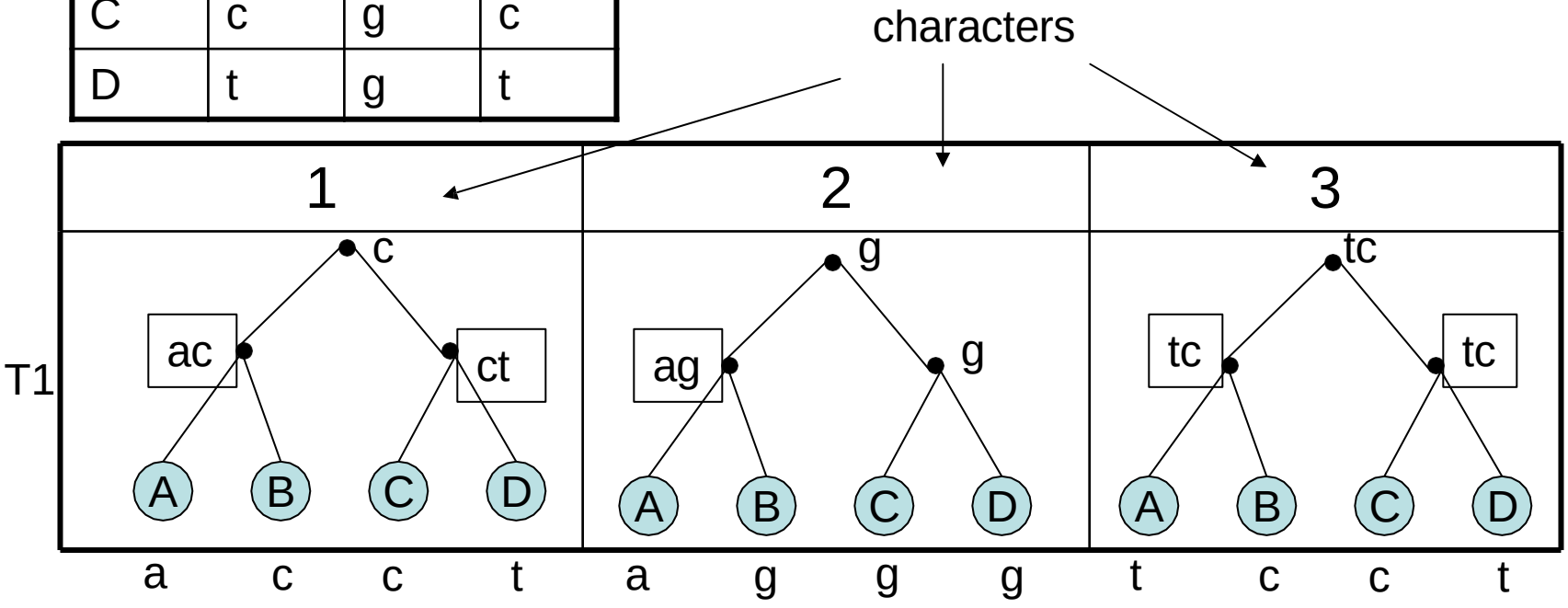
Perform ***post-order*** traversal of the tree (each node is evaluated only after all its children have been evaluated) and for each node *v* compute the candidate character set

Phase I: intuition

- If there is a state which fits both children, we take it as their common ancestor. If there is no such state (the intersection is empty), we take as the candidates the states of both children, since this is better than taking any other set which does not occur in any of the children

Phase I: example

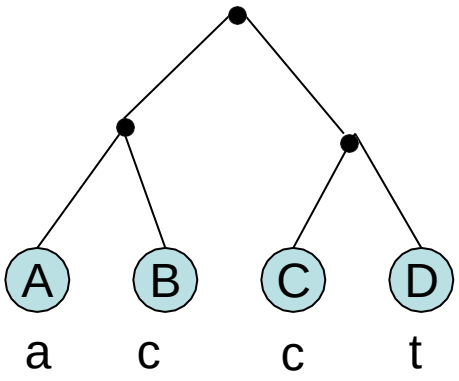
	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t



Phase I: code

	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t

j=1



Phase I.

For each column *j* of matrix ***C***:

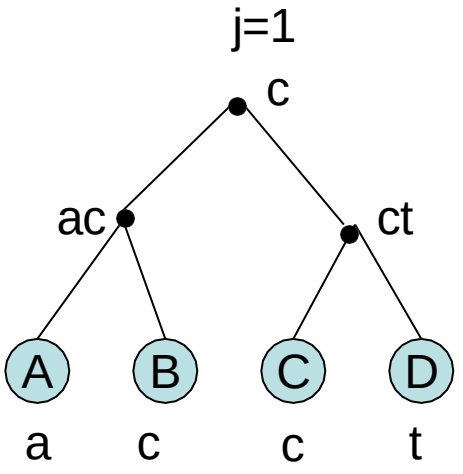
//initialize

for each leaf node *v* of species *i*:

$Set_v = \boldsymbol{C}_{ij}$

Phase I: code

	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t



Phase I.

For each column *j* of matrix ***C***:

//initialize

for each leaf node *v*:

$Set_v = \boldsymbol{C}_{ij}$

perform post-order traversal of *T*

for each internal node *v*

with children *u* and *w*:

if $Set_u \cap Set_w \neq \emptyset$

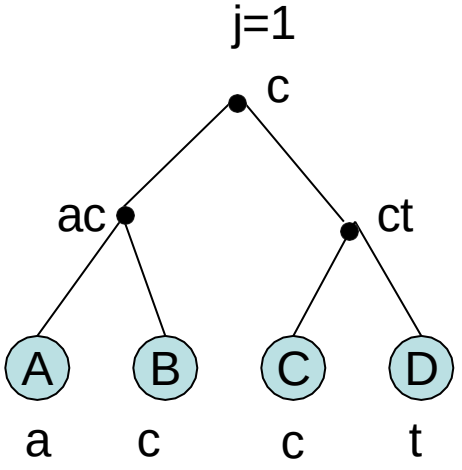
$Set_v = Set_u \cap Set_w$

else

$Set_v = Set_u \cup Set_w$

Phase II: intuition

	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t

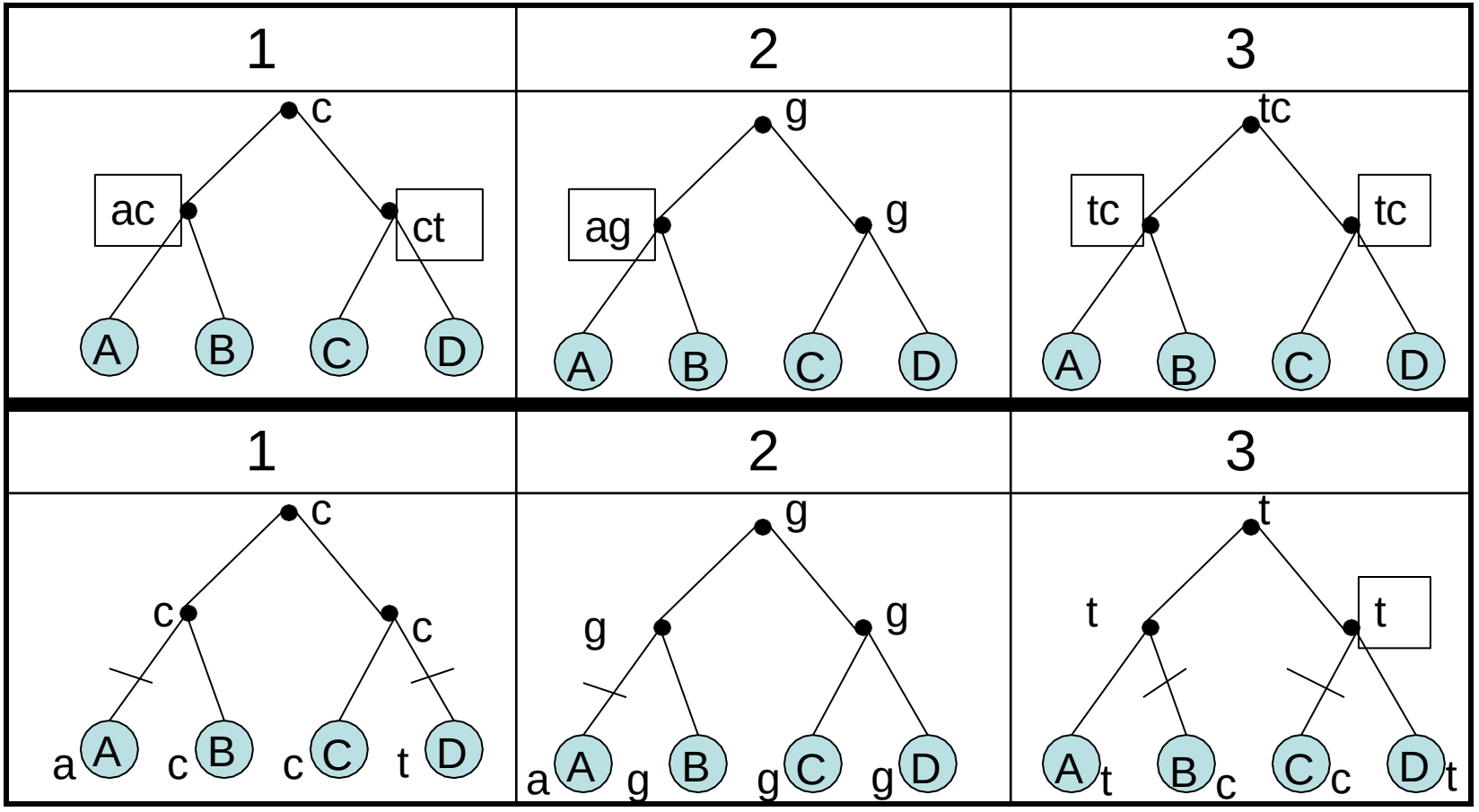


We determine value v_j to assign to each internal node, which we choose from the candidate set of characters in its parent

We perform pre-order traversal (each child is evaluated after its parent has been evaluated)

Phase II example

	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t



The total parsimony score *L* of this tree is 5

Phase II: code

	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t

For each character *j*

perform pre-order traversal of *T*

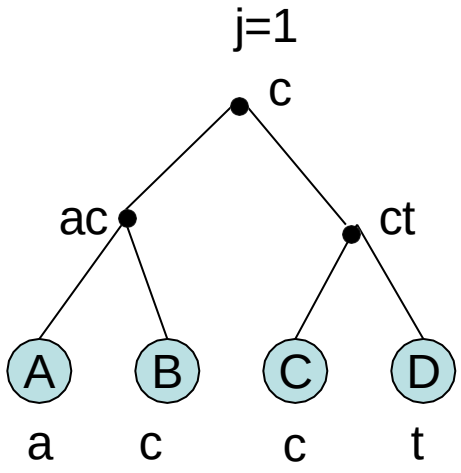
for each vertex *v* with parent *u*

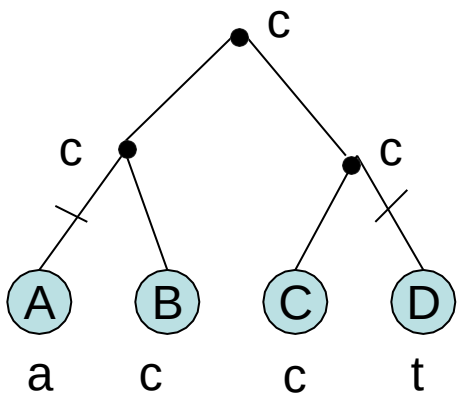
if $u_j \in \text{Set}_v$

$v_j = u_j$

else

v_j=any element from Set_v





The parsimony score for the first character=2

The Fitch algorithm: complexity

- If there are k possible values of each character, then for a single character we perform at most $2k$ operations, and with $2N$ total nodes in the tree, there is $O(Nk)$ work for a single character

- $O(NMk)$ for all M characters

The weighted parsimony: algorithm by Sankoff

- Different, application-specific costs are assigned for each change of character from state to state
- This is more realistic, since substitutions happen with different probabilities
- An overall algorithm is similar to the Fitch algorithm (you can read about it in your textbook)

The **large** parsimony problem

- Input: matrix ***C*** describing *M* characters for a set of *N* species

  M_{ij} – state of the *j*-th character for species *i*

  M_i – label of species *i*.

  All labels are distinct

- Goal: find the most parsimonous tree: topology, leaf labeling and labels for internal nodes

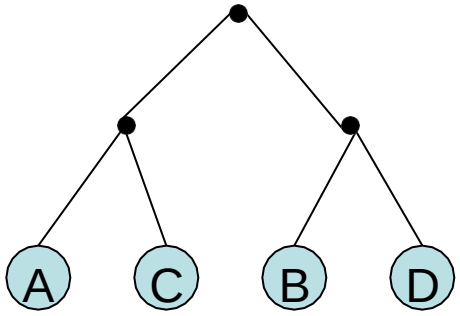
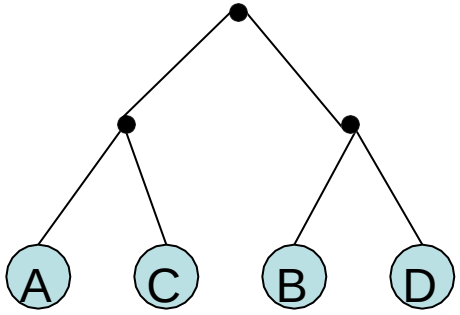
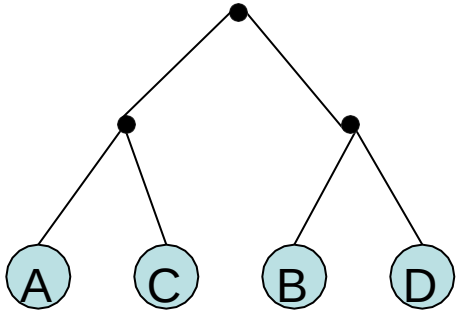
  The problem is NP-hard

Large Parsimony problem for 4x3 matrix

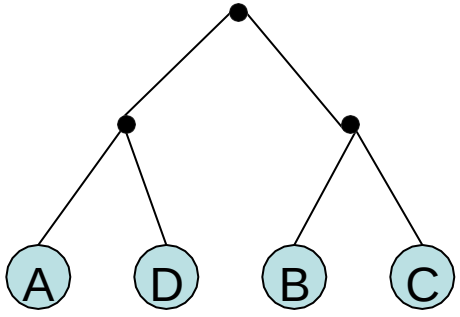
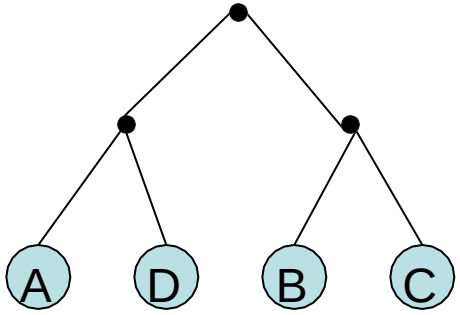
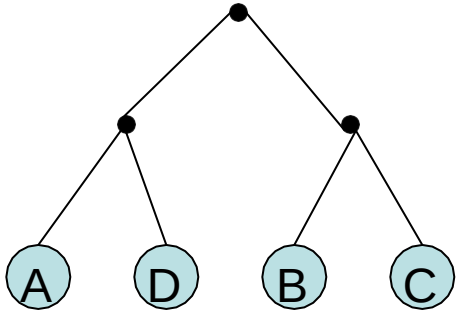
All possible trees need to be evaluated in order to find the most parsimonous tree

	1	2	3
A	a	a	t
B	c	g	c
C	c	g	c
D	t	g	t

T2

1	2	3	L(T)
			?

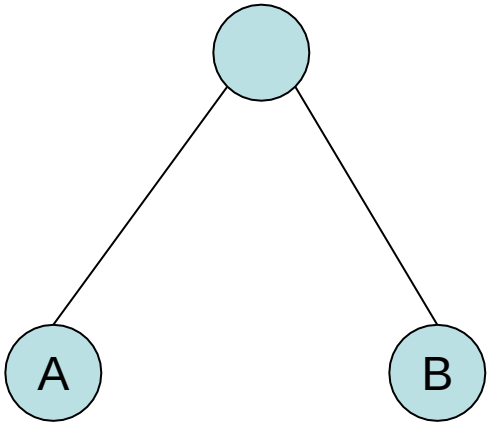
T3

1	2	3	L(T)
			?

Find the most parsimonous tree for this example: T1 (previously computed), T2 or T3 ?

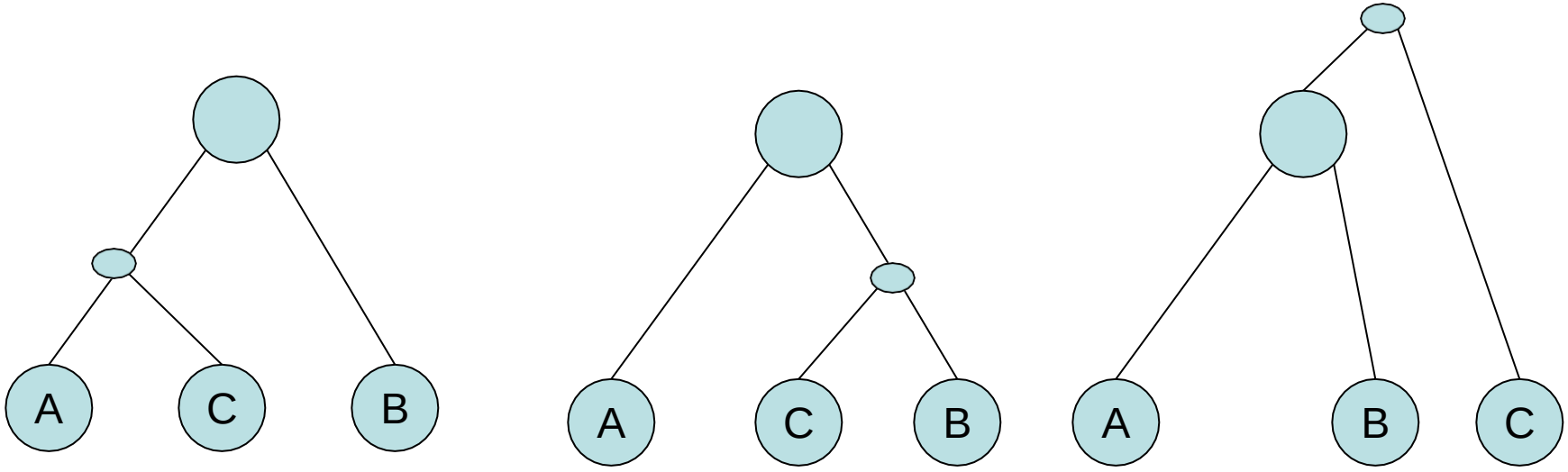
How many different trees?

- For 2 species (N=2) only 1 possible tree



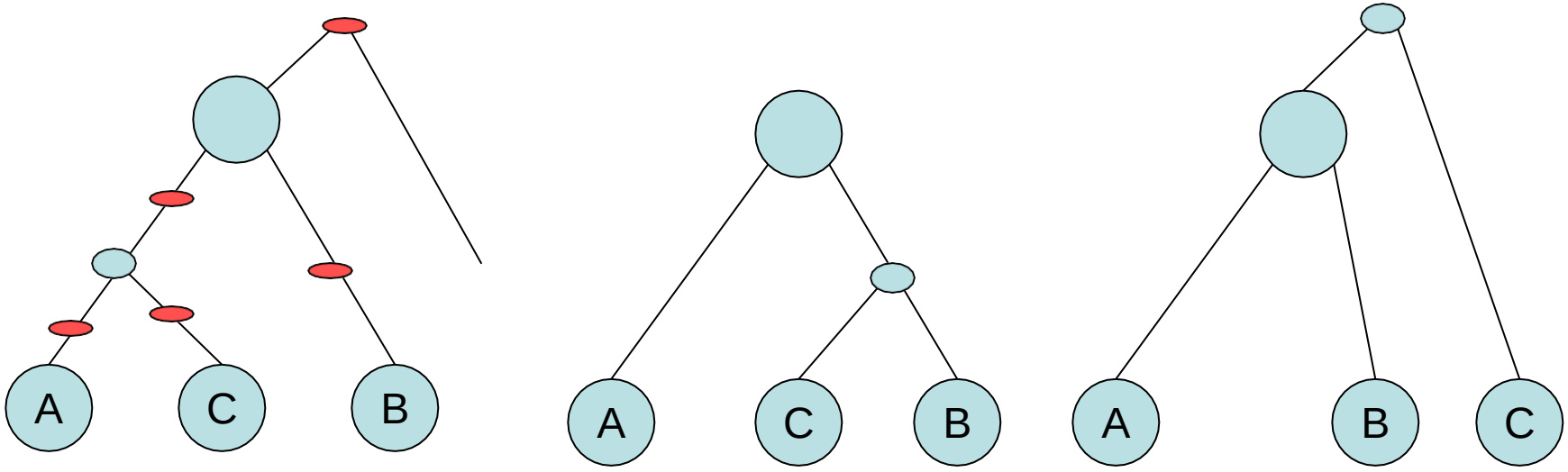
How many different trees?

- For 3 species (N=3): a new leaf can be added by splitting any of 2+1 branches



How many different trees

- For 4 species (N=4): for each of the previous 3 trees, a new leaf can be added by splitting any of 4+1 branches



1*3*5*…(2N-3) possible trees (2N-3)! – exponential number of different trees

Solution for the large parsimony problem

- Exhaustive solution: enumerate all possible trees, compute the P-Score of each tree, and choose the tree with a minimum score

- Optimization over the search space:
  - *Branch-and-bound*

The Branch-and-Bound technique

- The search is presented as the leaves of the search tree. Each node in this tree corresponds to some variant of a possible phylogenetic tree

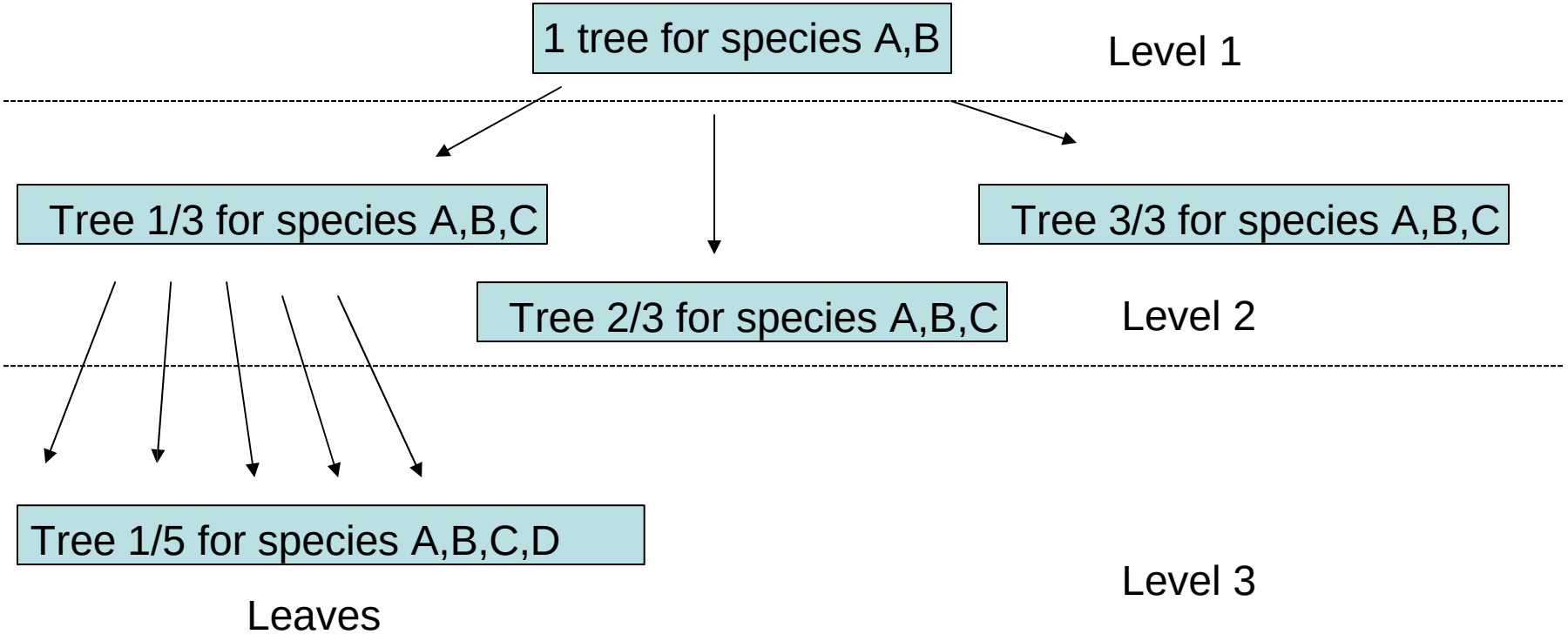
- In order to apply the B&B technique, the score of each search node must be ***monotonous***, i. e. the score of each node is >= the score of any of its ancestors

- In this case, the algorithm guarantees to find the best tree, but it does not guarantee that the search will be faster than the exponential time

- Performs quite good in practice

The Branch-and-Bound technique

- At level *k* of the tree we have nodes representing all possible phylogenetic trees for the first *k* species



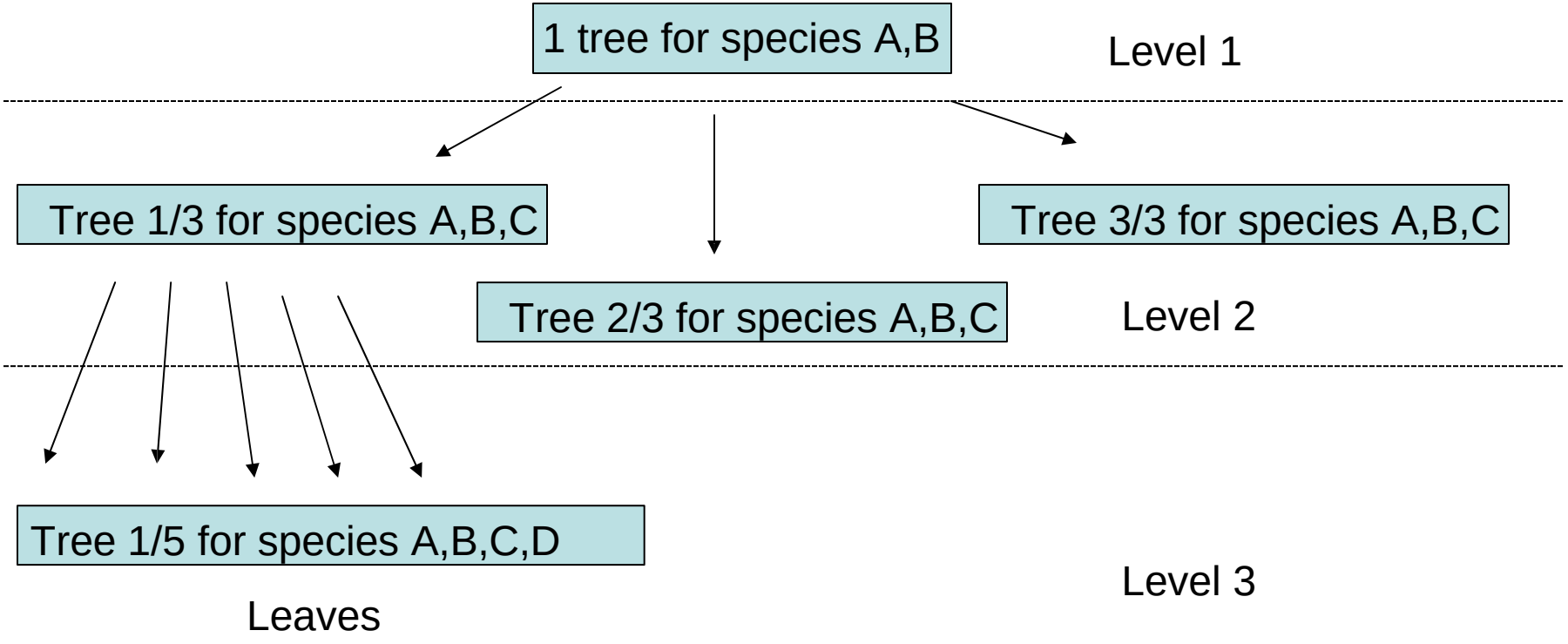
The Branch-and-Bound technique

- The search tree is traversed in order, and the score of the best leaf configuration found so far is kept as a bound *B*.

- Whenever a node is reached with the score >*B*, the search tree is pruned at this node, i.e. its subtree is not searched, since it is guaranteed that any leaf in its subtree cannot have score <=*B*

The Branch-and-Bound technique

- There are 2*k*-1 places to add a new species to an existing tree, thus each node at level *k* branches into 2*k*-1 children.
- The requirement for monotonicity is satisfied, since adding a new node cannot reduce the P-Score of the tree



The Branch-and-Bound technique

- The first leaf for all *N* species is found by computing a local minimum using one of the optimization techniques. This local minimum in many cases will be also a global minimum.
- The P-Score of this leaf is used as the bound on the rest of the search nodes, most of which are pruned and not expanded