

# Near-optimal Algorithm for Constructing Greedy Consensus Tree

Hongxun Wu

Institute for Interdisciplinary Information Sciences, Tsinghua University

# Phylogenetic tree

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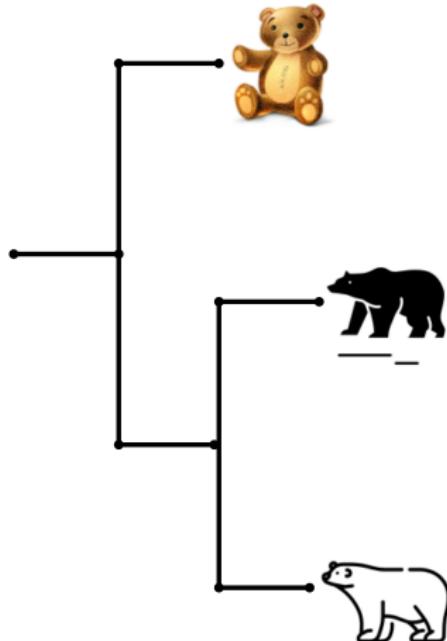


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- ▶ **Leaves** of the tree represent species.
- ▶ Each **inner node** represents the least common ancestor of all leaves in its subtree.



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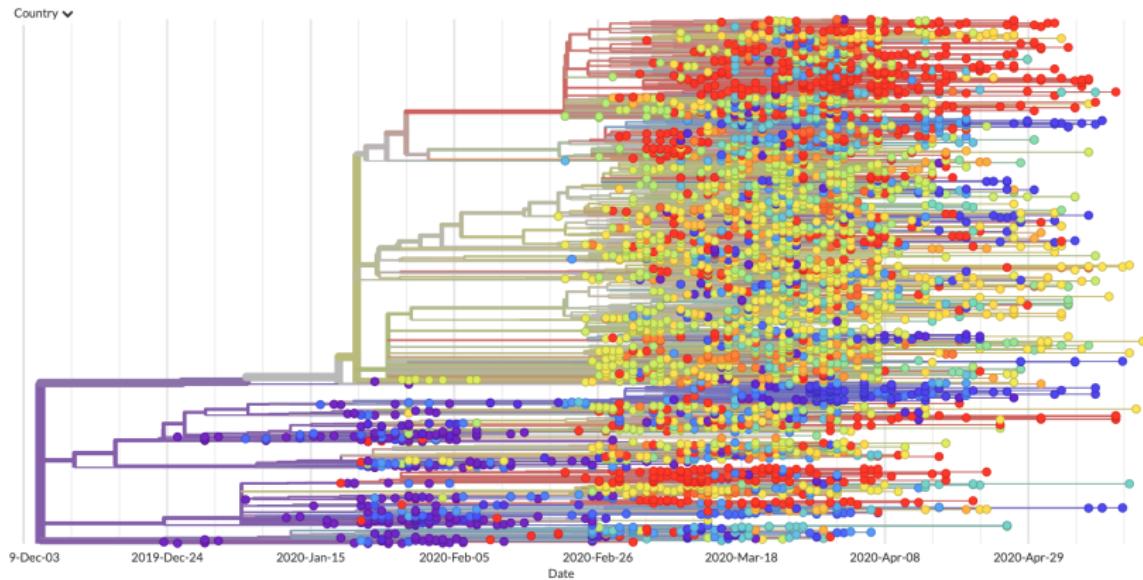
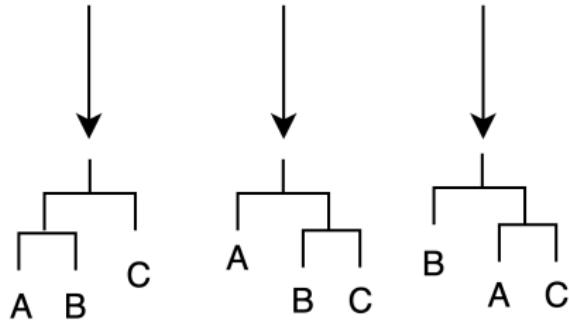


Figure: Phylogenetic Tree of Covid-19<sup>1</sup>

<sup>1</sup>Genomic epidemiology of novel coronavirus. 2020. URL:  
<https://nextstrain.org/ncov/global>.

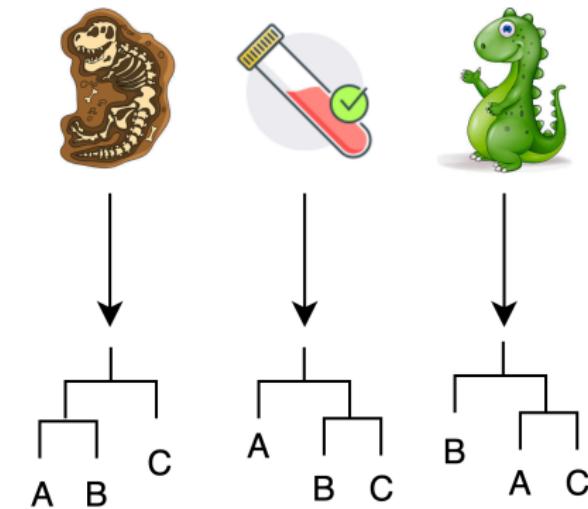
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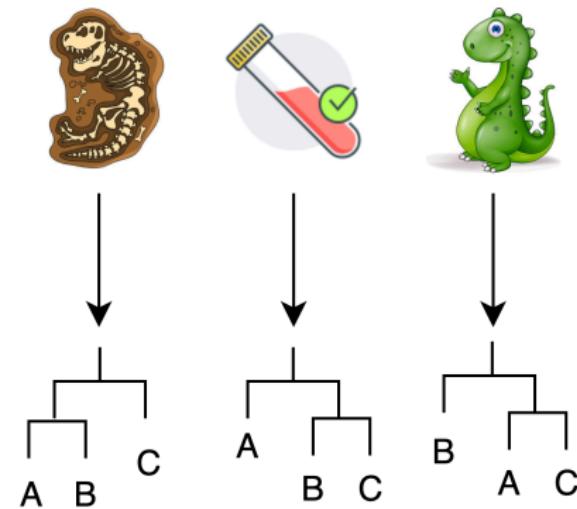
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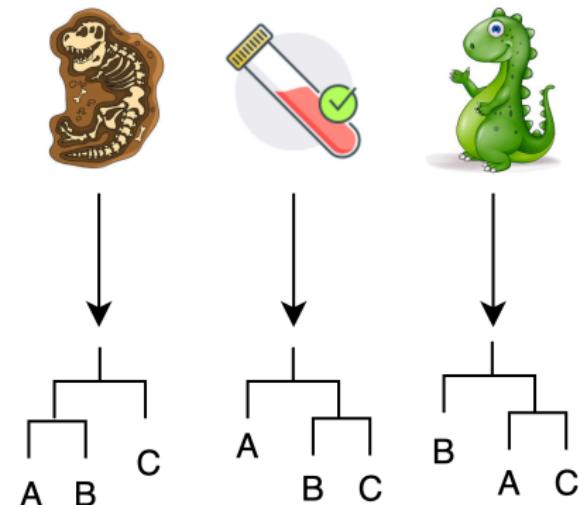
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- ▶ Let  $k$  be the number of phylogenetic trees in the input and  $n$  be the number of species in each of them.
- ▶ The input size is  $\Theta(kn)$ .



# Consensus tree

- ▶ Many consensus tree methods were proposed.

Consensus tree method	Running time
Adam's consensus tree	$O(kn \log n)$
Strict consensus tree	$O(kn)$
Loose consensus tree	$O(kn)$
Frequency difference consensus tree	$O(kn \log^2 n)$
Majority-rule consensus tree	$O(kn \log k)$ , Randomized $O(kn)$
Majority-rule (+) consensus tree	$O(kn)$
Local consensus tree	$O(kn^3)$
$R^*$ consensus tree	$O(n^2 \log^{k+2} n)$
<b>Greedy consensus tree</b>	$O(kn^{1.5})$ , $O(k^2 n)$

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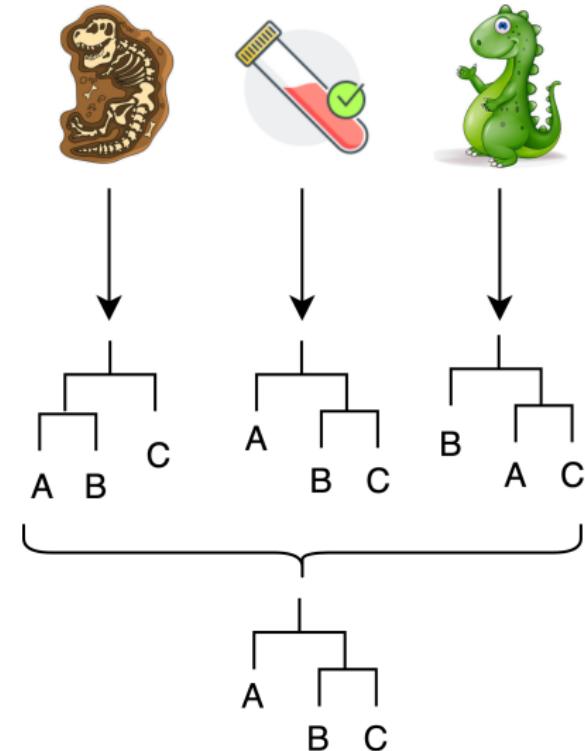
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- ▶ Most of them have near-optimal running time. Greedy consensus tree is one of the exceptions.

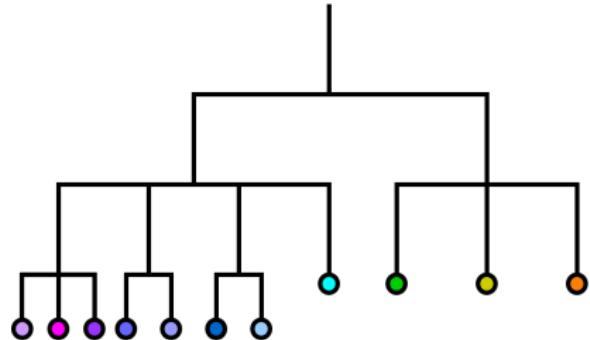
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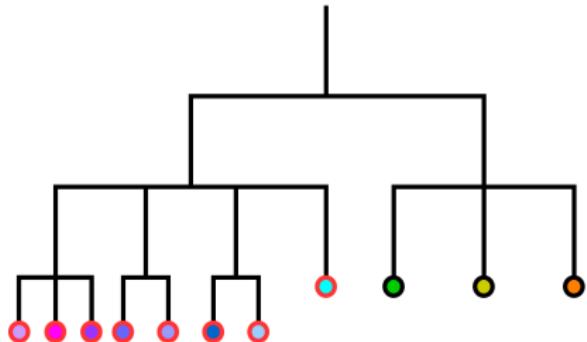
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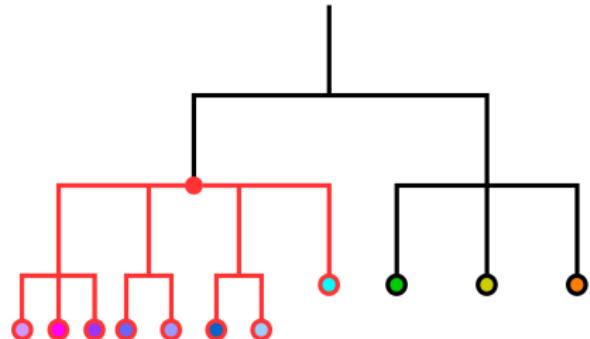
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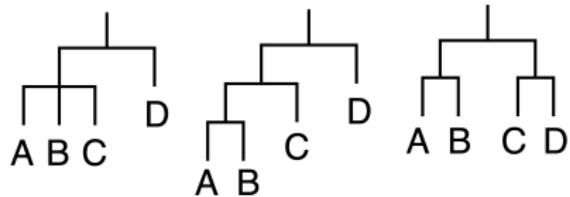
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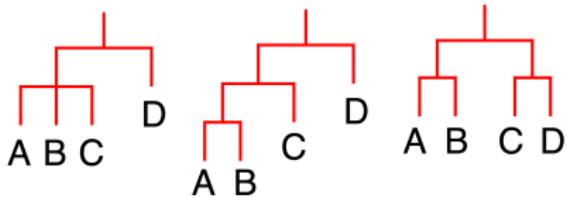
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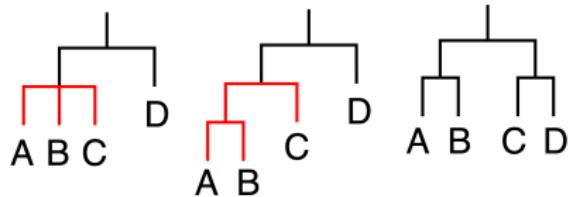
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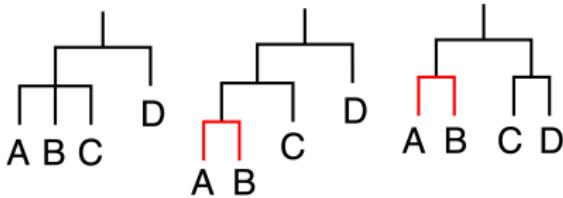
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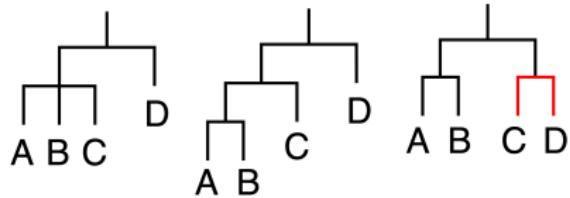
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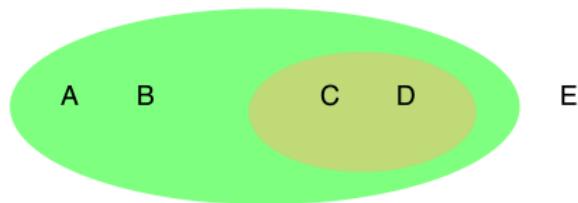
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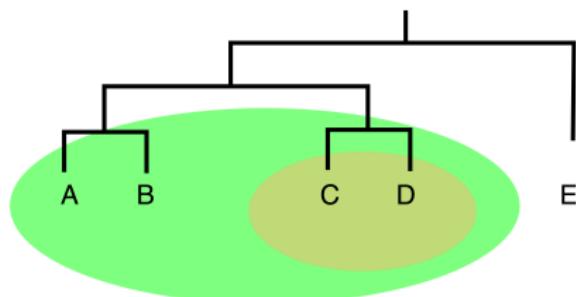
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  - ▶ They are disjoint.
  - ▶ One contains the other.



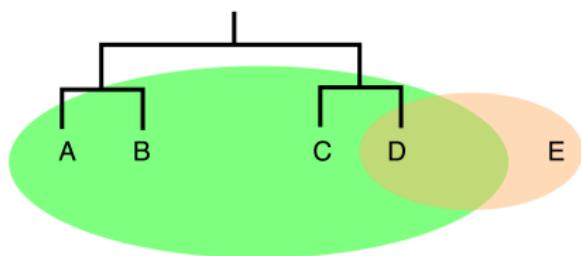
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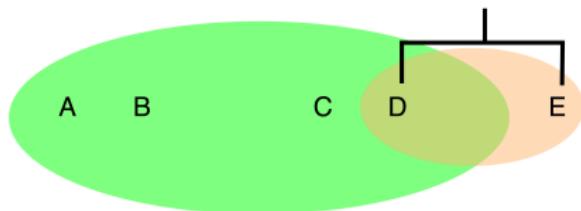
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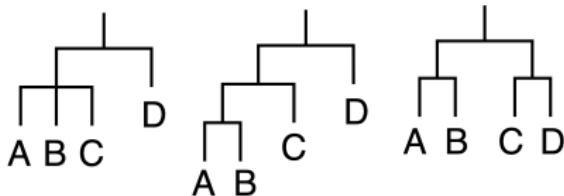
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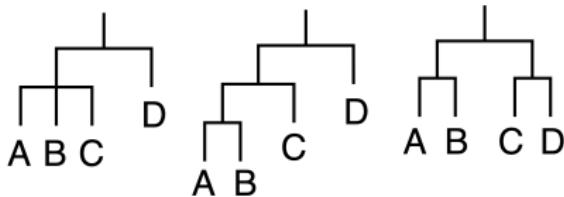
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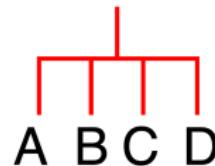
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A B C D

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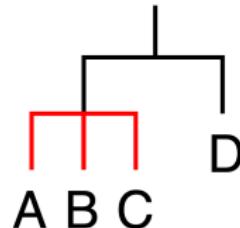
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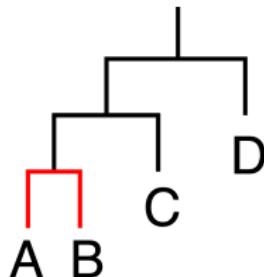
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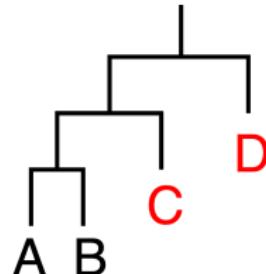
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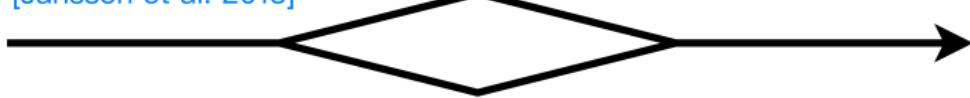
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## Previous Works

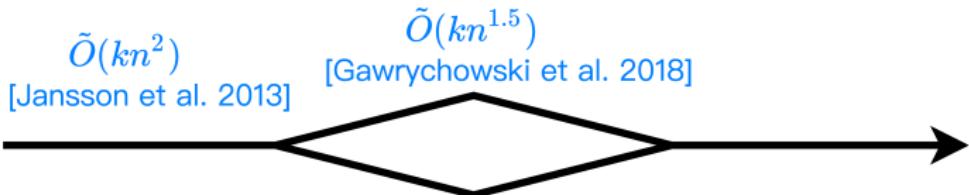
$\tilde{O}(kn^2)$

[Jansson et al. 2013]



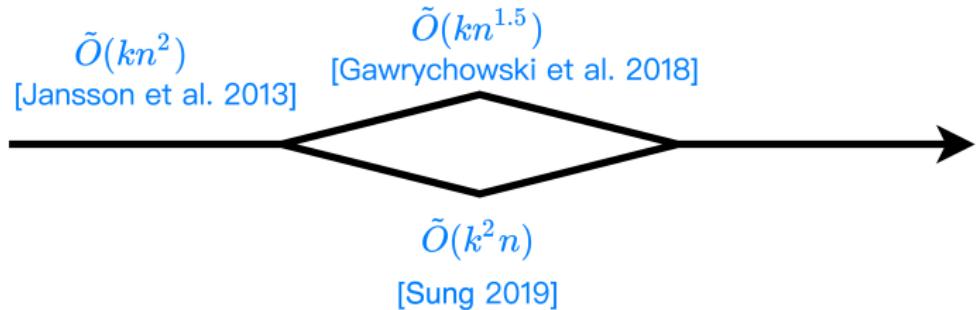
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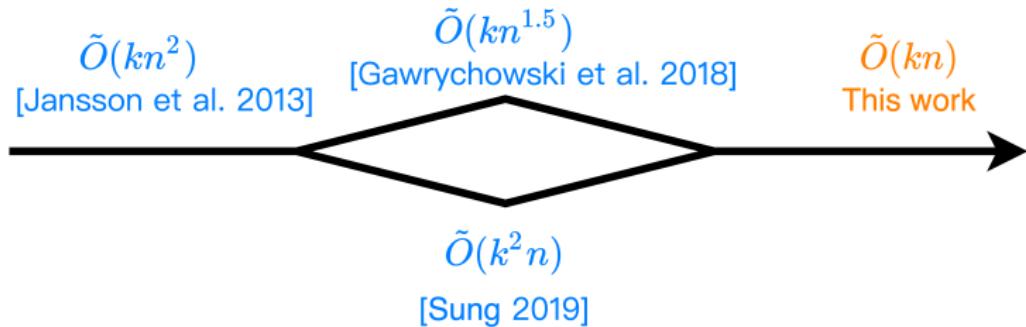
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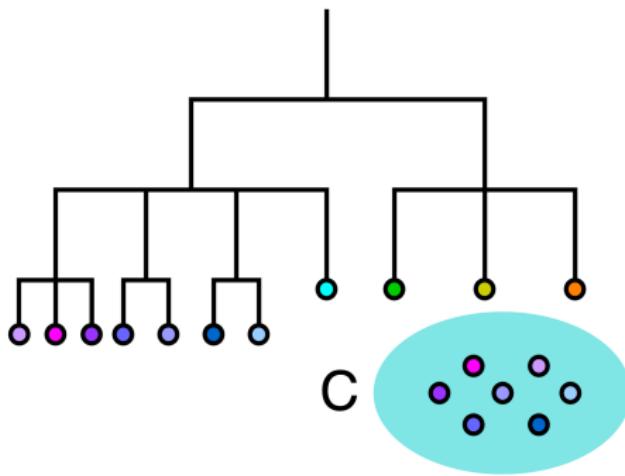
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- ▶ Handle first part within  $\tilde{O}(kn)$  time is simple.
- ▶ The hard part is to determine whether each cluster is consistent with our current consensus tree.

# Characterization of consistency

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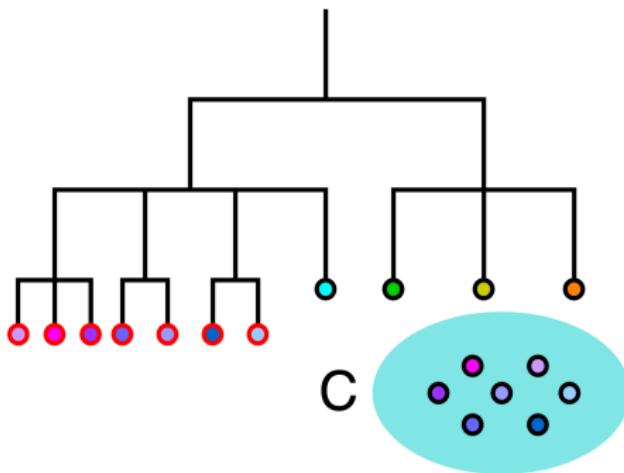
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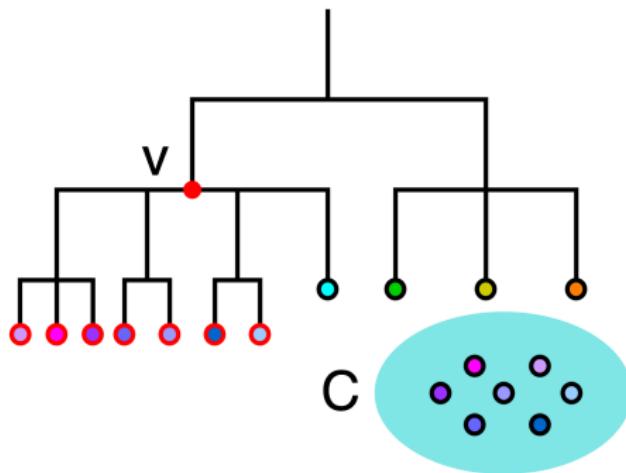
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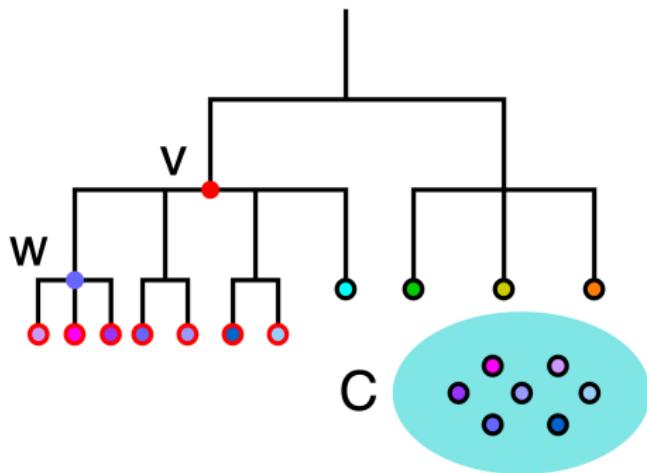
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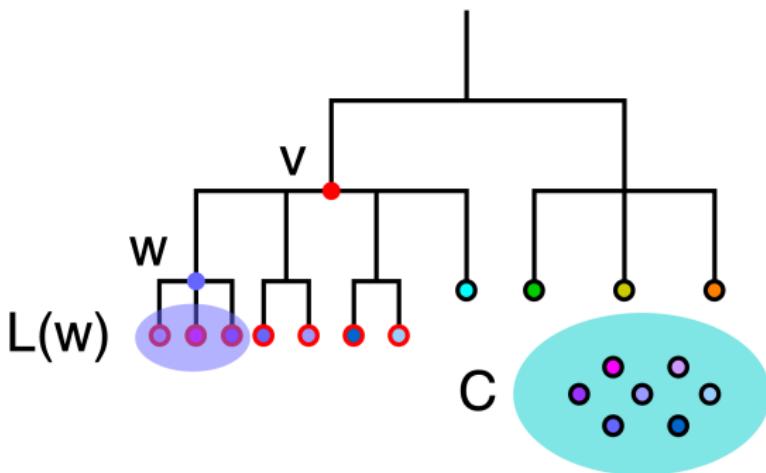
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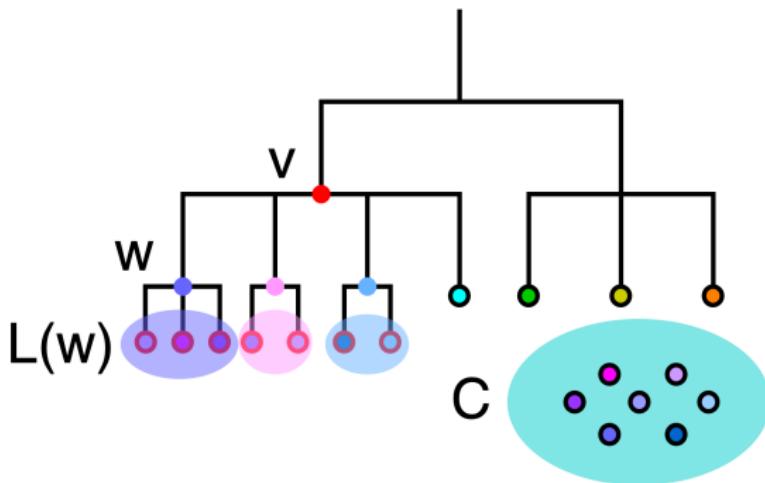


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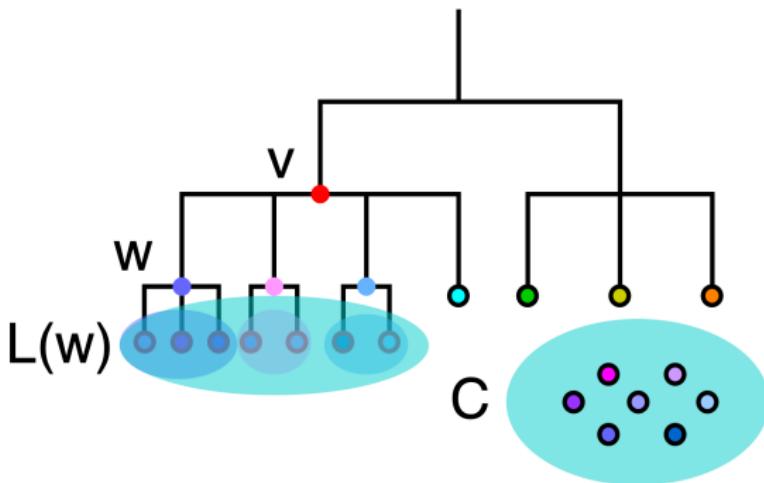


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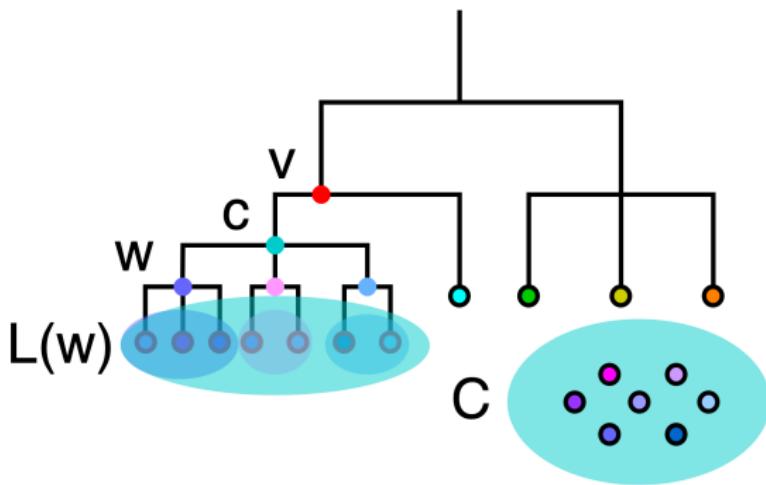


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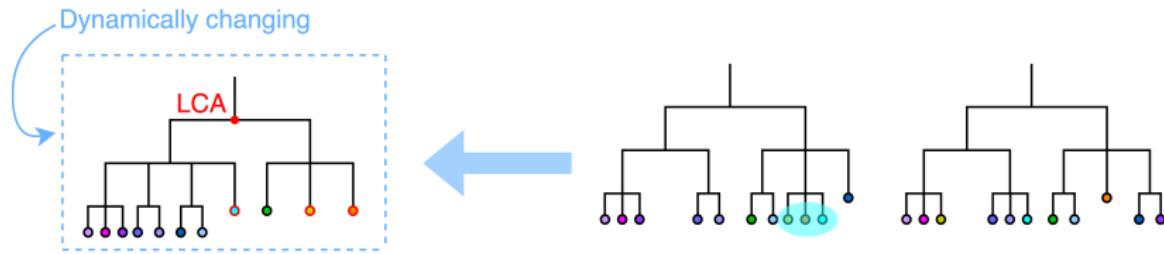
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  2. If consistent, insert a new node to the consensus tree.

## Main difficulty

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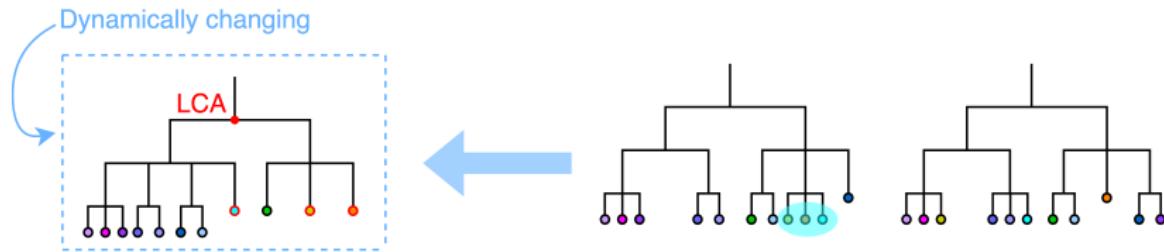
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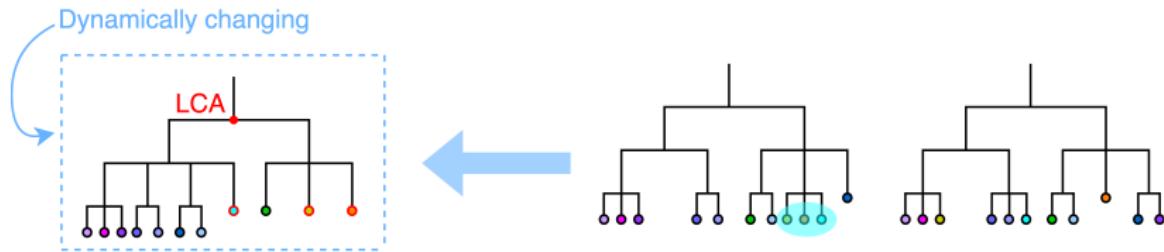
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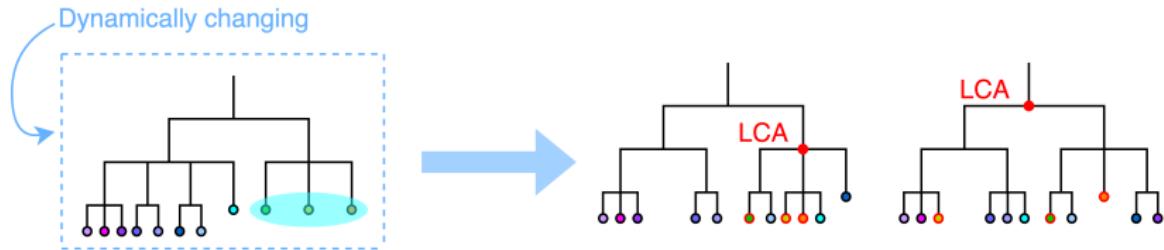
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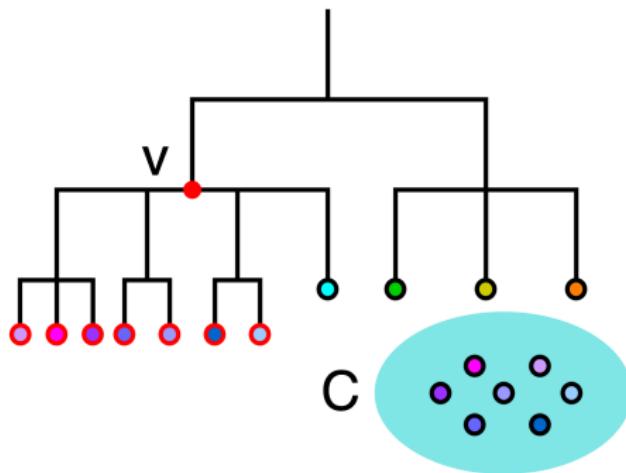


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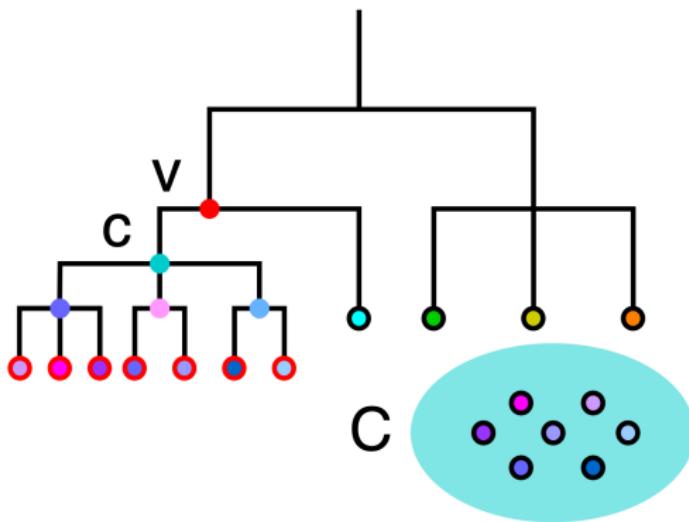


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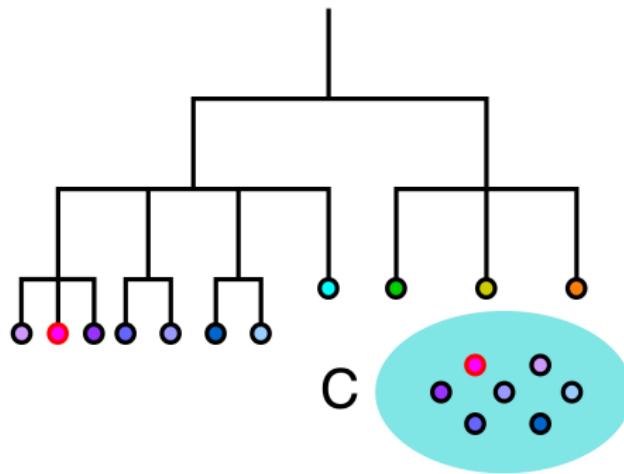


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Let  $v$  be the deepest ancestor of a leaf  $x_0 \in C$  s.t.  $L(v) \not\subseteq C$  and  $w$  be a child of  $v$ .  $L(w)$  is defined as the cluster of all species in its subtree.

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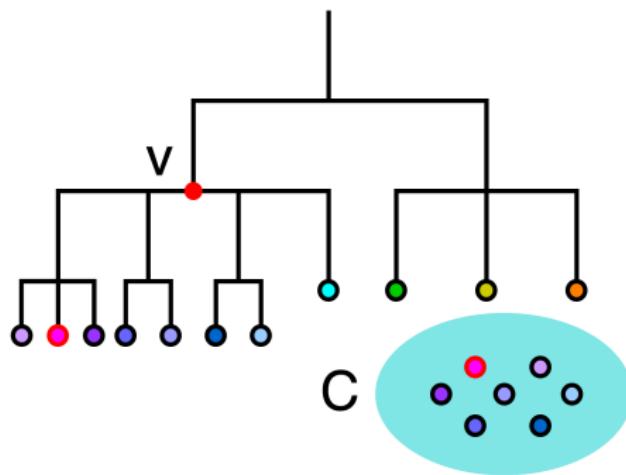


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Let  $v$  be the deepest ancestor of a leaf  $x_0 \in C$  s.t.  $L(v) \not\subseteq C$  and  $w$  be a child of  $v$ .  $L(w)$  is defined as the cluster of all species in its subtree.

$C$  is consistent with the consensus tree if and only if it is the union of several such  $L(w)$ .

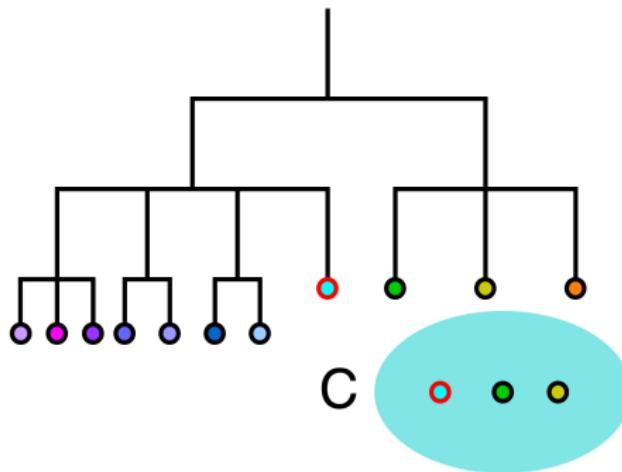


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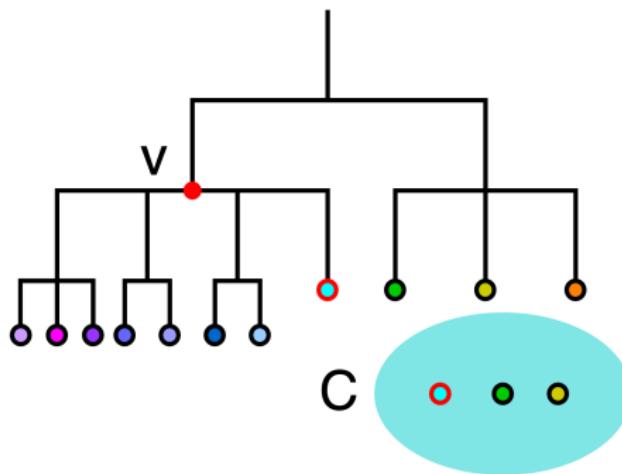


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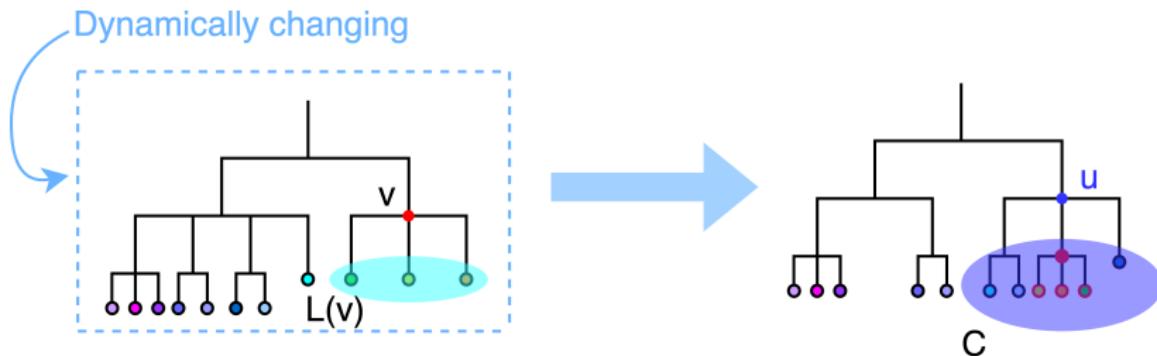
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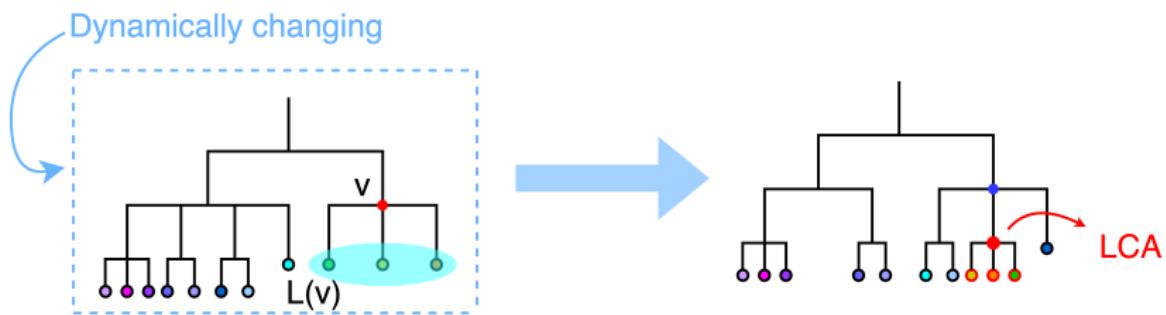
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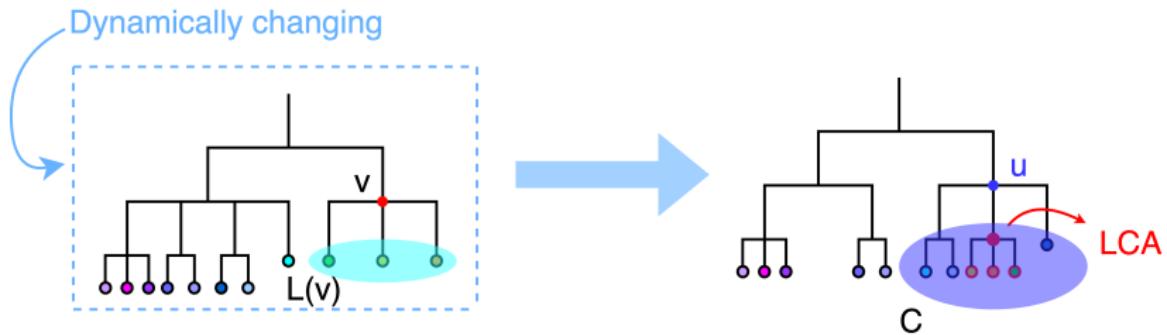
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Suppose  $C$  is  $L(u)$  of inner node  $u$  on input phylogenetic tree  $T_i$ .  
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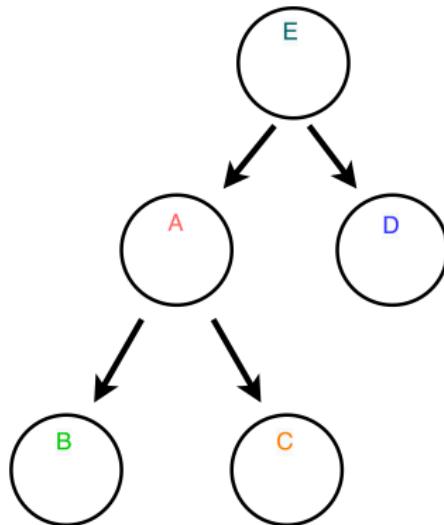
- ▶ To find deepest such ancestor we can binary search the path from  $x_0$  to root.
- ▶ As a result, the modified characterization can be implemented by maintaining LCAs of clusters in the dynamic tree on  $k$  static trees.

# BST

- ▶ Given a dynamic set  $S$  of nodes on static tree  $T_i$ , how do we support dynamic addition, deletion, and query  $LCA(S)$ ?

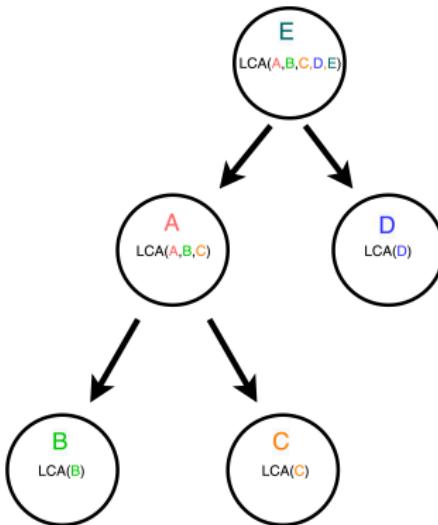
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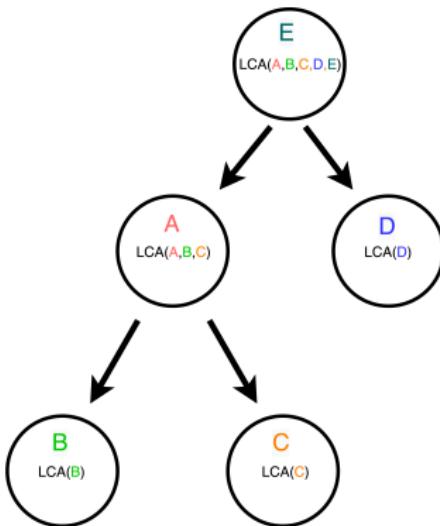
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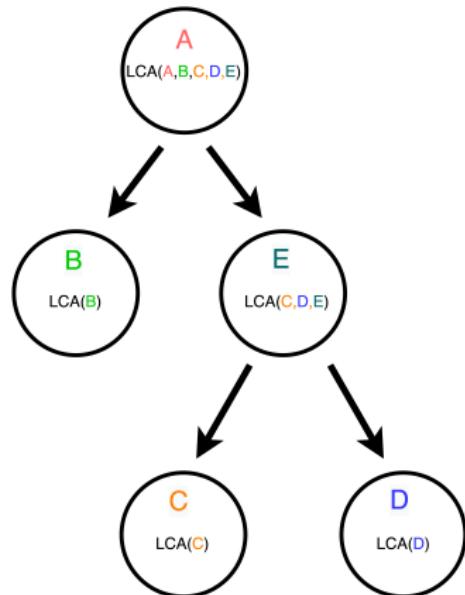
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- ▶ When the children of a node changes, we recompute the LCA of its two children.

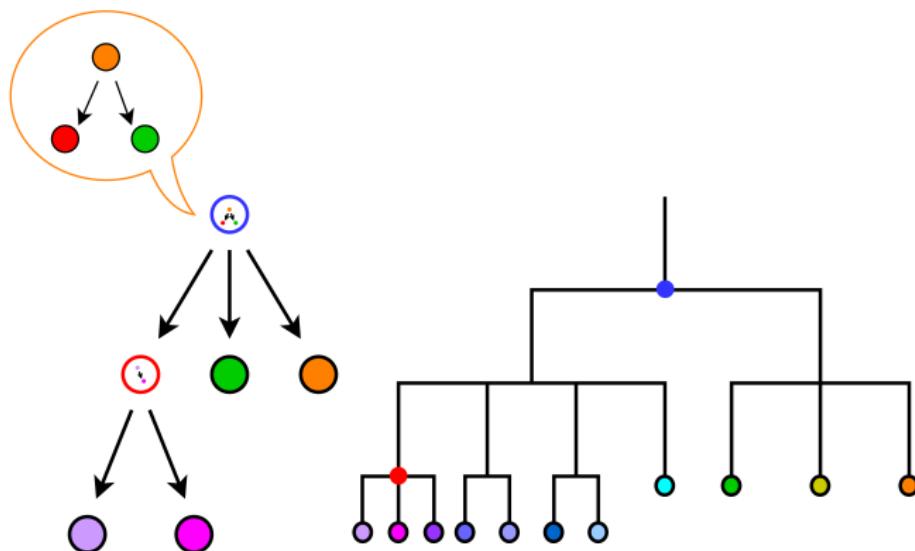


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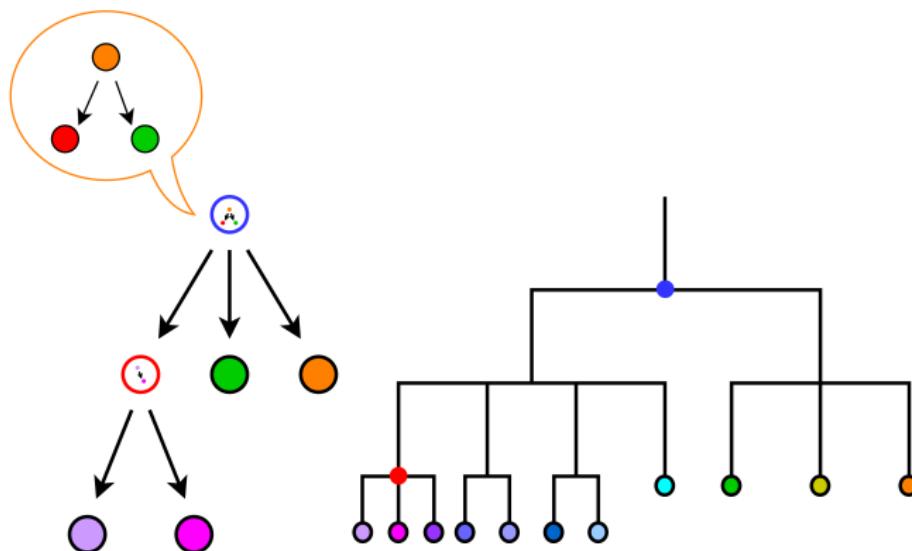
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  - ▶ Each node of the BST is the LCA of one of its children.

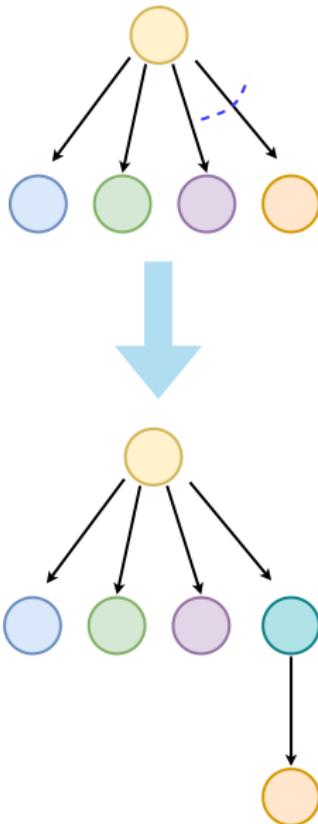


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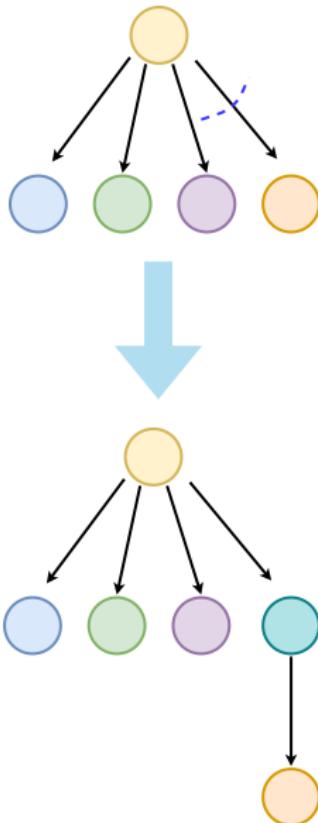
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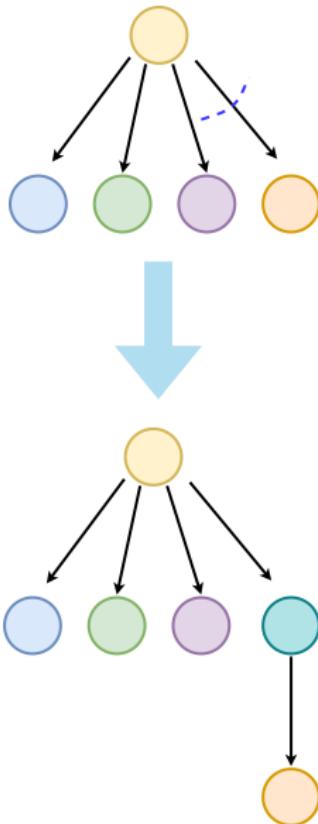
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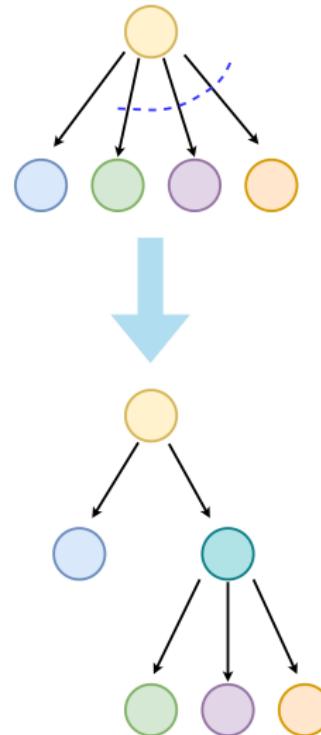
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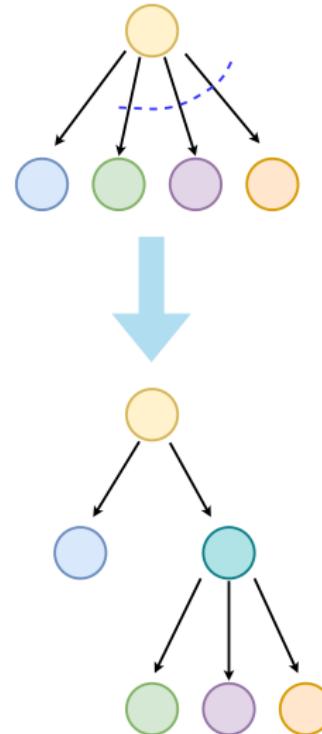
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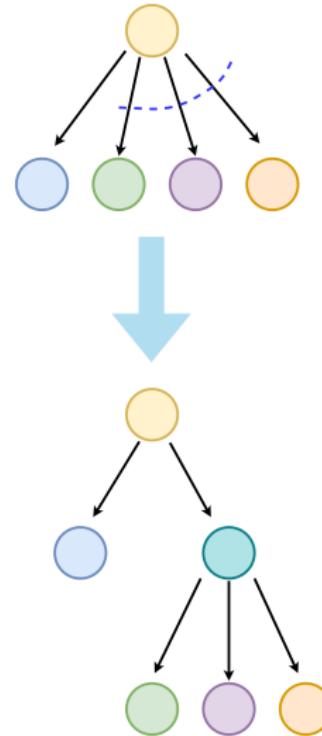
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- ▶ Since we always enumerate the smaller part, in total  $O(kn \log n)$  deletions in BSTs.



# Q & A

Questions?

Thank you!