A Faster Construction of Greedy Consensus Trees

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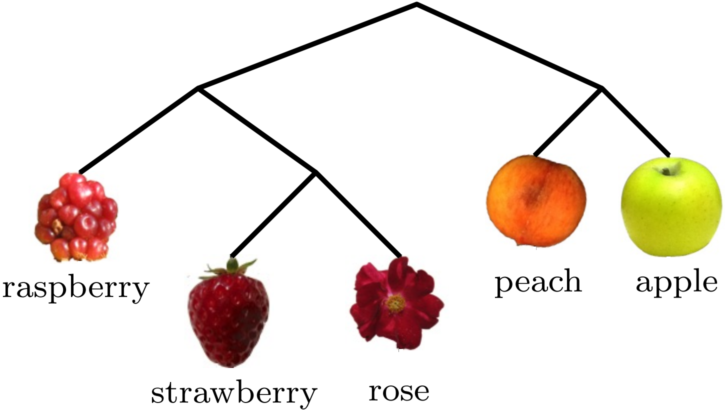
Slides by Paweł Gawrychowski

Phylogenetic trees



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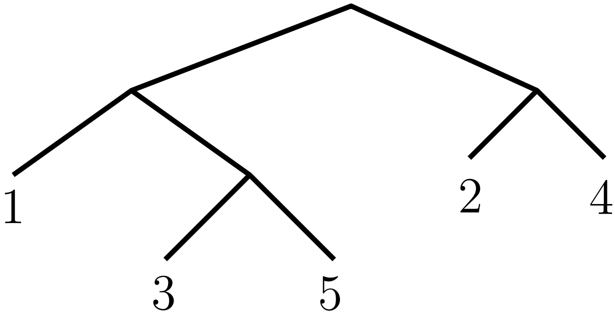

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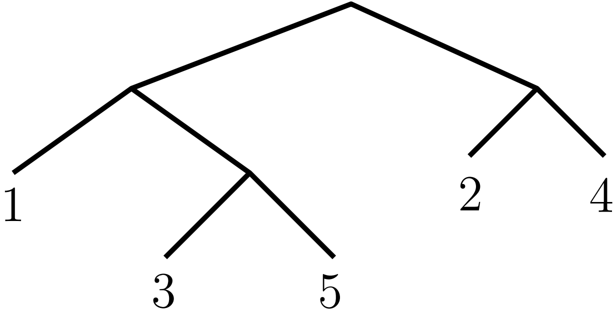

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2. No unary nodes, but the degrees are unbounded.
3. Each leaf correspond to a species and has a distinct label from $[n]$.

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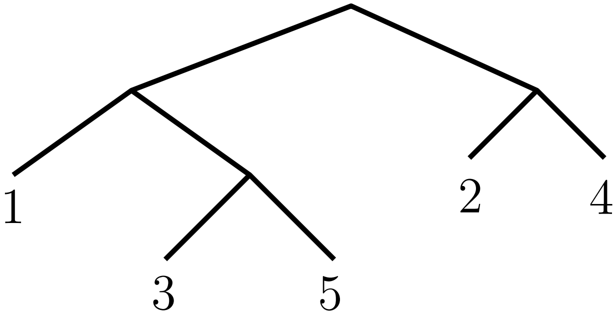

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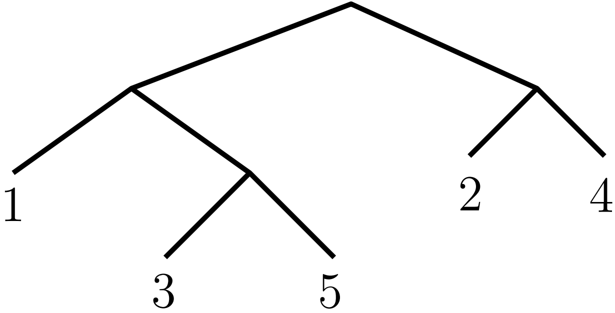

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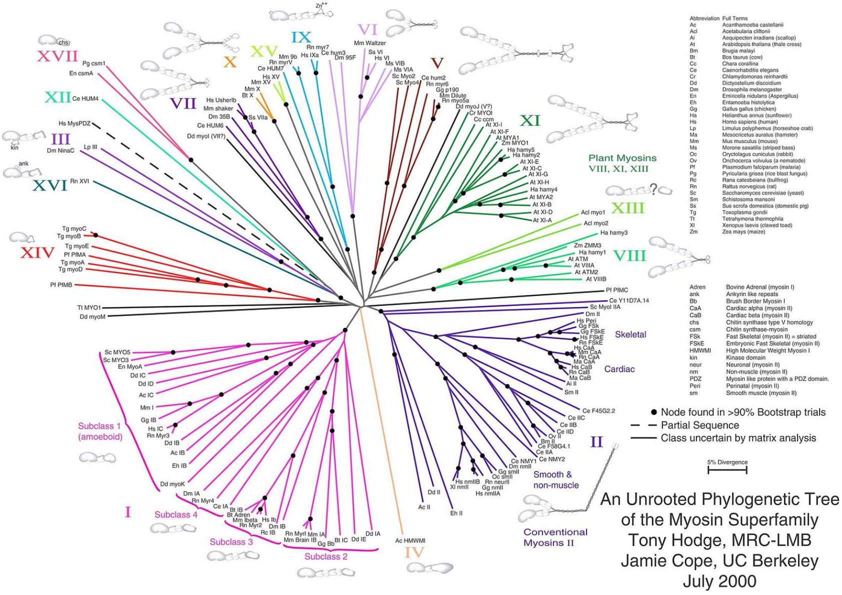
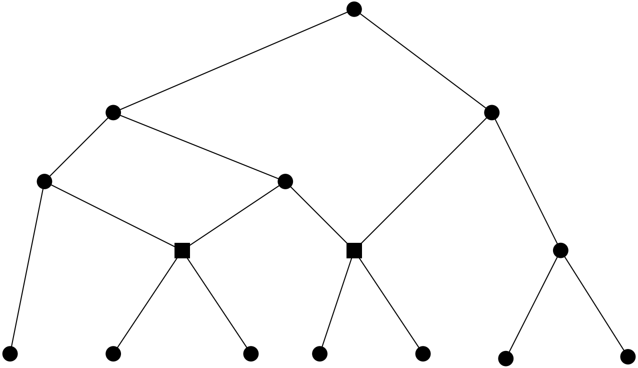
Not in this talk: unrooted phylogenetic trees



Not in this talk: phylogenetic networks



Motivation

By applying different reconstruction methods or using different data sources we might obtain multiple phylogenetic trees. How to combine them into a single tree?

For any node of T_1 or T_2, there is a node of the combined tree with exactly the same set of leaf labels.

In practice, the set of leaf labels in a tree might be a proper subset of $[n]$, but we assume that it is exactly $[n]$ as in the previous work.

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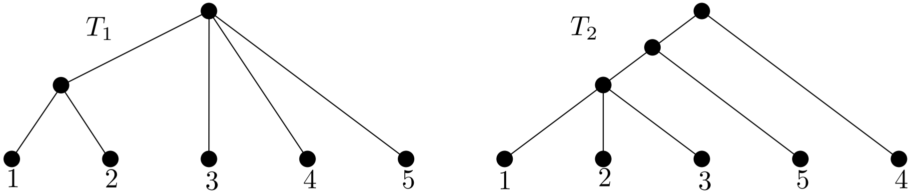

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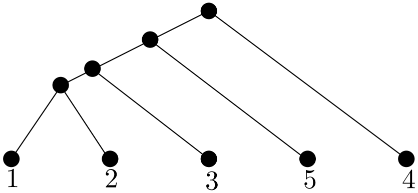

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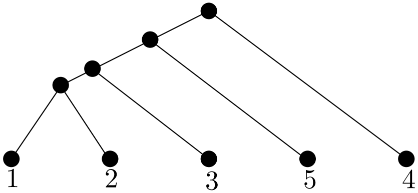

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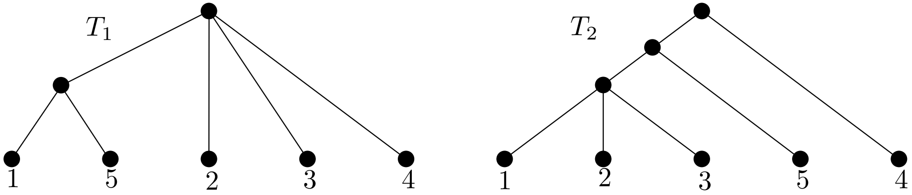

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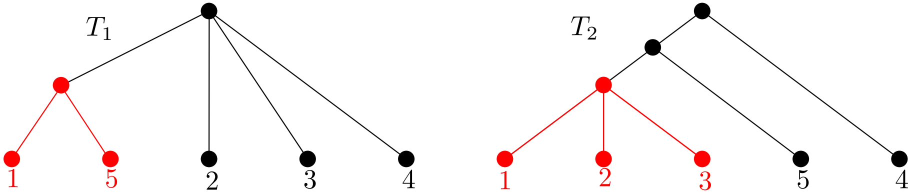

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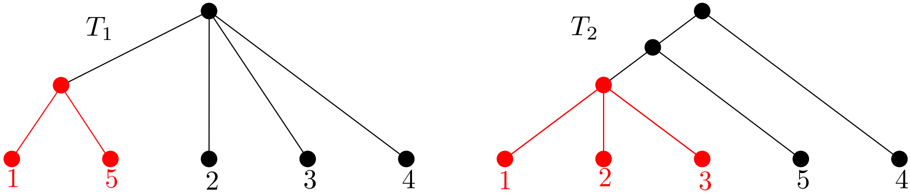

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Notation

Input: k trees $T_1, \ldots, T_k$ on n leaves with distinct labels from $[n]$.
Output: a single tree T_r on n leaves with distinct labels from $[n]$.

Cluster

$\mathrm{L}(u)$ = labels of all leaves in the subtree rooted at u

$$\mathrm{L}(u) = \{1, 2\}$$

We identify a tree with the set of its clusters.

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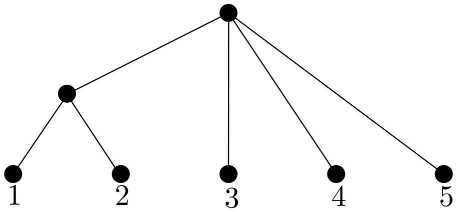

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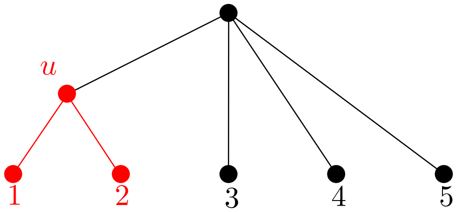

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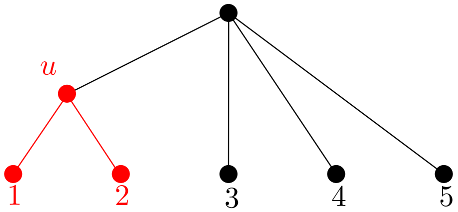

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Different methods of combining trees

1. Majority consensus tree,
2. loose consensus tree,
3. frequency difference consensus tree,
4. greedy consensus tree.

and Adam's consensus tree, strict consensus tree, asymmetric median consensus tree...

Compatible clusters

C_1 and C_2 are compatible if $C_1 \cap C_2 = \emptyset$, $C_1 \subseteq C_2$ or $C_2 \subseteq C_1$.

$\{1, 2\}$ and $\{3, 4\}$ are compatible, and so are $\{1, 2, 3\}$ and $\{2, 3\}$, but $\{1, 2\}$ and $\{2, 3\}$ are not.

A collection of clusters corresponds to a tree iff they are pairwise compatible.

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A collection of clusters corresponds to a tree iff they are pairwise compatible.

Majority consensus tree

We choose all clusters that appear in more than $k/2$ of the trees.

For any two chosen clusters C_1 and C_2, there is a tree T_i containing both C_1 and C_2, so they must be compatible.

Hence, chosen clusters correspond to a single tree T_r.

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Loose consensus tree

Compatible cluster

A cluster C is compatible with a tree T if it is compatible with cluster $\mathrm{L}(u)$, for every $u \in T$.

We choose all clusters that appear in at least one tree and are compatible with all trees. By definition, chosen clusters correspond to a single tree T_r.

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Frequency difference consensus tree

Frequency

The frequency of a cluster C is the number of trees T_i such that $C = \mathrm{L}(u)$ for some $u \in T_i$.

For every cluster $\mathrm{L}(u)$, where $u \in T_i$ for some i, we choose $\mathrm{L}(u)$ if its frequency is strictly larger than the frequency of any cluster $\mathrm{L}(v)$, where $v \in T_j$ for some j, such that $\mathrm{L}(u)$ is not compatible with $\mathrm{L}(v)$.

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Greedy consensus tree

1. We consider all clusters that appear in at least one tree in decreasing order of their frequencies.
2. Consider one such cluster $\mathrm{L}(u)$, where $u \in T_i$ for some i. If $\mathrm{L}(u)$ is consistent with $\mathcal{C}$, add $\mathrm{L}(u)$ to $\mathcal{C}$.
3. Return the tree corresponding to $\mathcal{C}$.

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3. Return the tree corresponding to $\mathcal{C}$.

Known bounds

Majority	$\mathcal{O}(k \cdot n)$	Jansson, Shen, Sung JACM 2016
Loose	$\mathcal{O}(k \cdot n)$	Jansson, Shen, Sung JACM 2016
Frequency	$\tilde{\mathcal{O}}(\min\{n, k\} \cdot k \cdot n)$	Jansson et al. TCBB 2016
Greedy	$\mathcal{O}(k \cdot n^2)$	Jansson, Shen, Sung JACM 2016
Frequency	$\tilde{\mathcal{O}}(k \cdot n)$	This paper
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Frequency difference consensus tree

Previous algorithm:

1. Compute the frequency of every cluster $\mathrm{L}(u)$, where $u \in T_i$ for some i, in $\mathcal{O}(\min\{n,k\} \cdot k \cdot n)$ time.
2. Given the frequency of every cluster, construct the frequency difference consensus tree in additional $\mathcal{O}(k \cdot n \log^2 n)$ time.

Only need to compute identifiers $\mathrm{id}(u)$, where $u \in T_i$ for some i, such that $\mathrm{id}(u) = \mathrm{id}(v)$, where $u \in T_i$, $v \in T_j$ for some i and j, iff $\mathrm{L}(u) = \mathrm{L}(v)$.

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Computing identifiers

We proceed in phases, in the ℓ-th phase assigning ids to all nodes u with $|\mathrm{L}(u)| \in [2^{\ell}, 2^{\ell+1})$, where $u \in T_i$ for some i.

Total number of artificial nodes over all phases = $\mathcal{O}(k \cdot n \log n)$.

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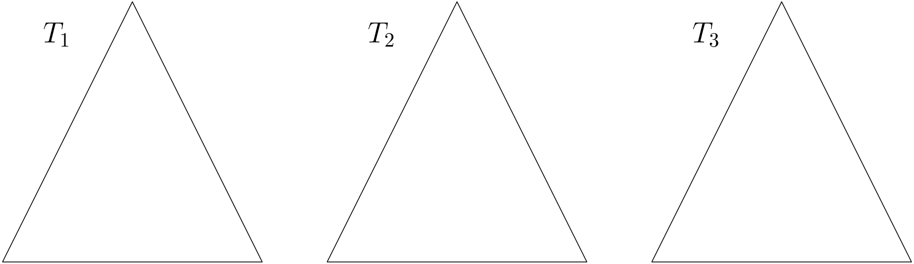

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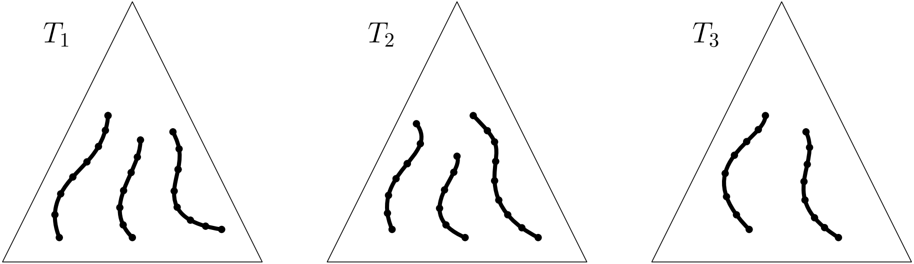

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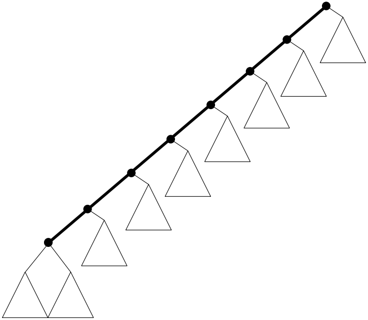

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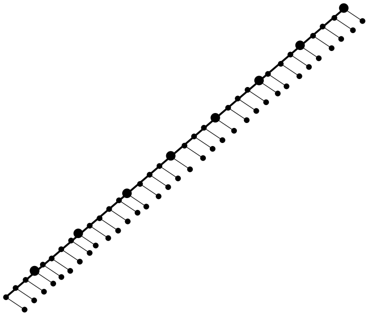

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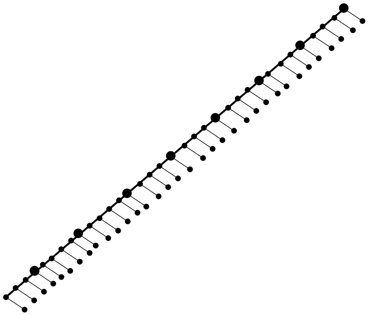

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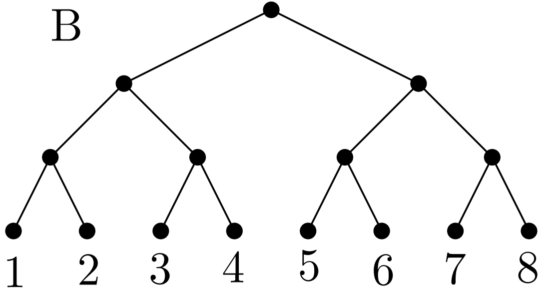

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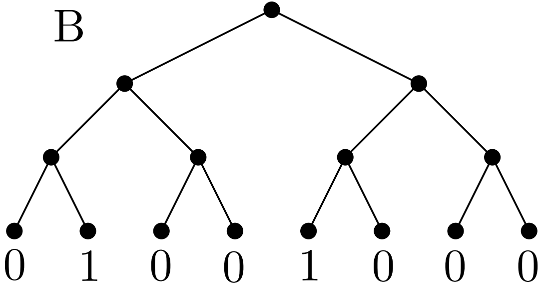

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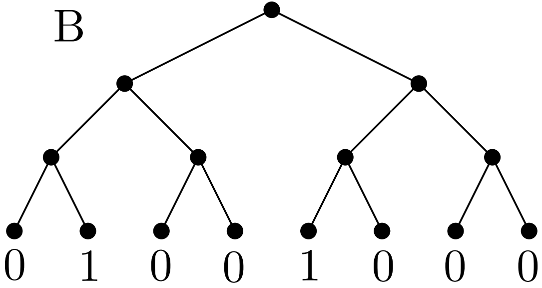

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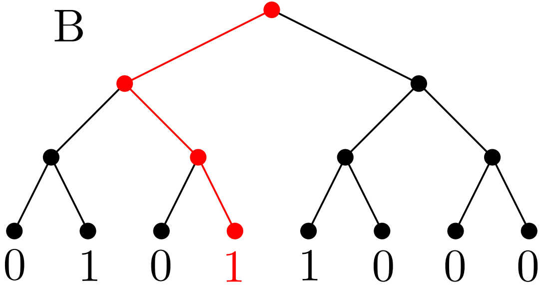

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1. B is implemented persistently, so after an insert we need to recompute only $\log n$ identifiers.
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3. This would give us insertions $\mathcal{O}(\log^2 n)$, so $\mathcal{O}(k \cdot n \log^3 n)$ overall.
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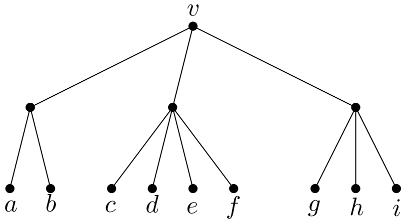
Greedy consensus tree

We consider the clusters $\mathrm{L}(u)$, where $u \in T_i$ for some i in the appropriate order and maintain the current tree T_c. We need to:

1. Efficiently check if $\mathrm{L}(u)$ is compatible with all clusters of T_c,
2. if so update T_c.

Updating T_c

Adding $\{a, b, g, h, i\}$:



1. We always need to add a new child v' to some node v and reconnect some of the children of v to v'.
2. We implement this in time proportional to $\min\{\#\text{ reconnected children}, \#\text{ not reconnected children}\}$.
3. Then, the overall complexity of updating T_c is $O(n \log n)$.

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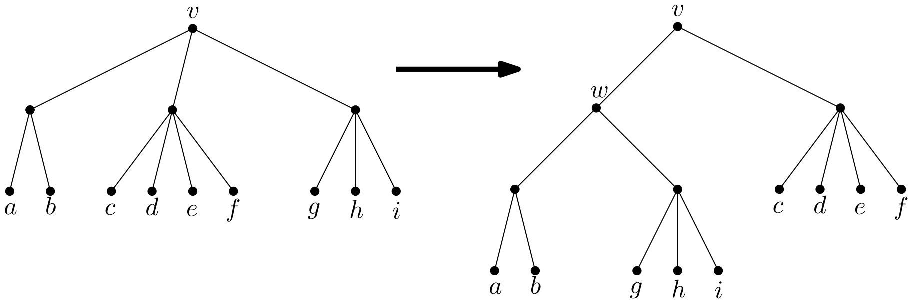

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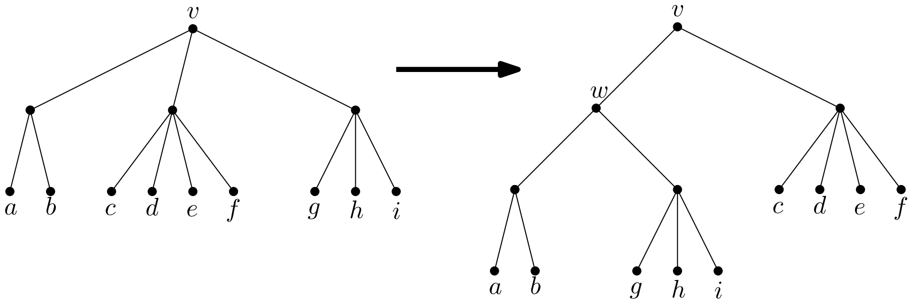

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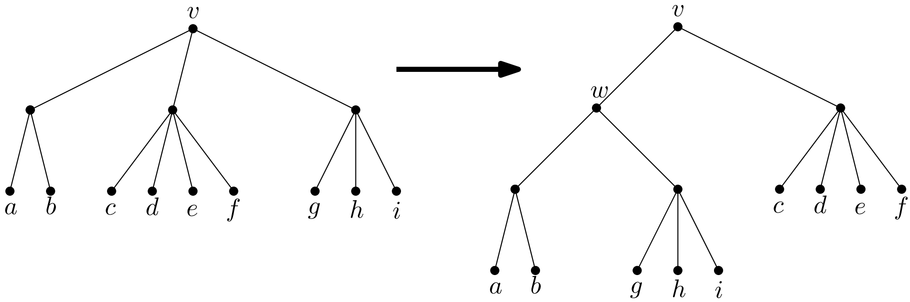

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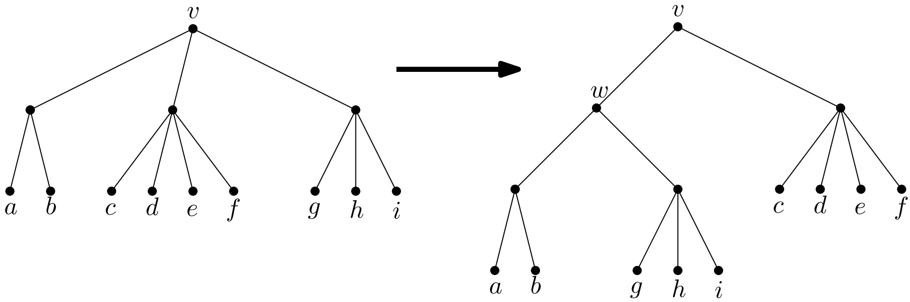

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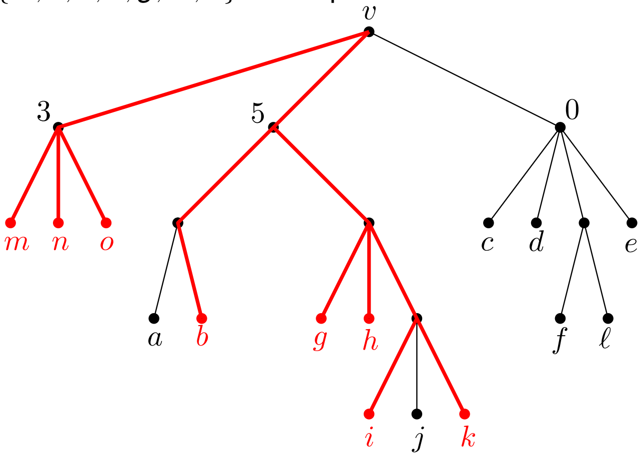

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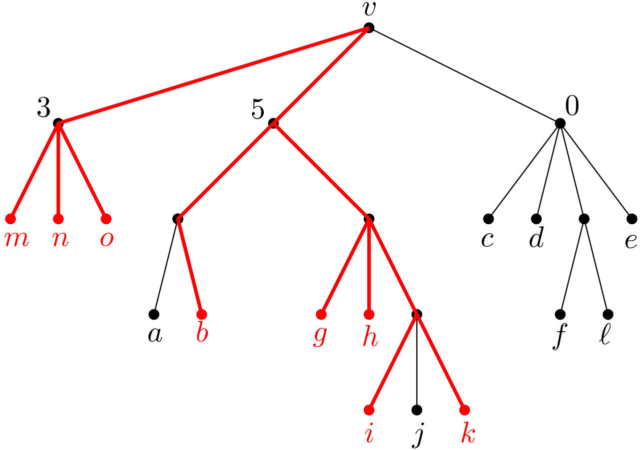

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We apply micro-macro decomposition of every T_i into $\mathcal{O}(n^{0.5})$ micro-trees of size $\mathcal{O}(n^{0.5})$:

We maintain the LCA for all leaves in a subtree of every boundary node. This requires some bookkeeping.

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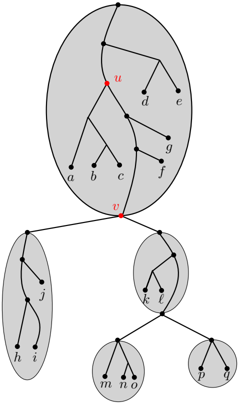

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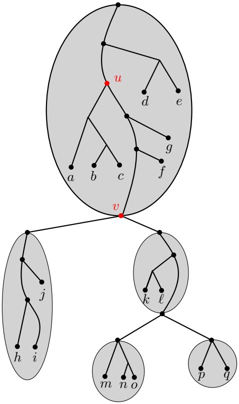

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