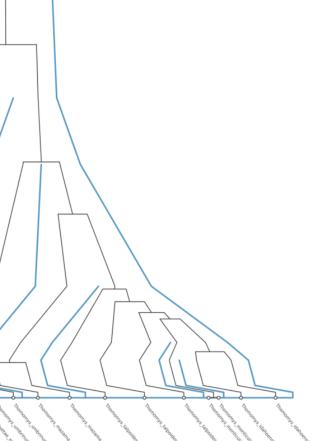
Visualizing Multispecies Coalescent Trees: Drawing Gene Trees Inside Species Trees

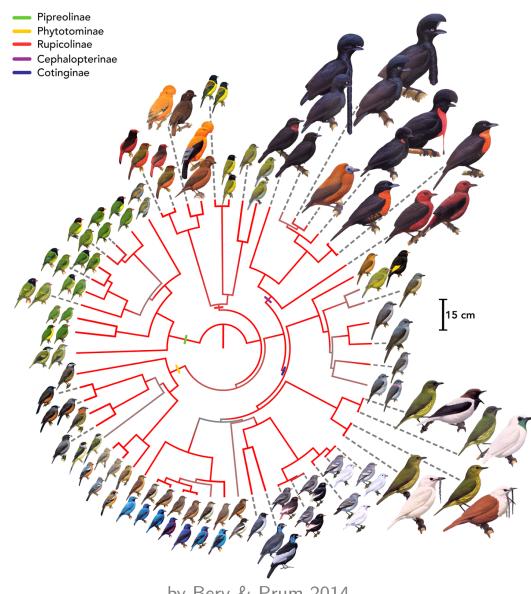
Jonathan Klawitter Felix Klesen Moritz Niederer Alexander Wolff



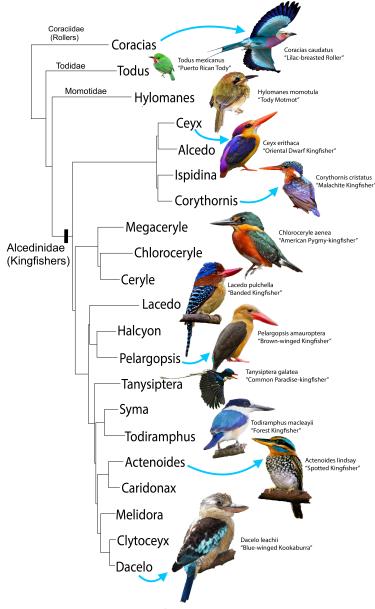
htw saar



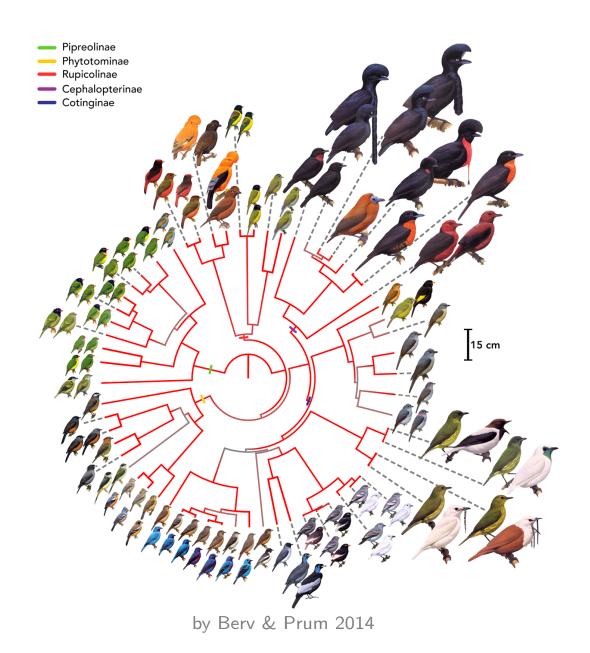




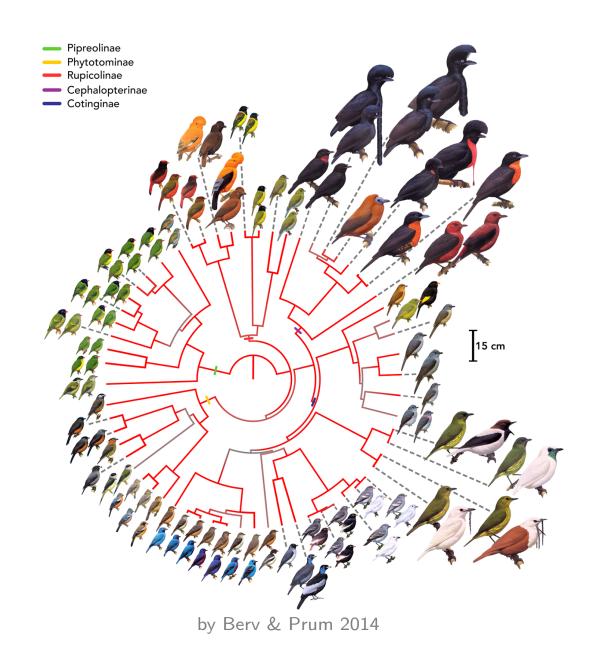
by Berv & Prum 2014



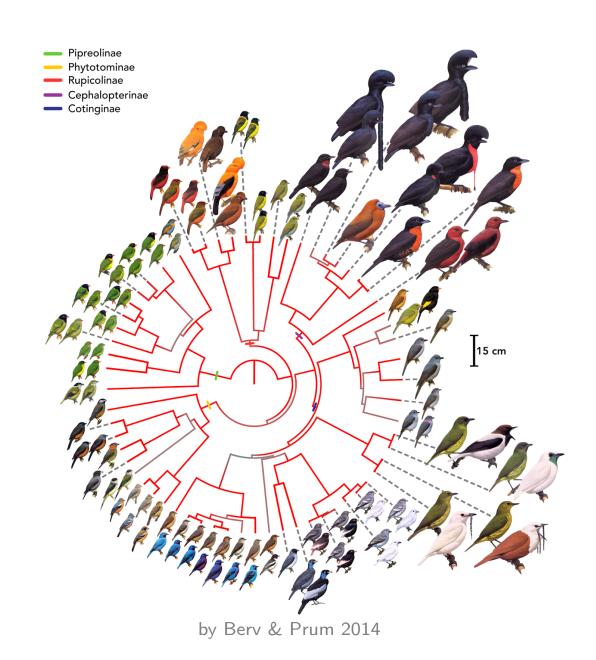
by Jenna McCullough 2016



A phylogenetic tree T is a rooted, binary tree with labelled leaves and vertex heights.



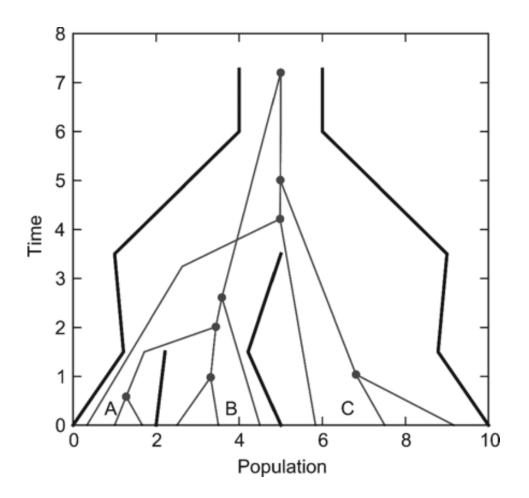
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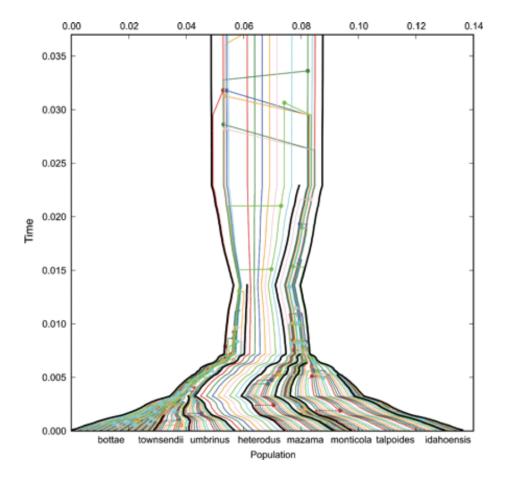


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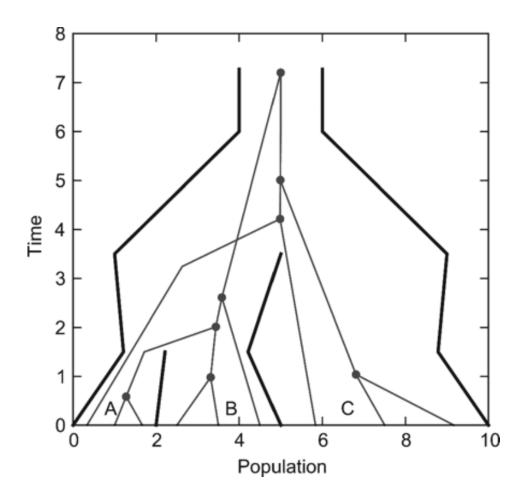
Call T a **species/gene tree** if the leaves represent species/biological sequences.

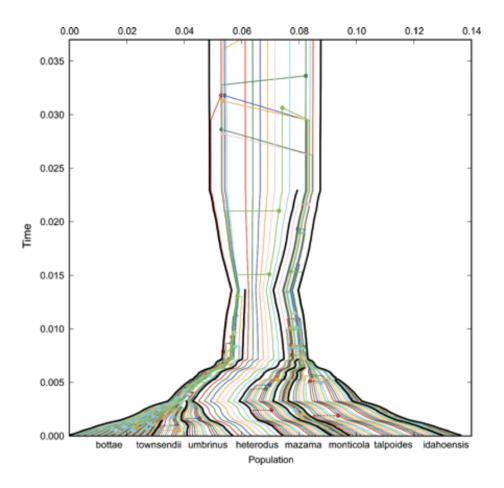
■ In practice, a species tree and its gene trees *differ*.



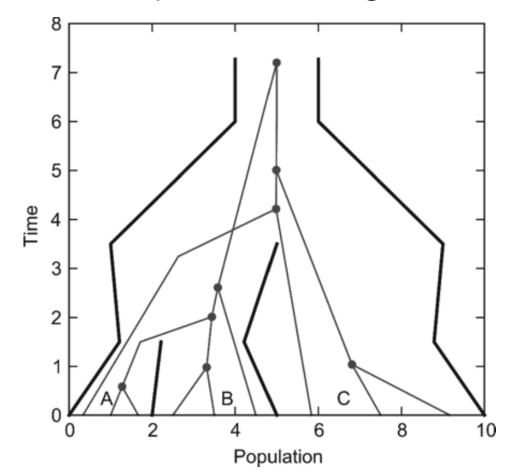


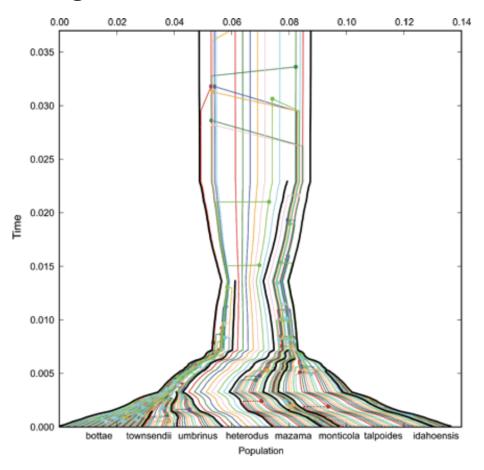
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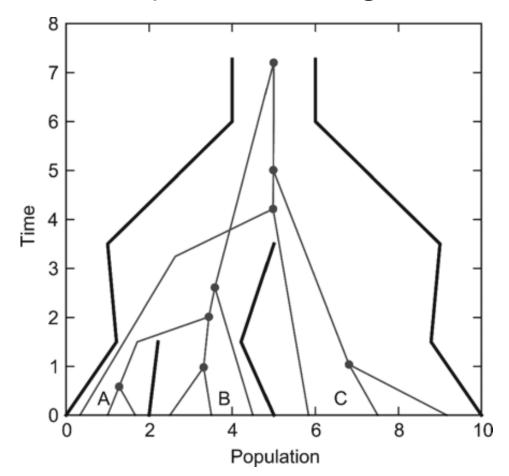


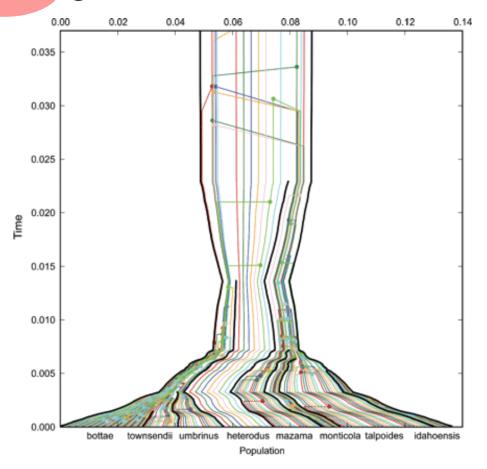
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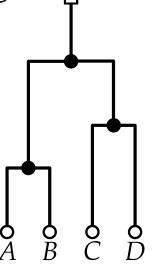
A multispecies coalescent tree $\langle S, T, \varphi \rangle$ consists of

Species tree S

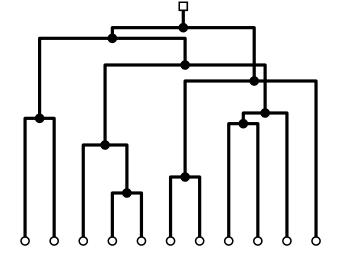
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Species tree S



Gene tree T

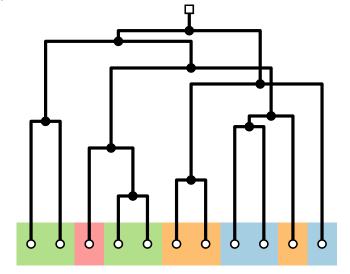


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- \blacksquare a species tree S,
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Species tree S

Gene tree T

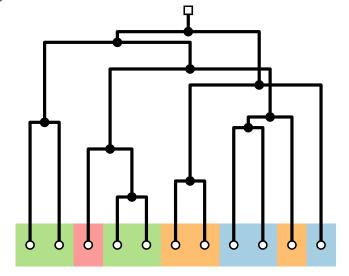


A multispecies coalescent tree $\langle S, T, \varphi \rangle$ consists of

- \blacksquare a species tree S,
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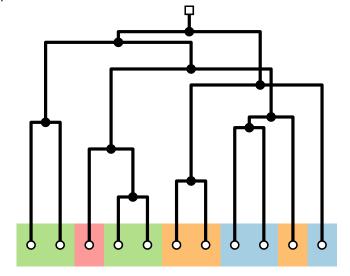
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Additionally:

■ Effective population size — branch widths

Species tree S

Gene tree T



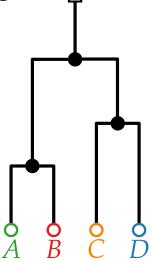
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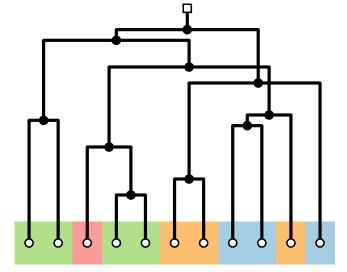
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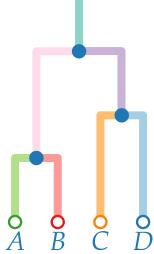
Species tree S



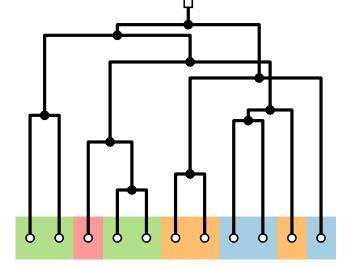
Gene tree T

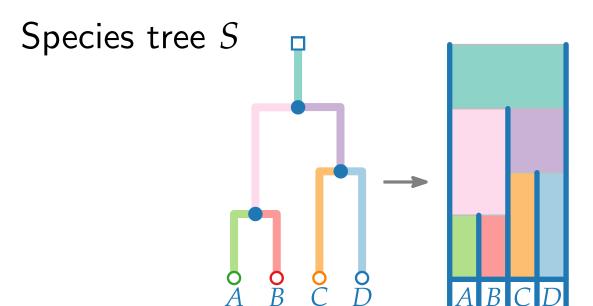


Species tree S

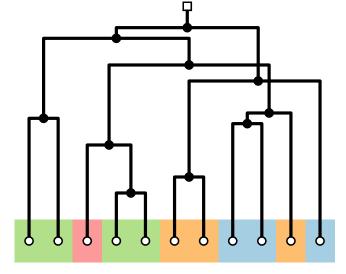


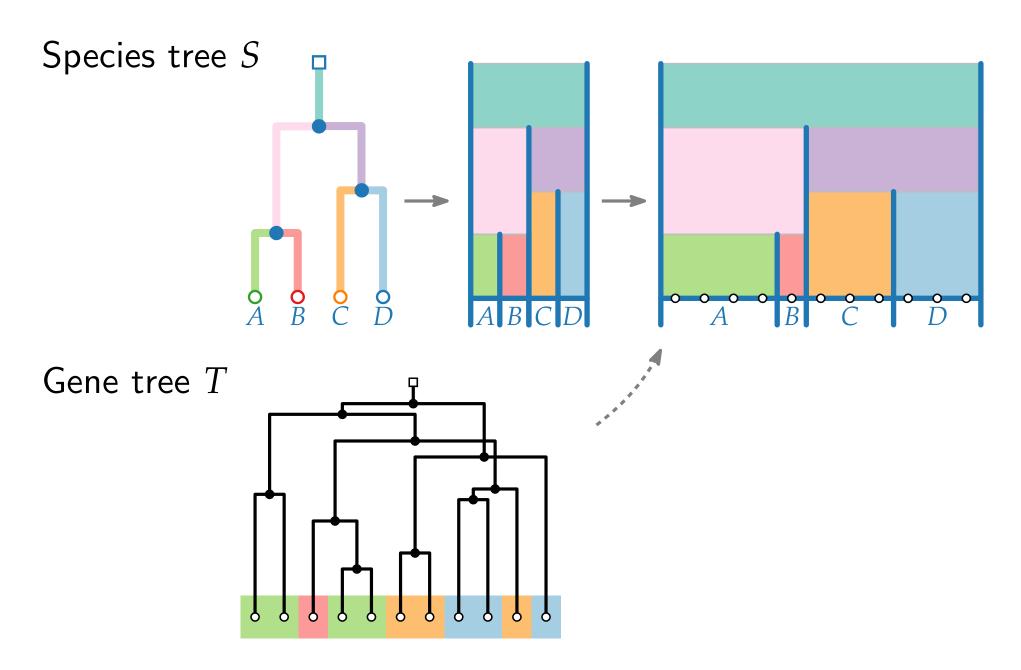
Gene tree T

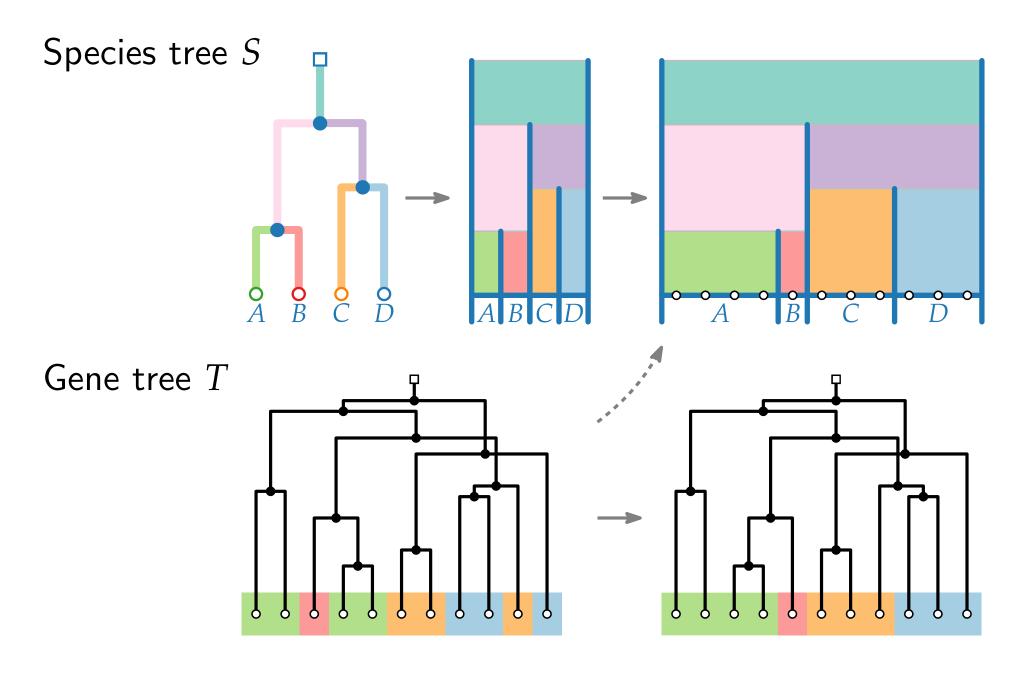


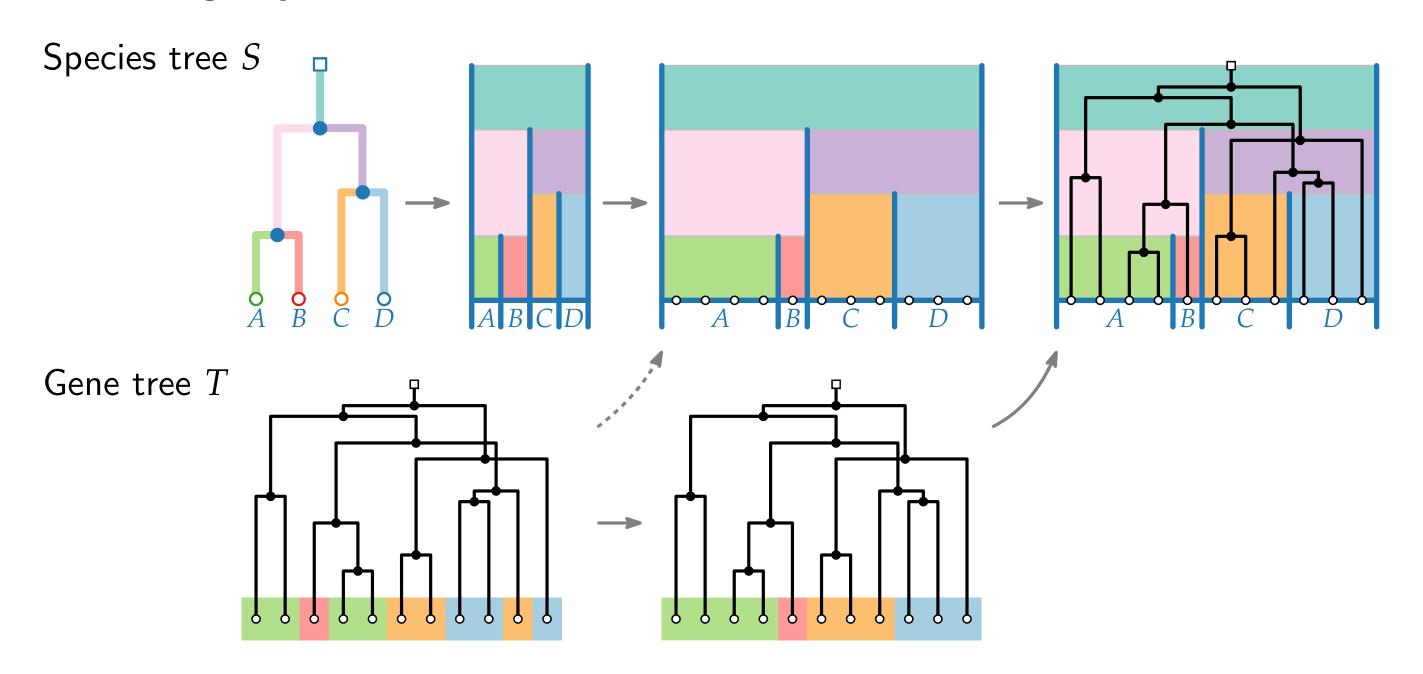


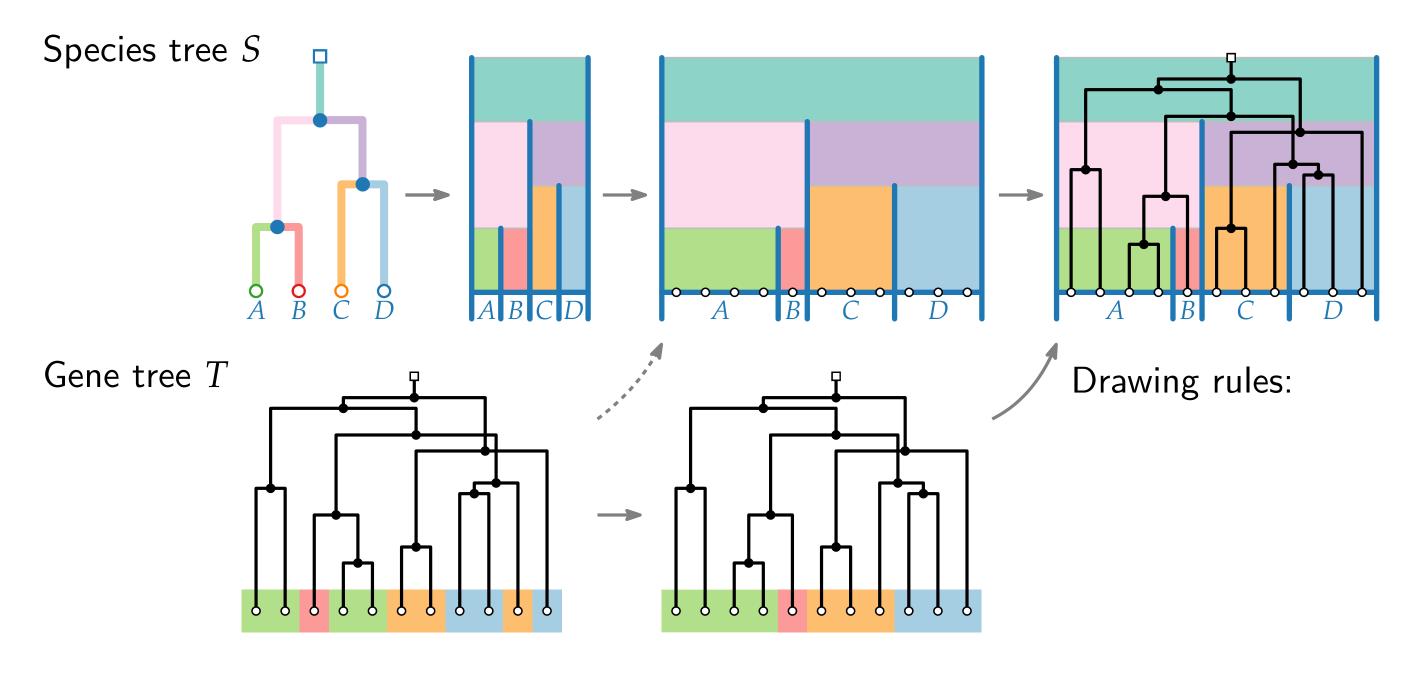
Gene tree T

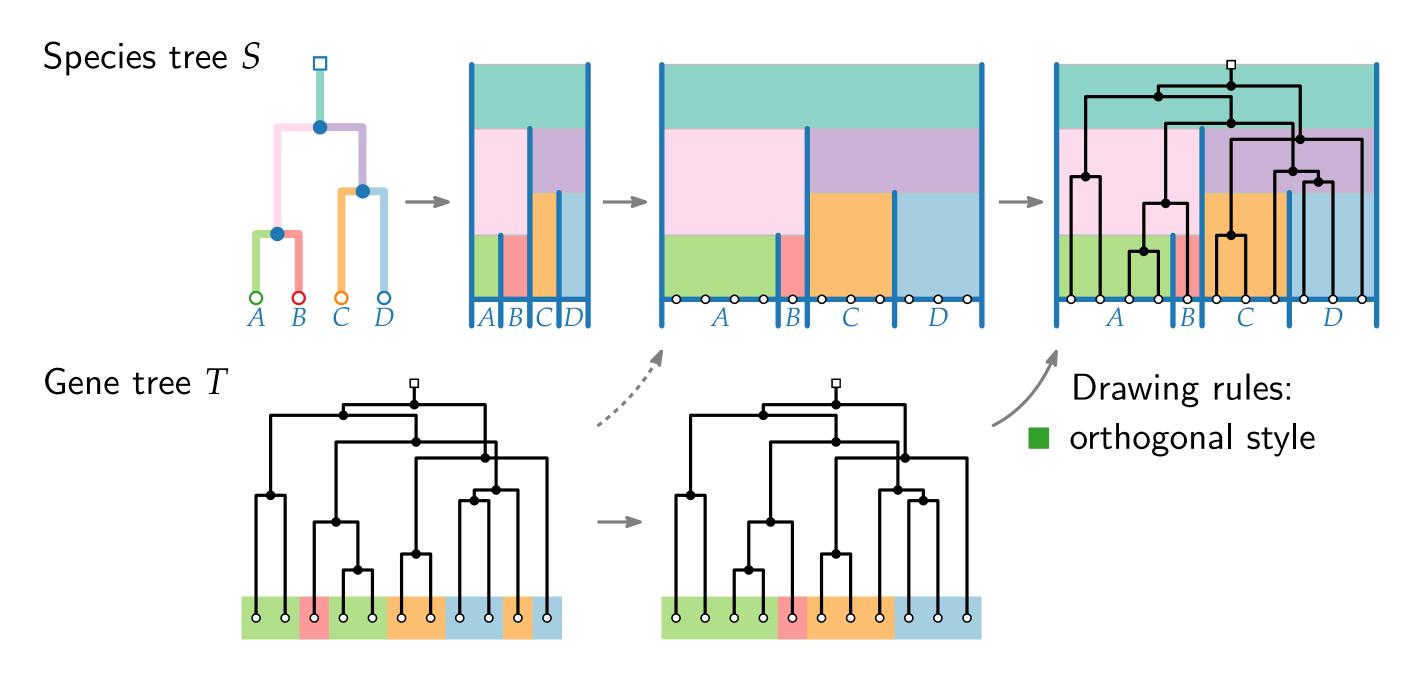


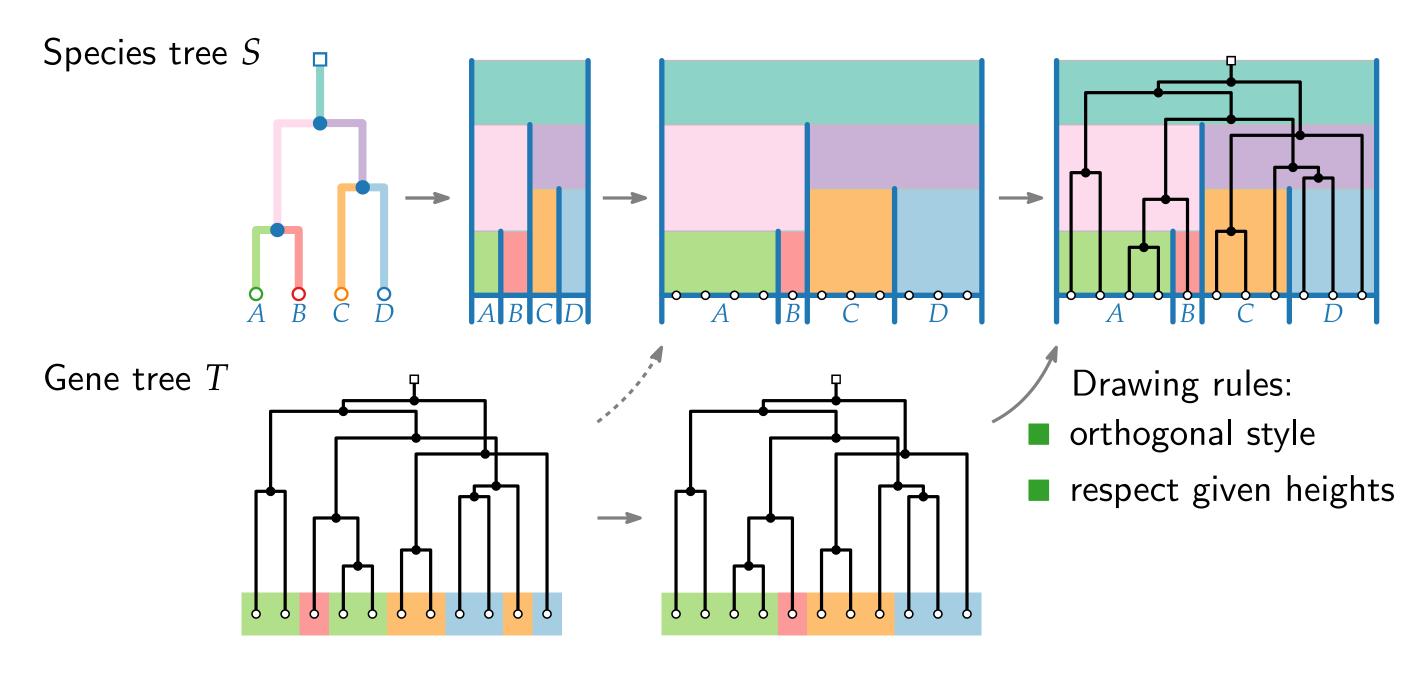


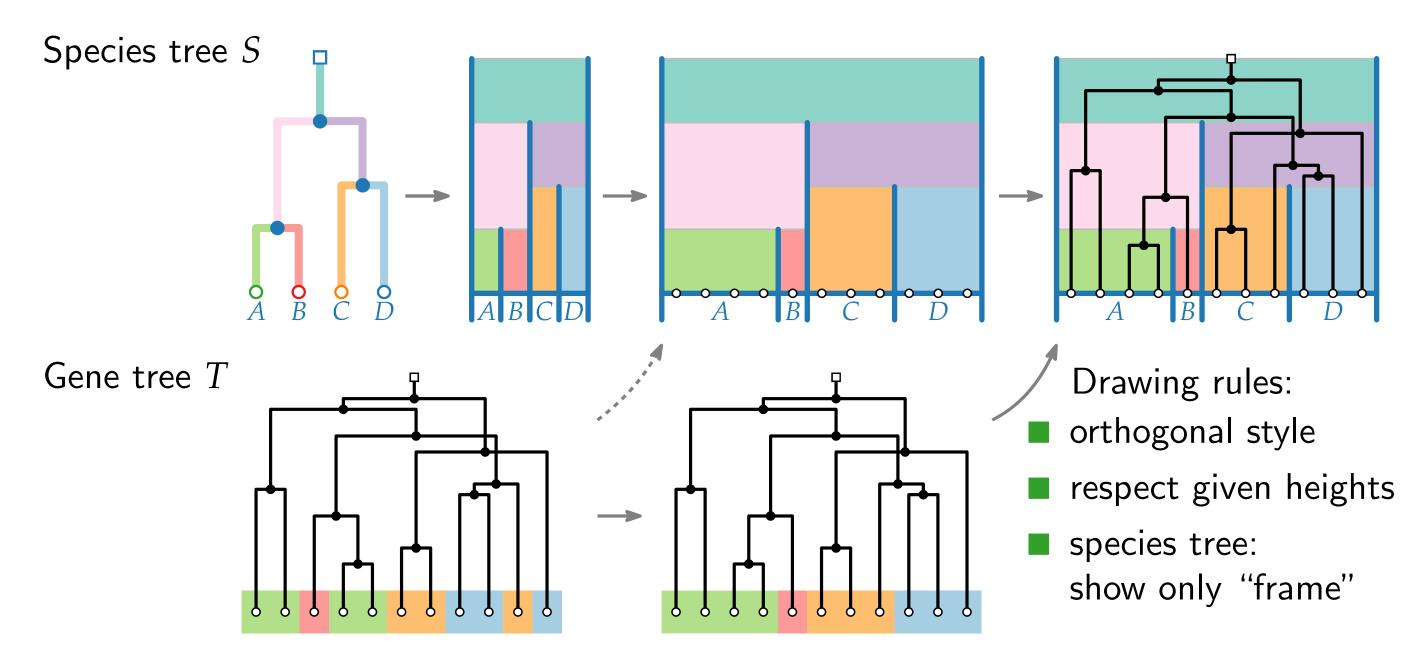


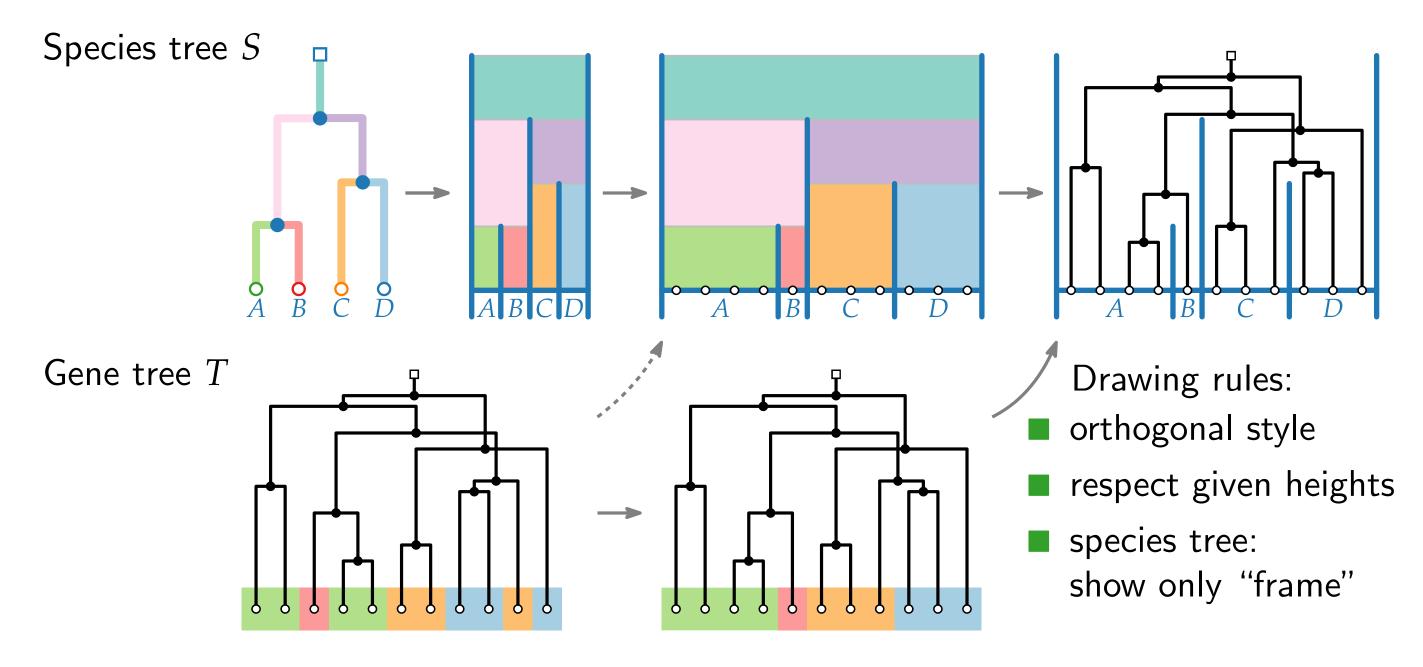


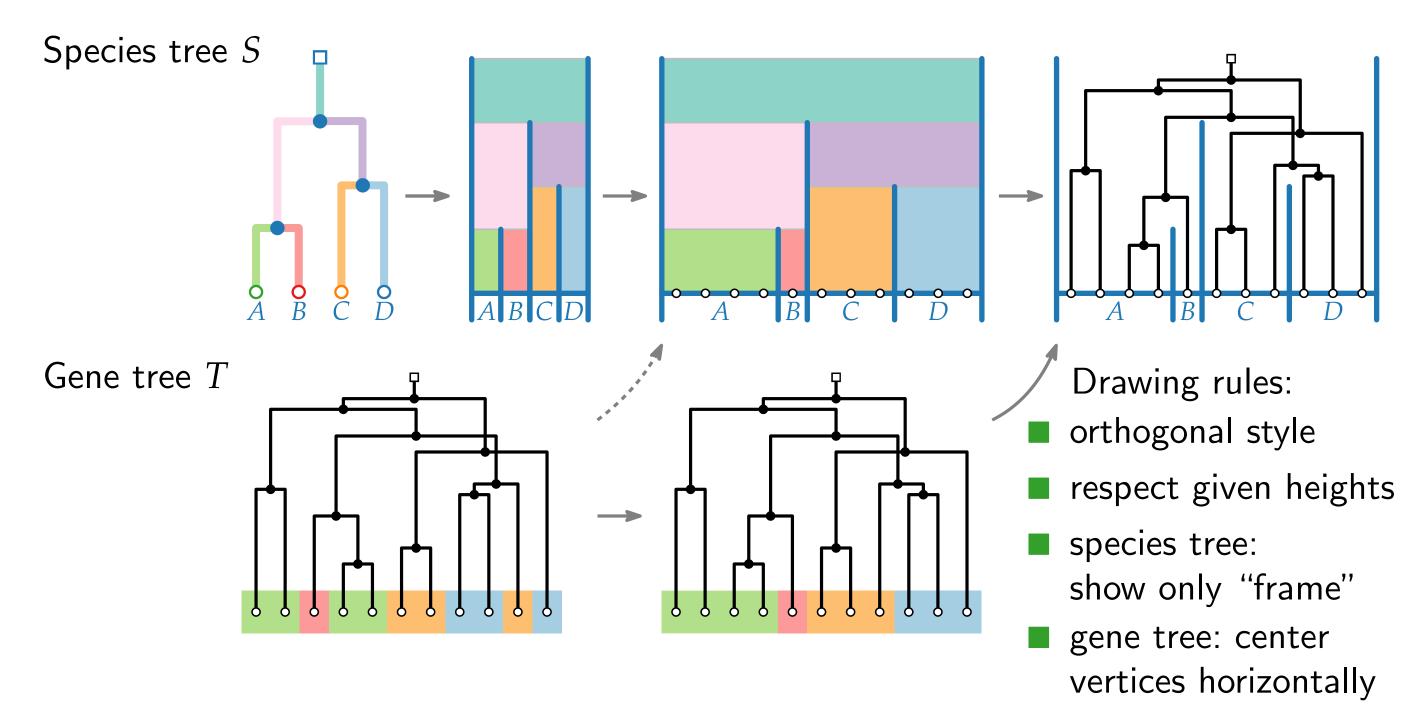


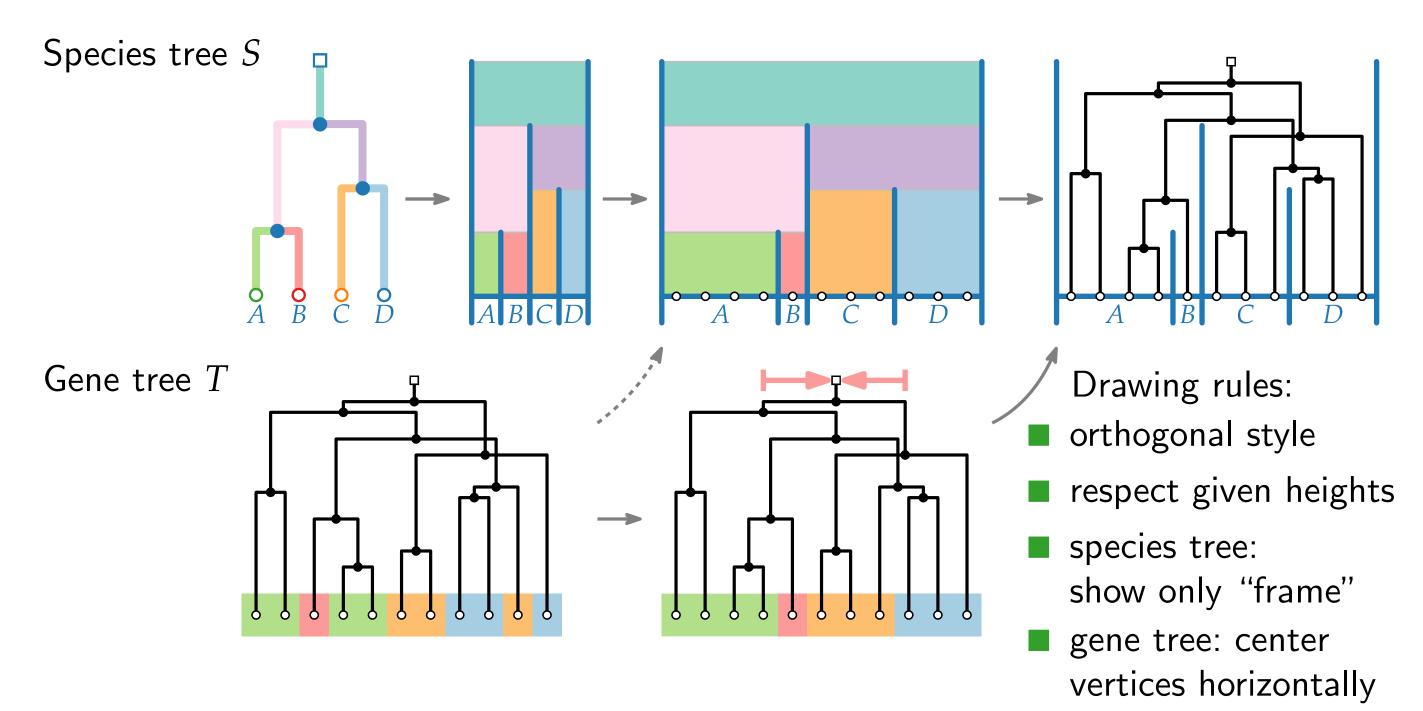




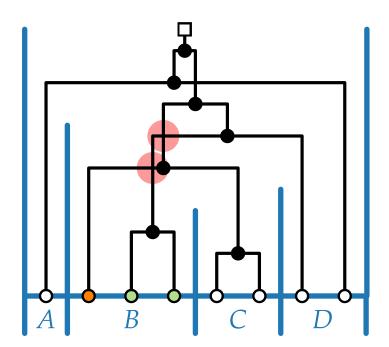






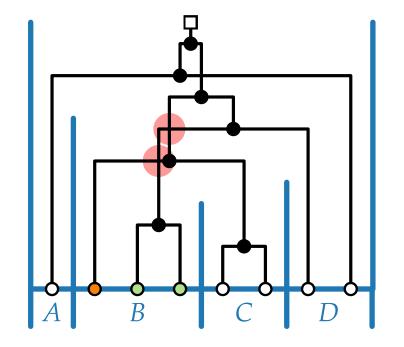


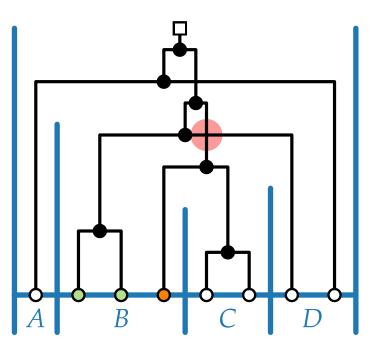
Minimize the number of crossings by...



Minimize the number of crossings by...

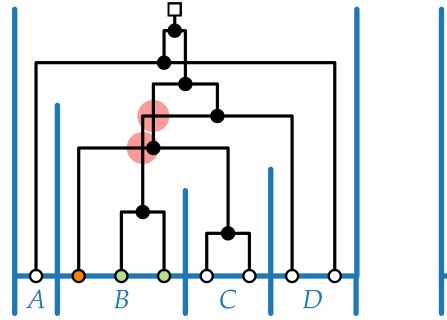
changing gene order

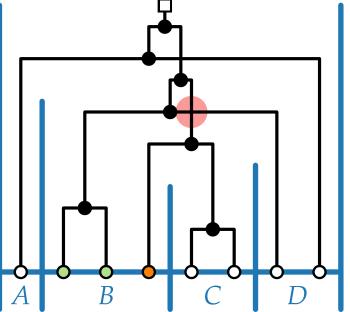




Minimize the number of crossings by...

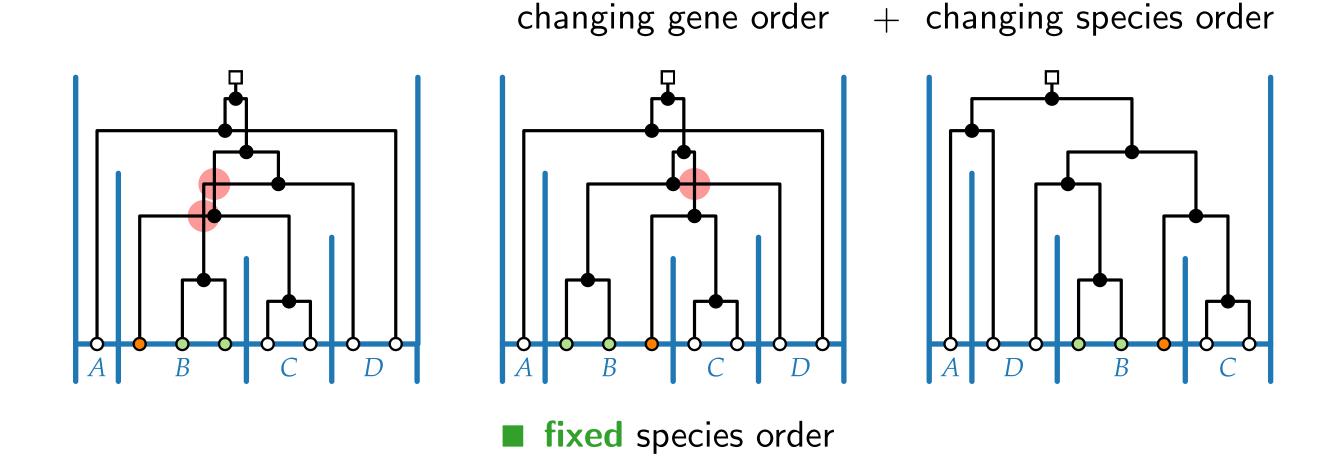
changing gene order



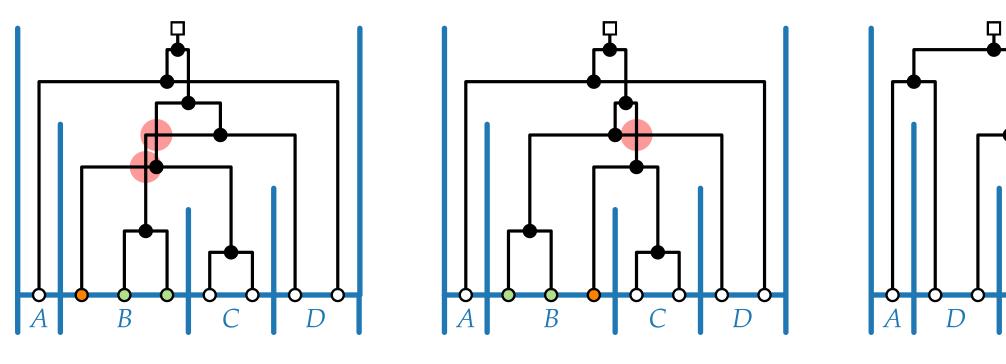


fixed species order

Minimize the number of crossings by...



Minimize the number of crossings by...



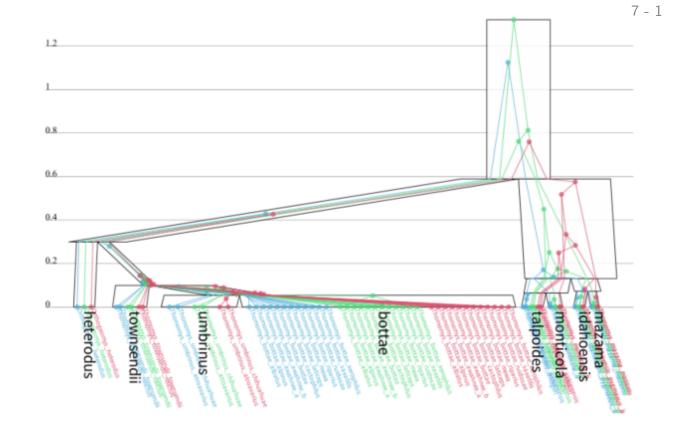
changing gene order + changing species order

fixed species order

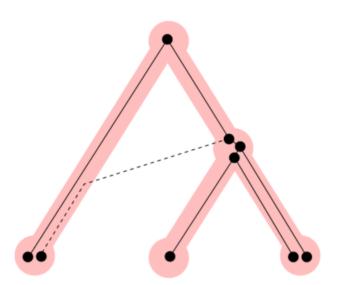
variable species order

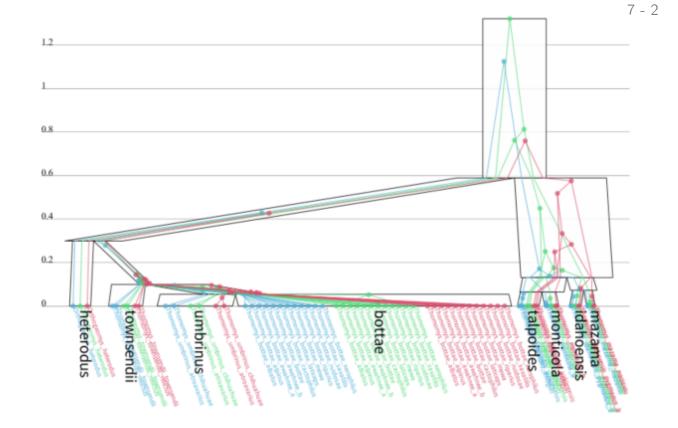
Related work

■ Tool *UglyTrees* by Douglas uses a different model of MSC trees.



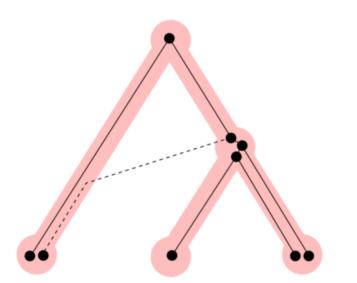
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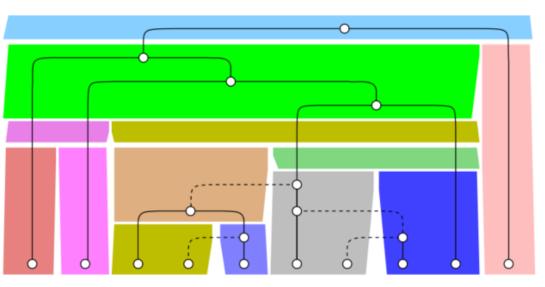


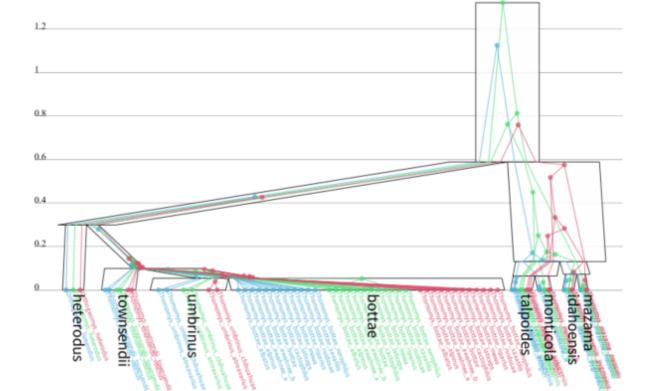


Related work

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- Co-phylogenetic trees
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 - Space-filling approach by Calamoneri, Di Donato, Mariottini, Patrignani [TCS'20]







Our contribution

- We have defined drawing style for MSC trees.
- Planarity testing is easy.
- Crossing minimisation is NP-hard (for fixed & variable species order).
- We present two simple heuristics and an integer linear program (ILP).
- We do an experimental evaluation of the heuristics.

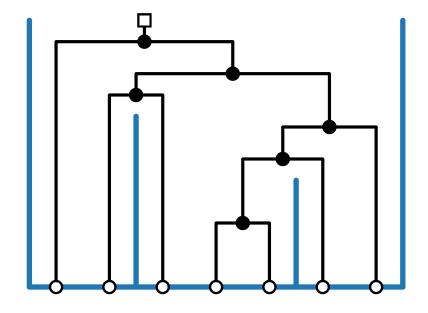
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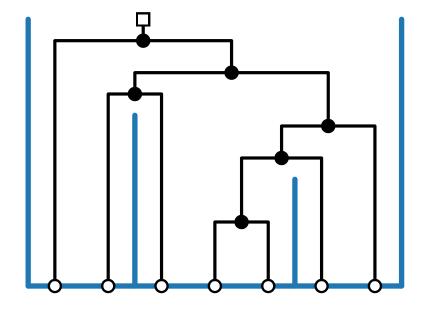
variable species order

fixed species order

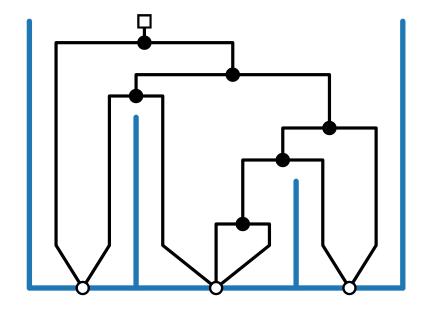
variable species order



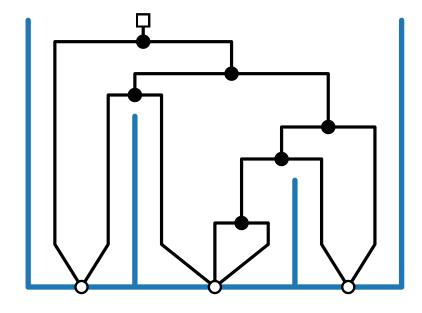
fixed species order



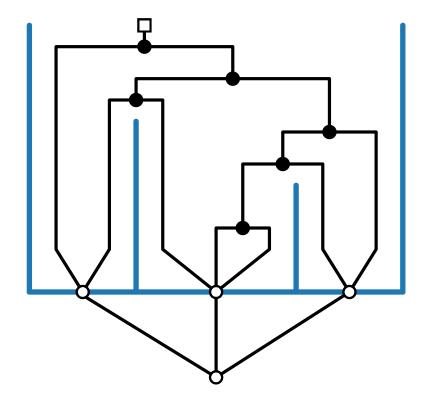
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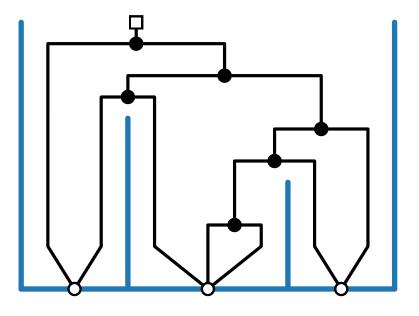
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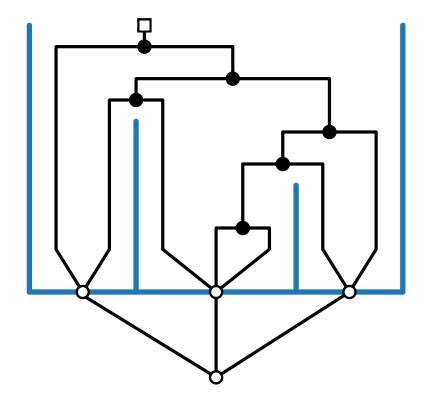
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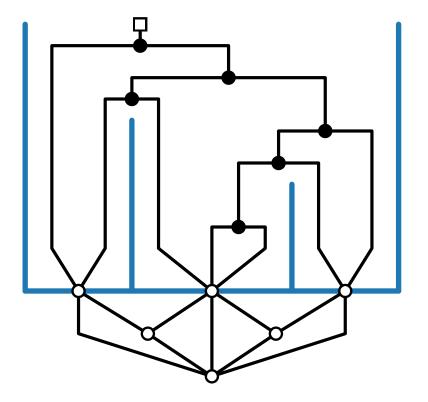
fixed species order



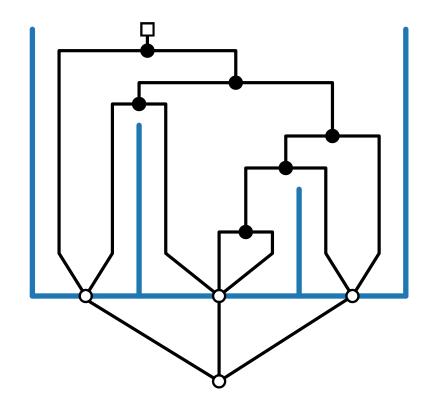
variable species order



fixed species order

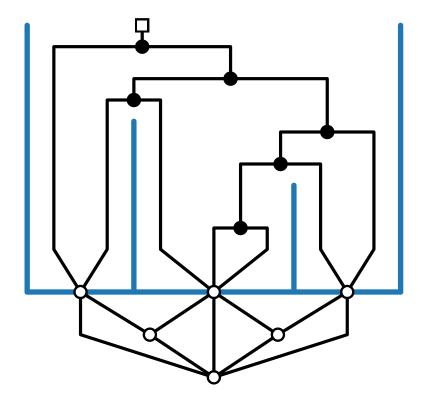


variable species order

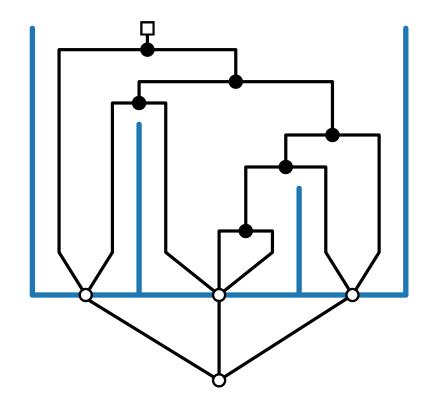


Upward planar!

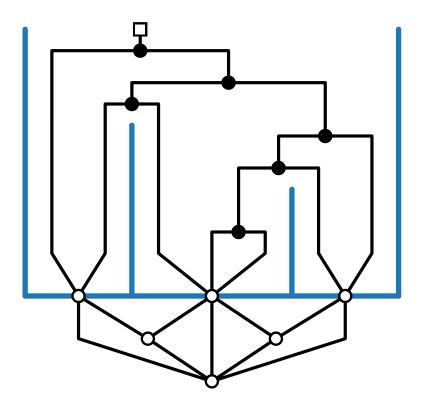
fixed species order



variable species order



fixed species order



Upward planar! ----

Testing upward planarity of single-source digraphs can be done in linear time.

[Bertolazzi, Di Battista, Mannino, Tamassia: SIAM J. Comput. '98]

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NP-Hardness

Theorem.

Crossing minimisation for tree-in-tree drawings of MSC trees with *variable* species order is **NP-hard**.

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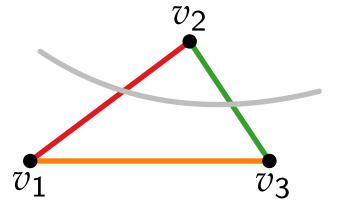
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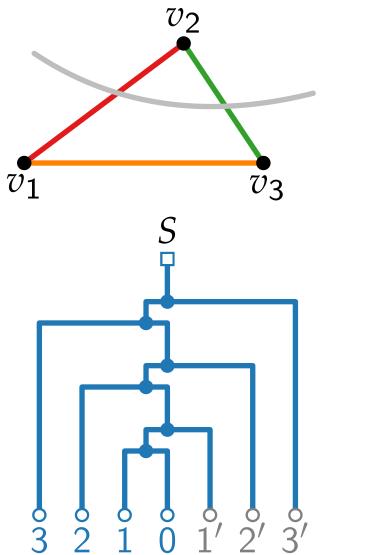
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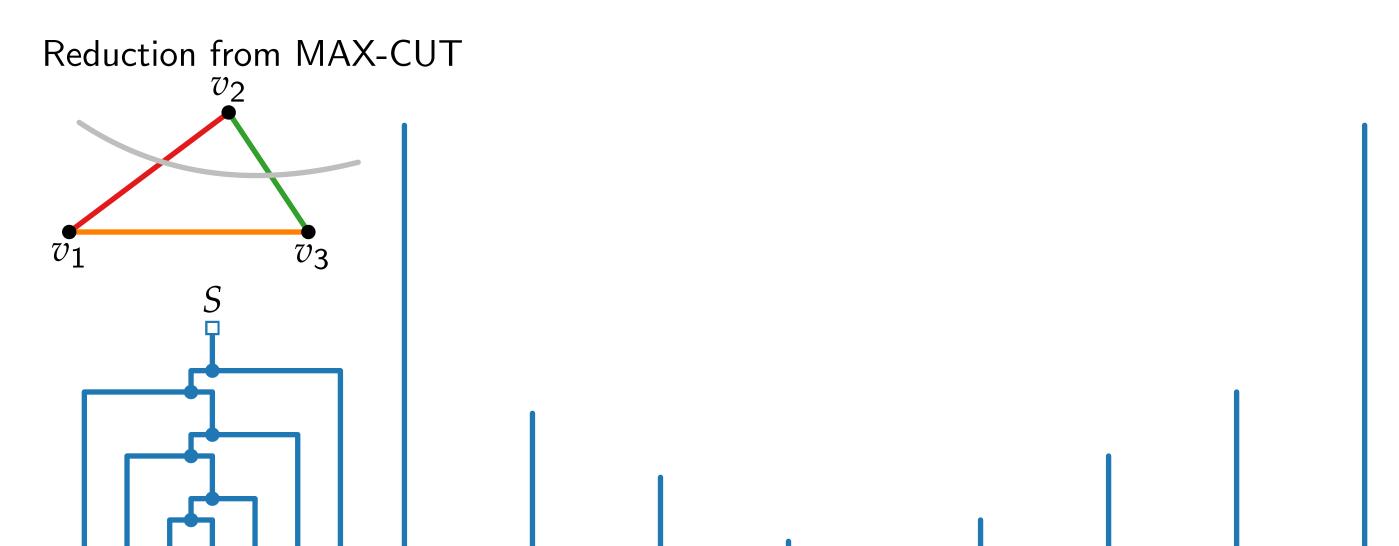
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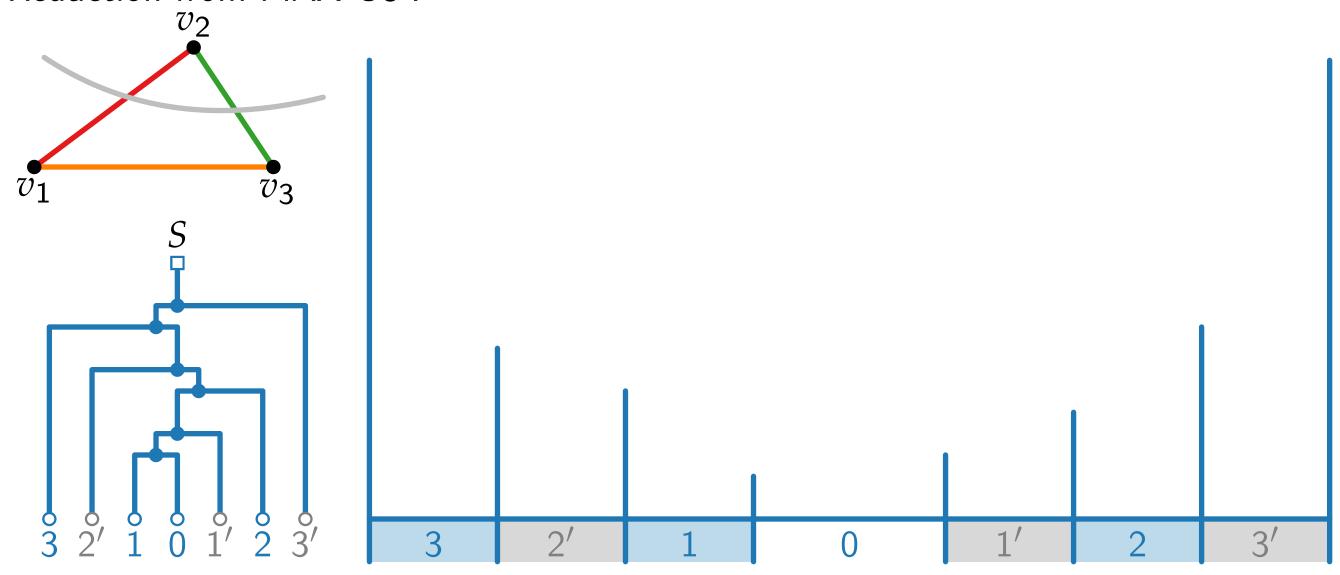
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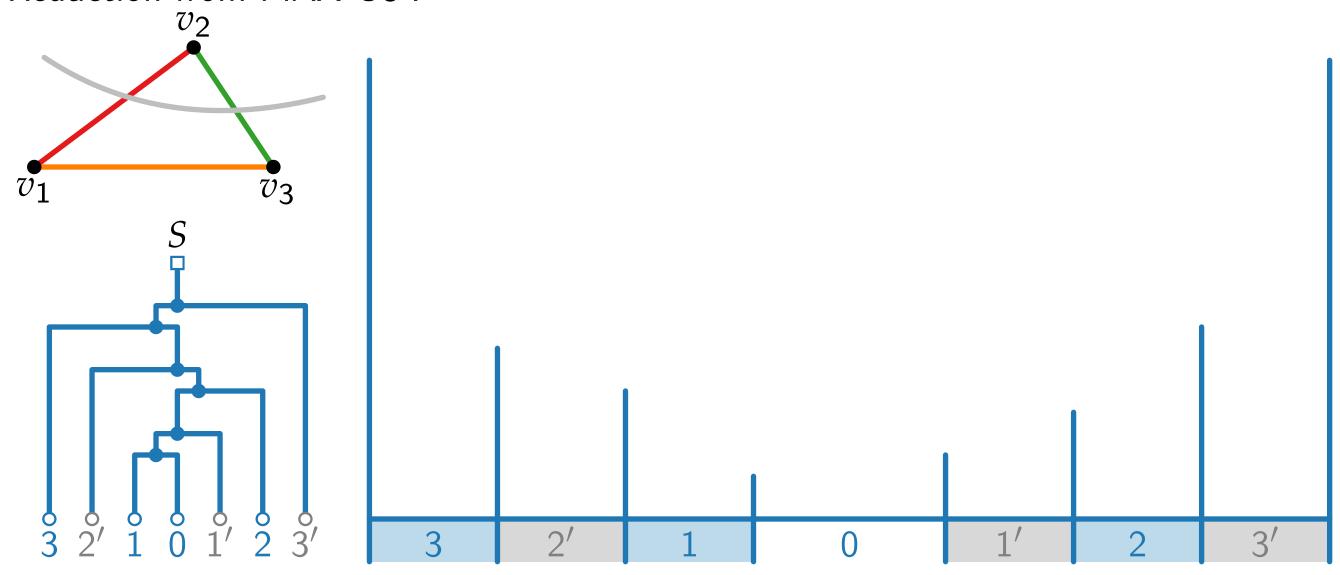




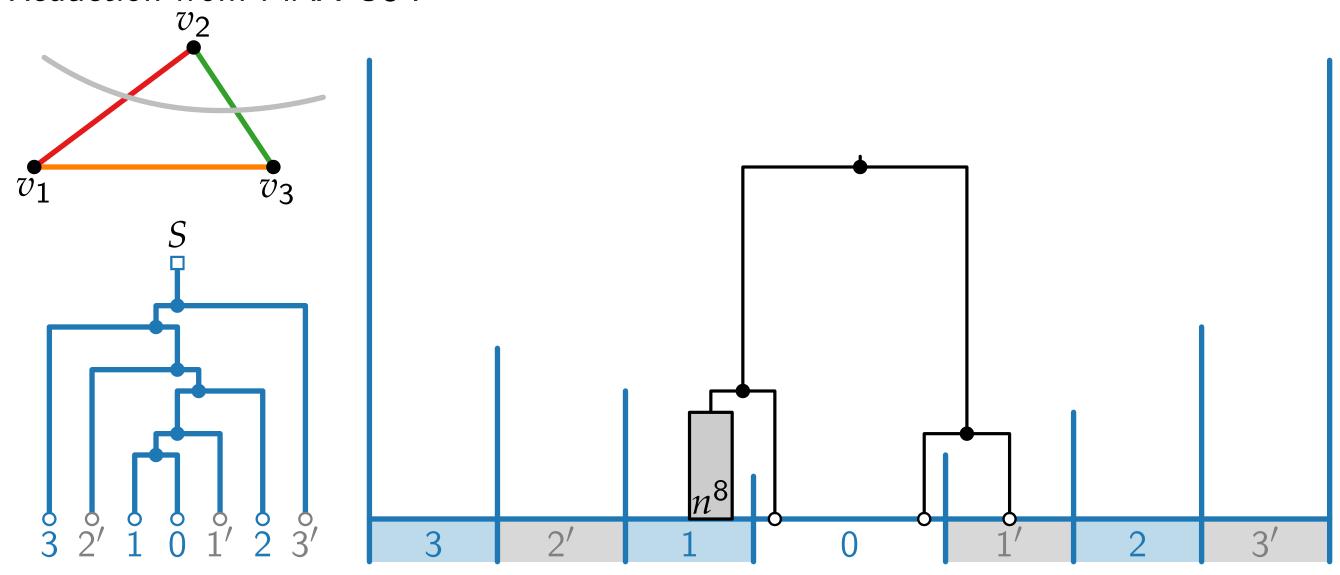


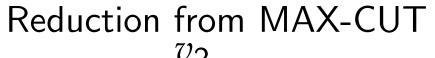


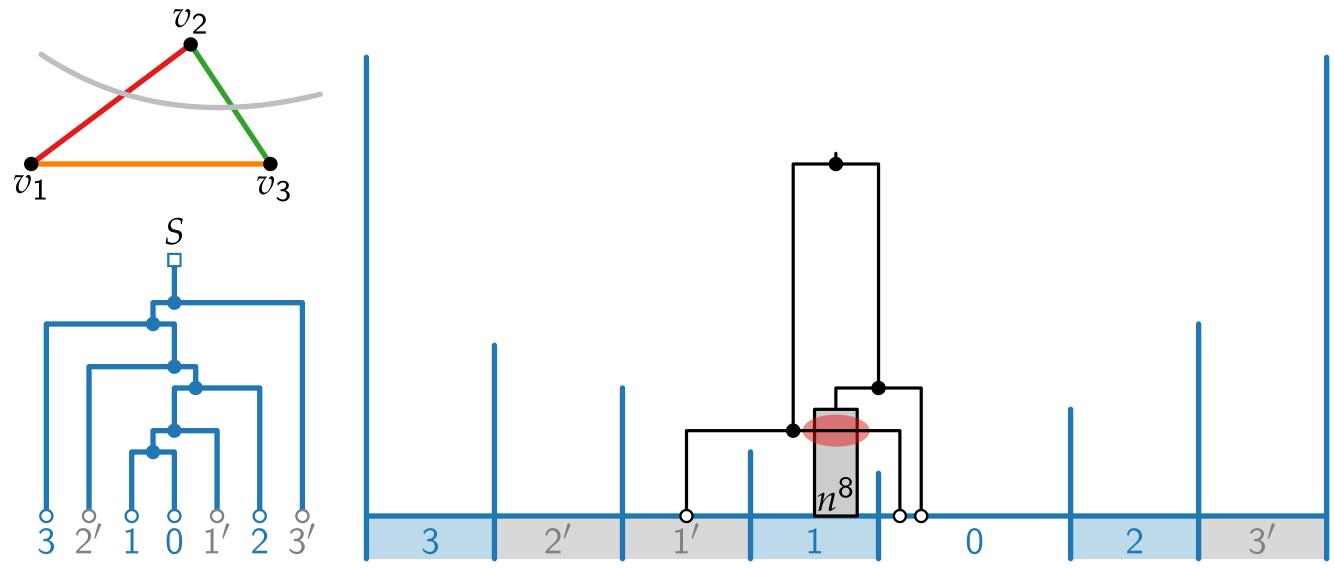




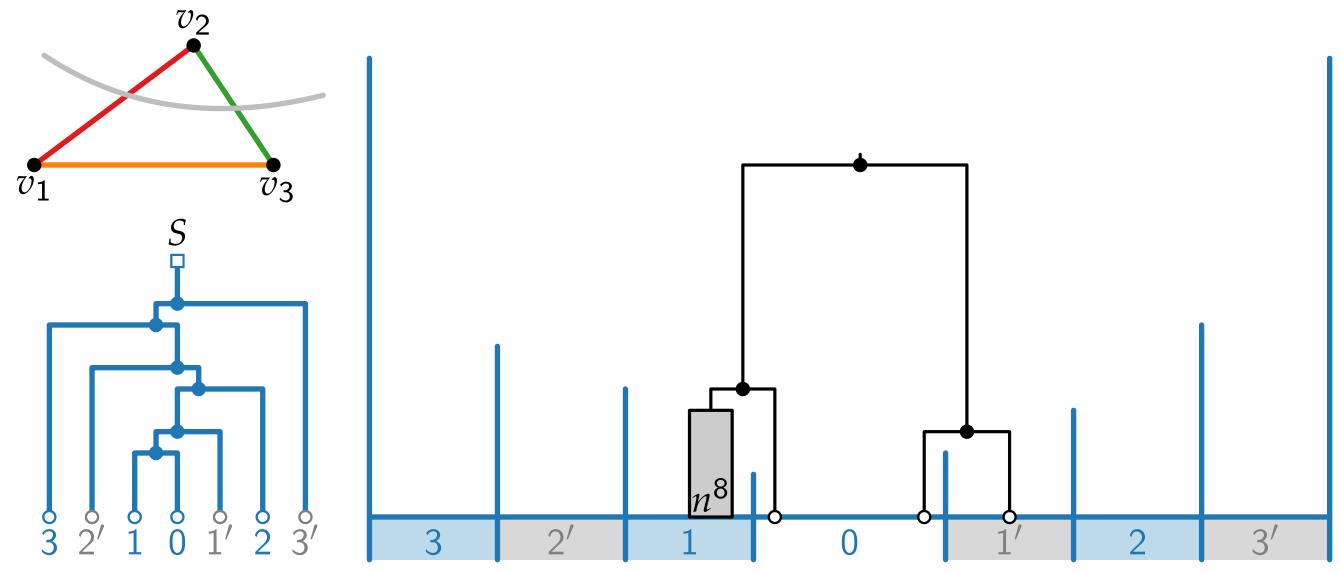




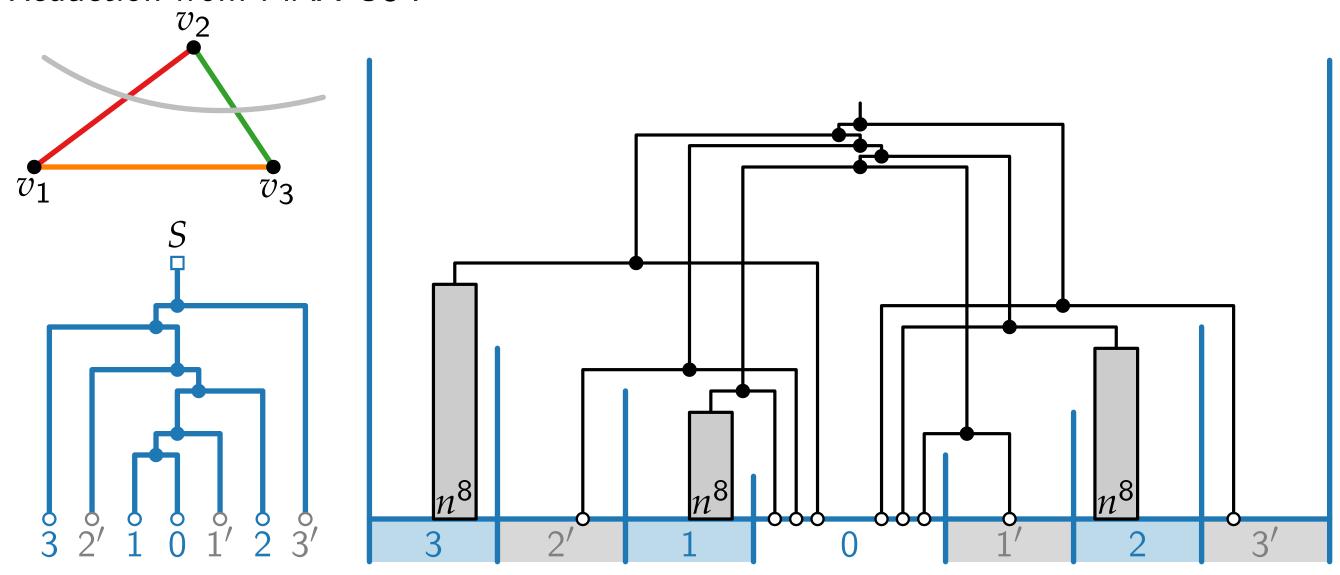


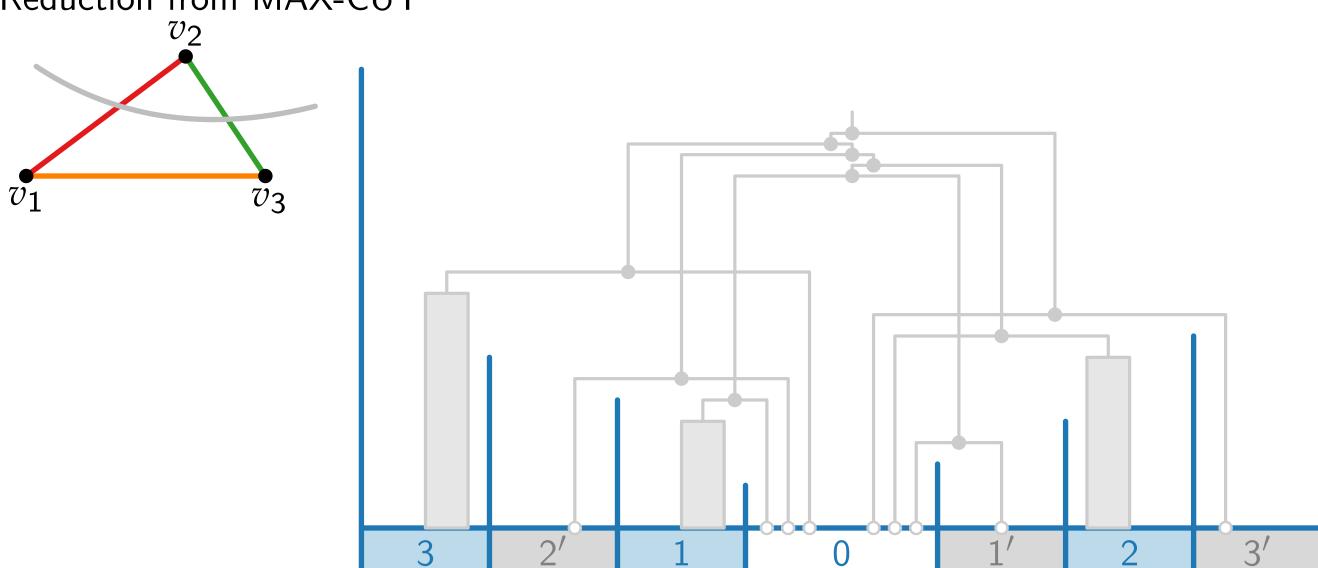


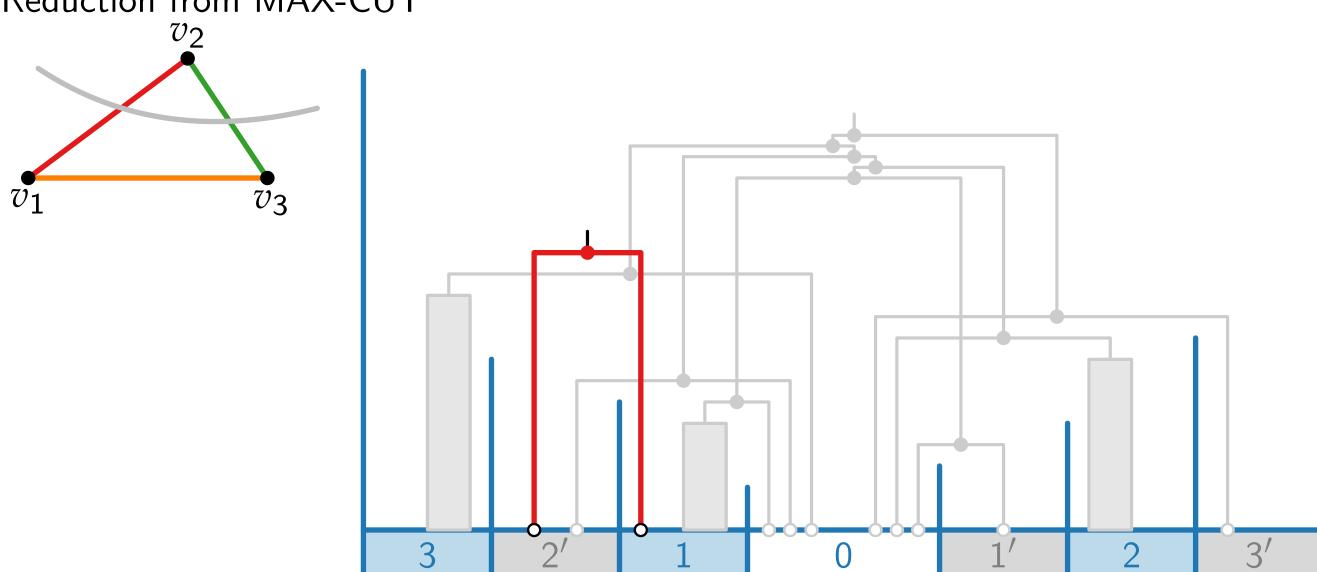


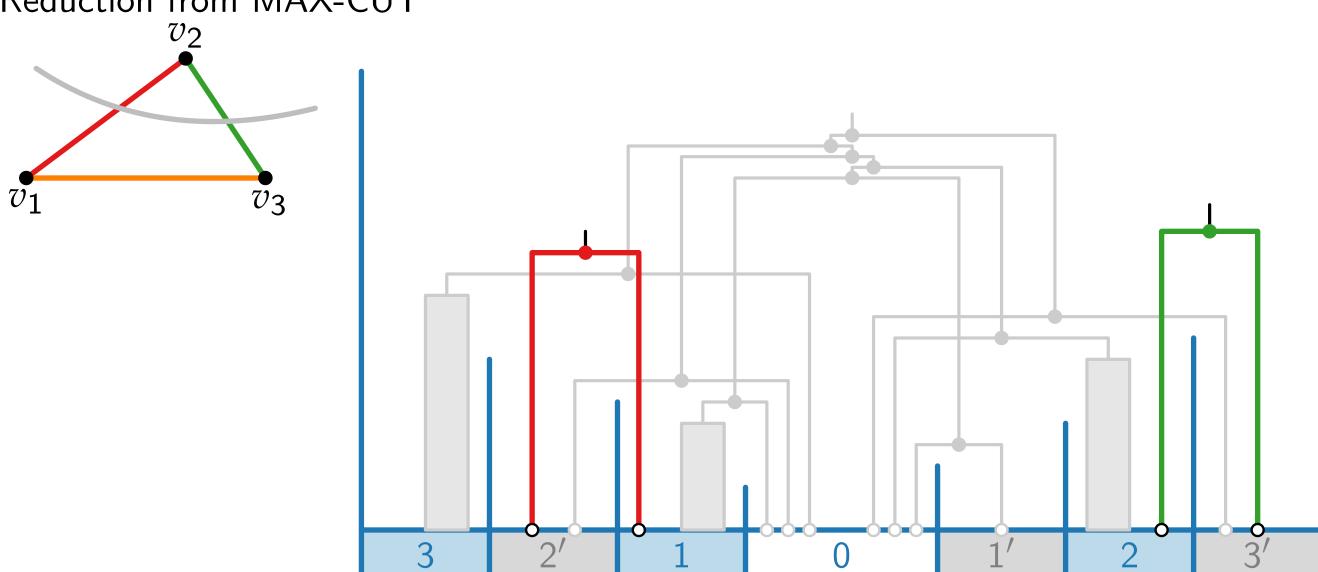


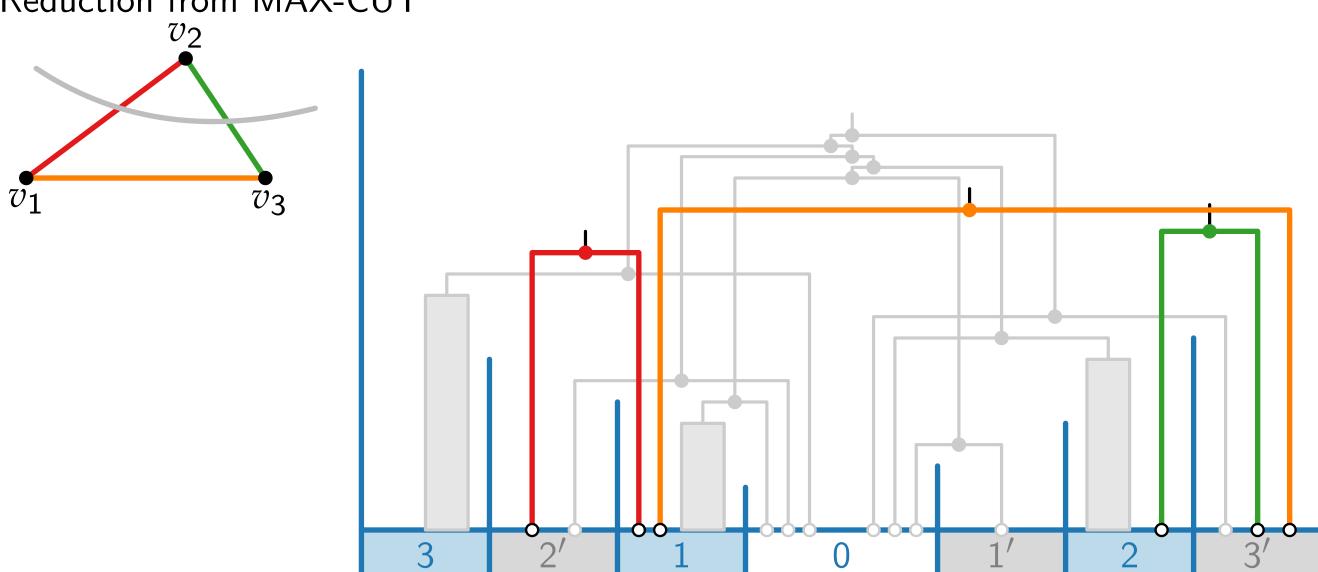


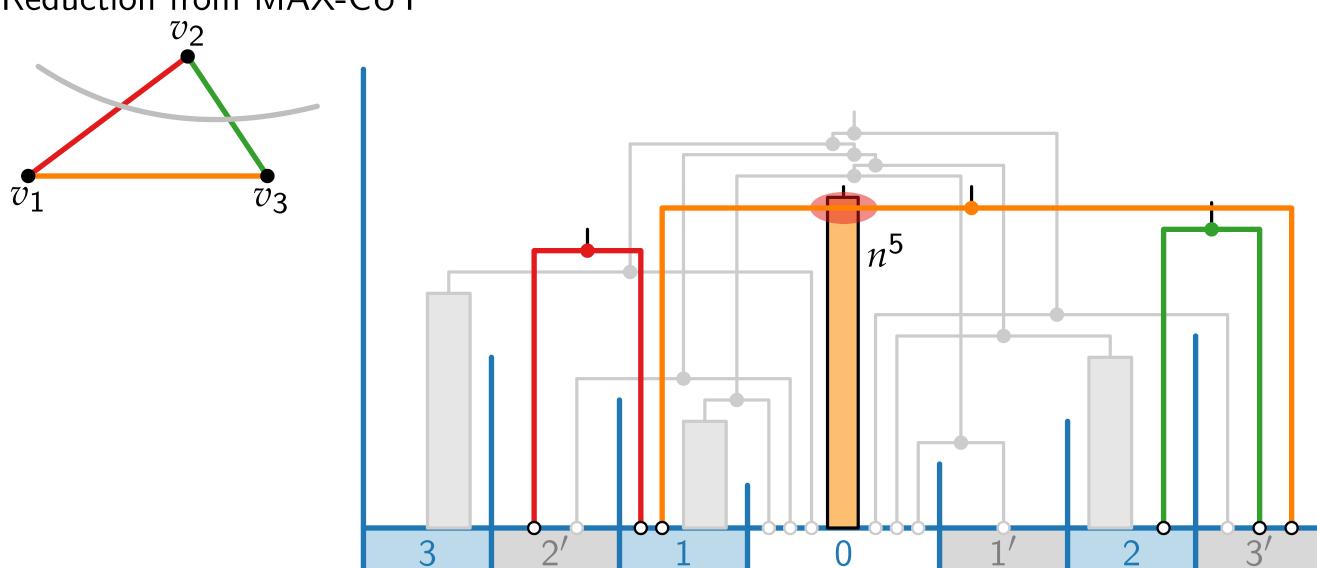


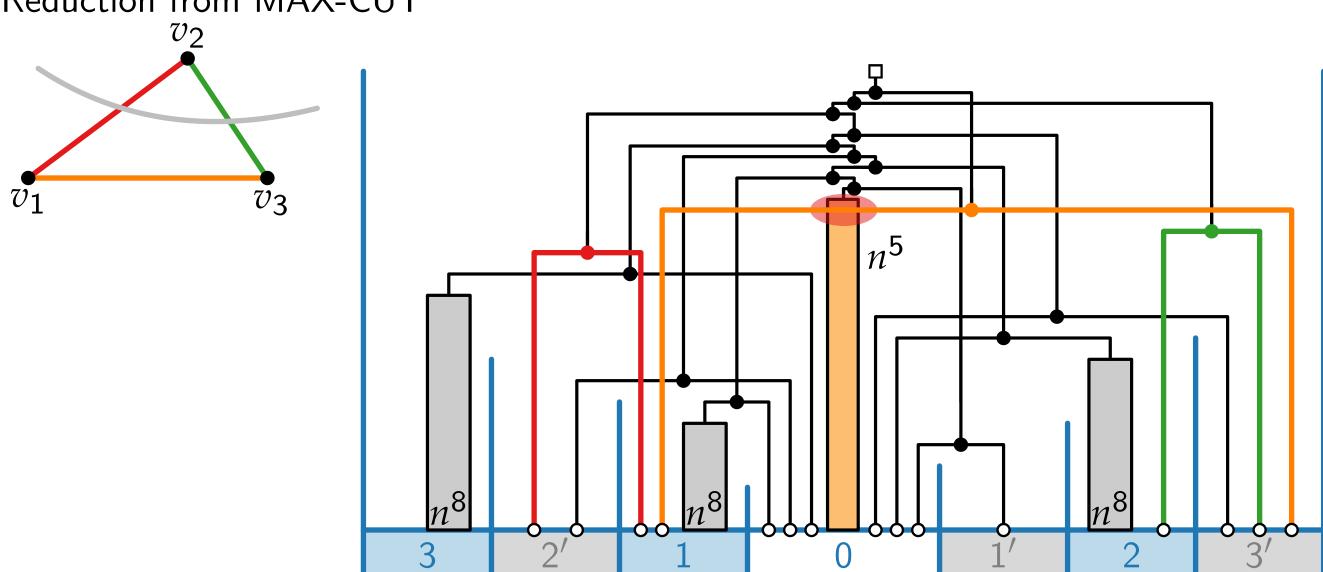




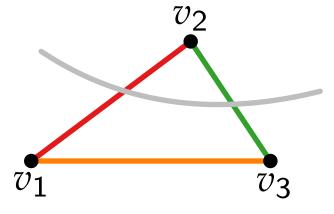








Reduction from MAX-CUT



Done! :-)

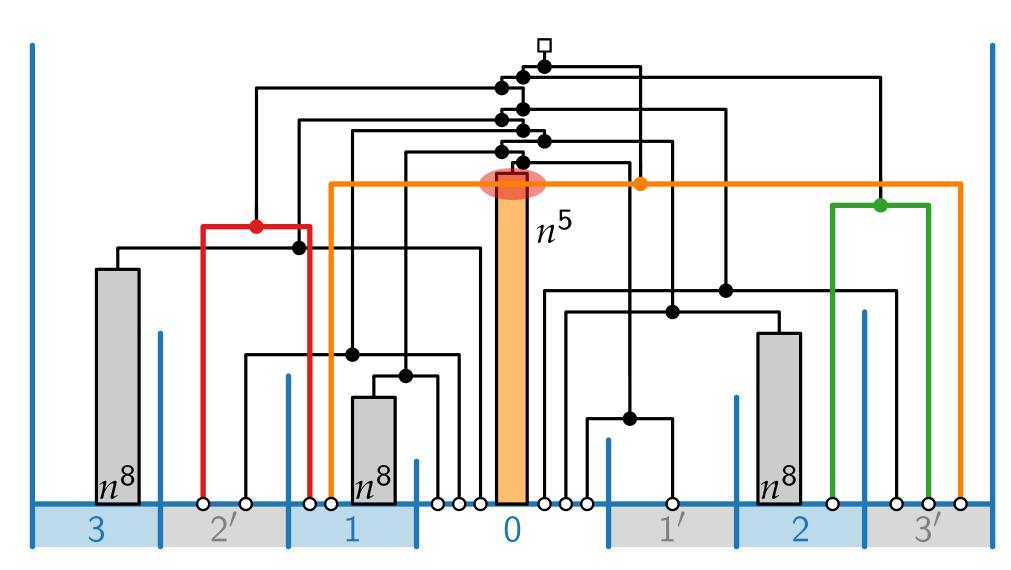
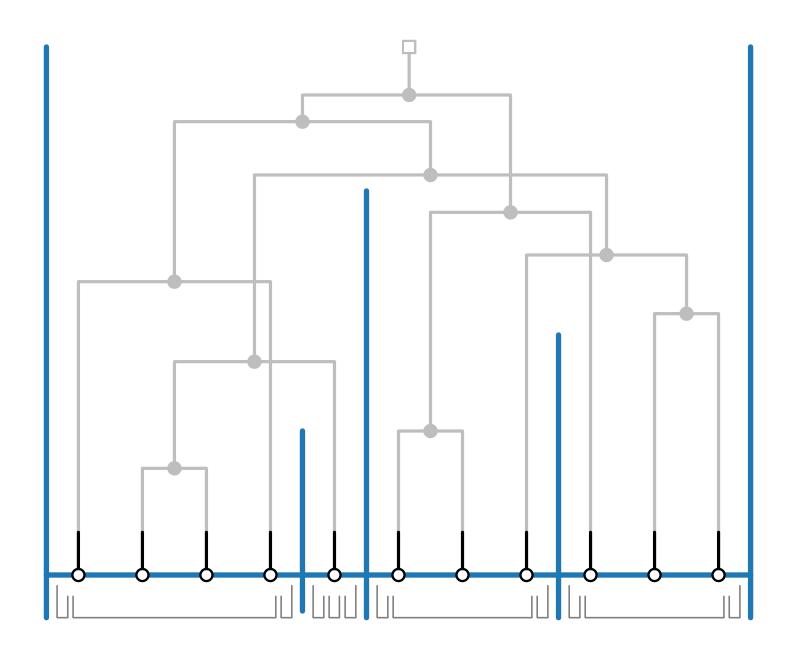


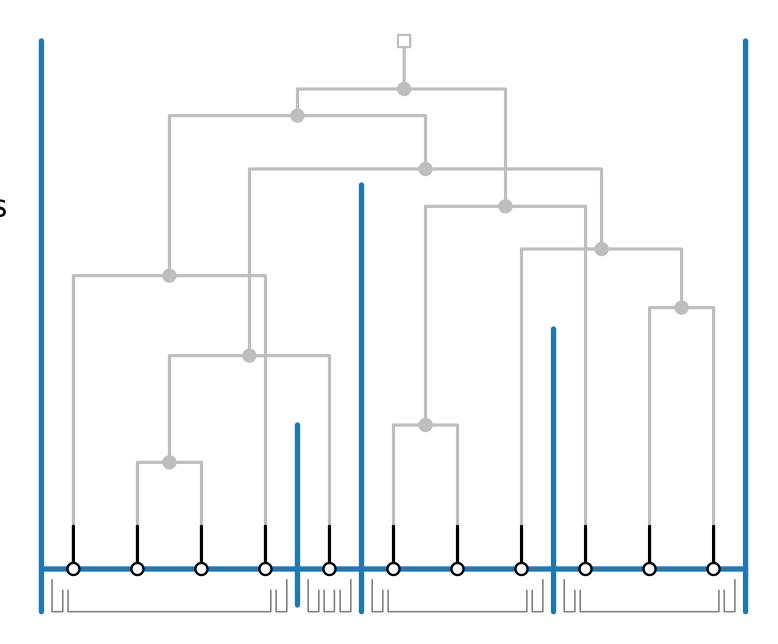
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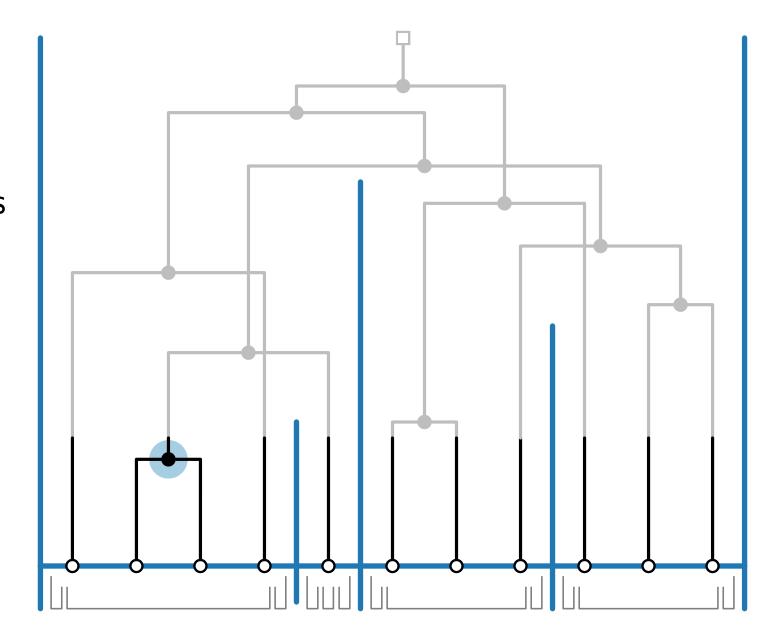
bottom-up



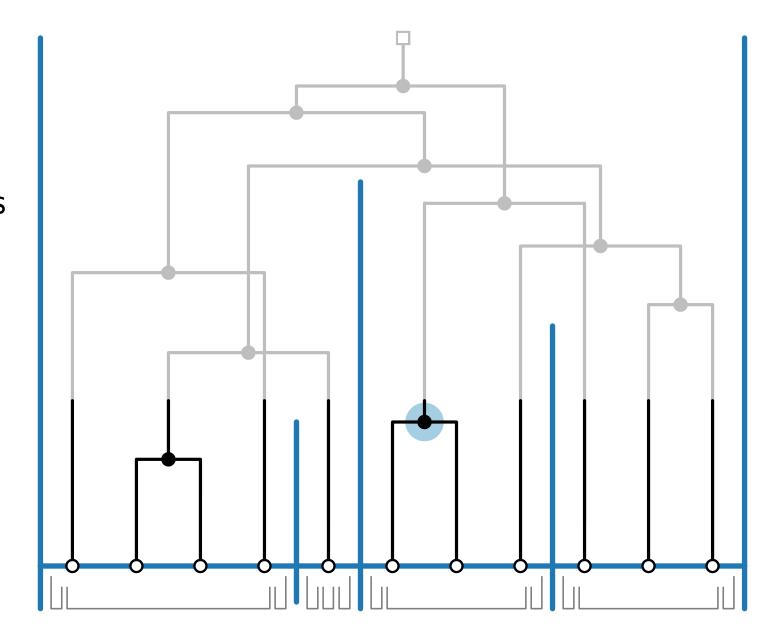
- bottom-up
- left stack, mid bucket, and right stack for each species



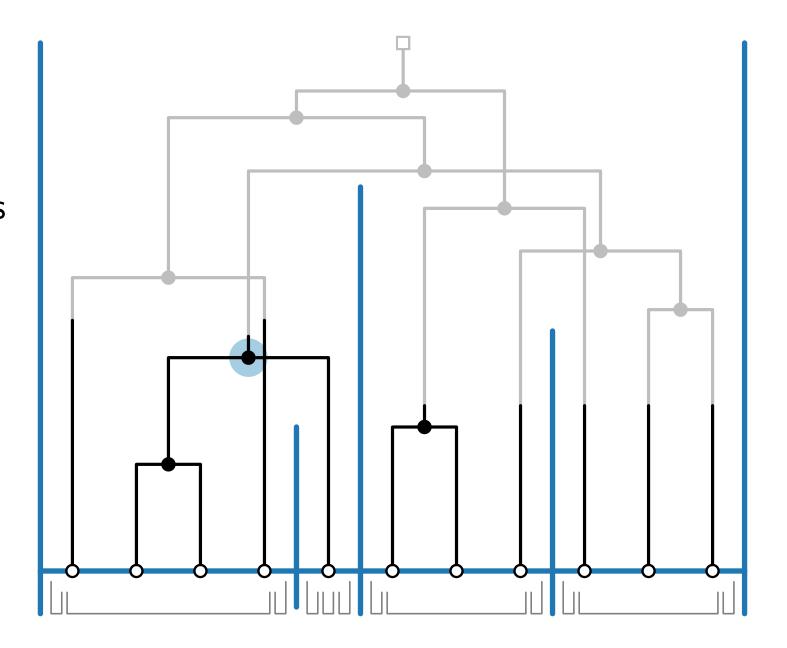
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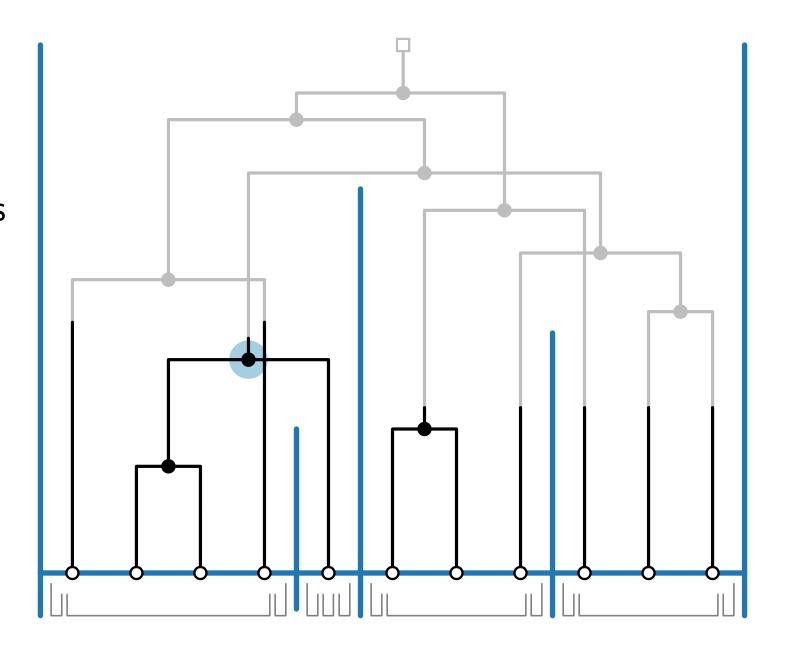
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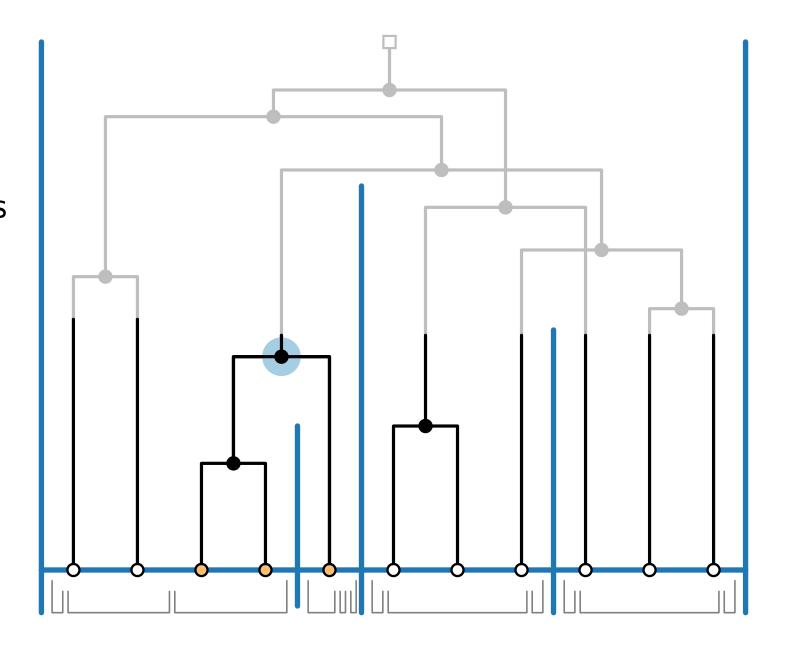
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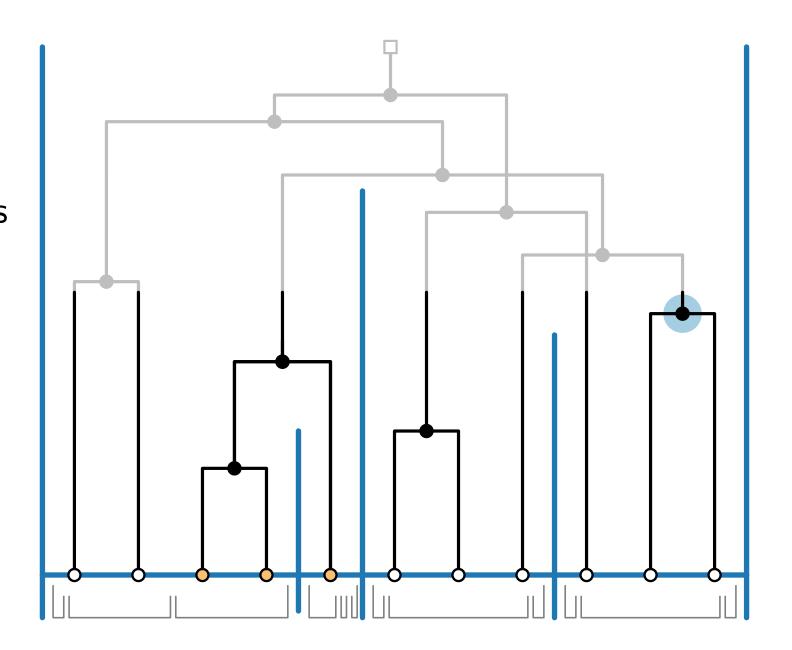
- bottom-up
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- move subtrees together



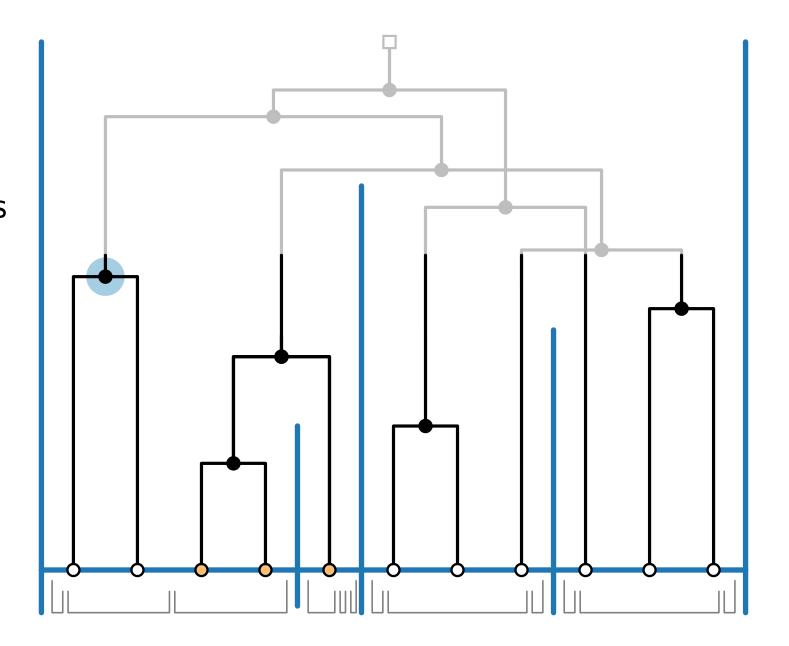
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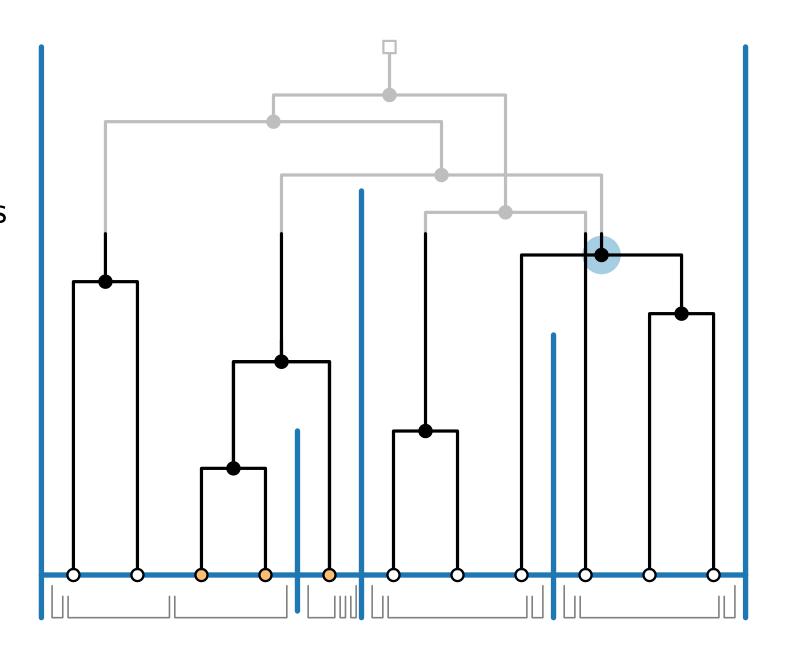
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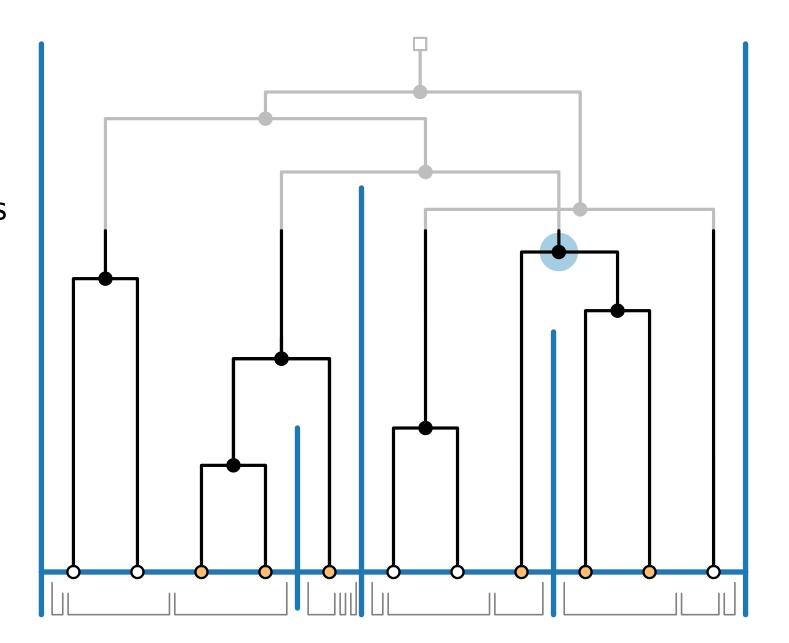
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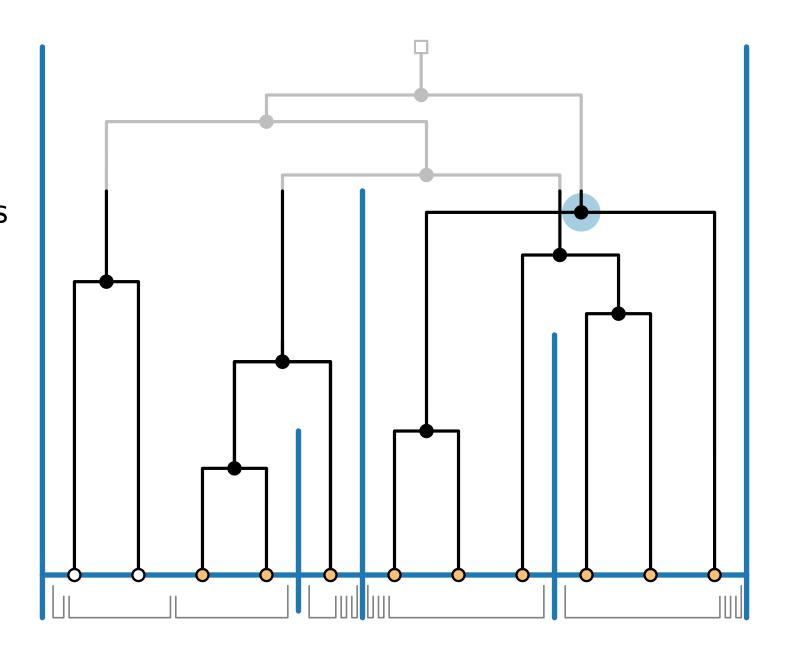
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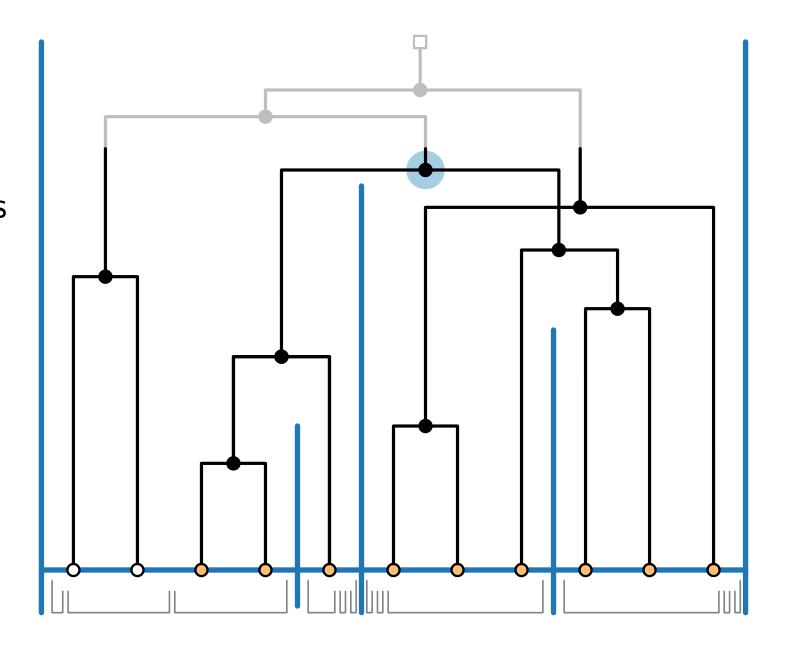
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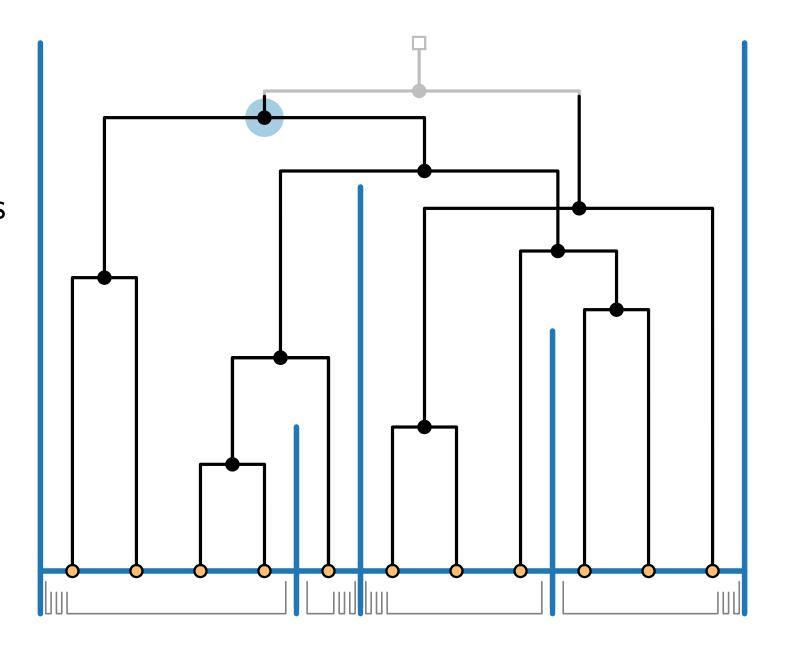
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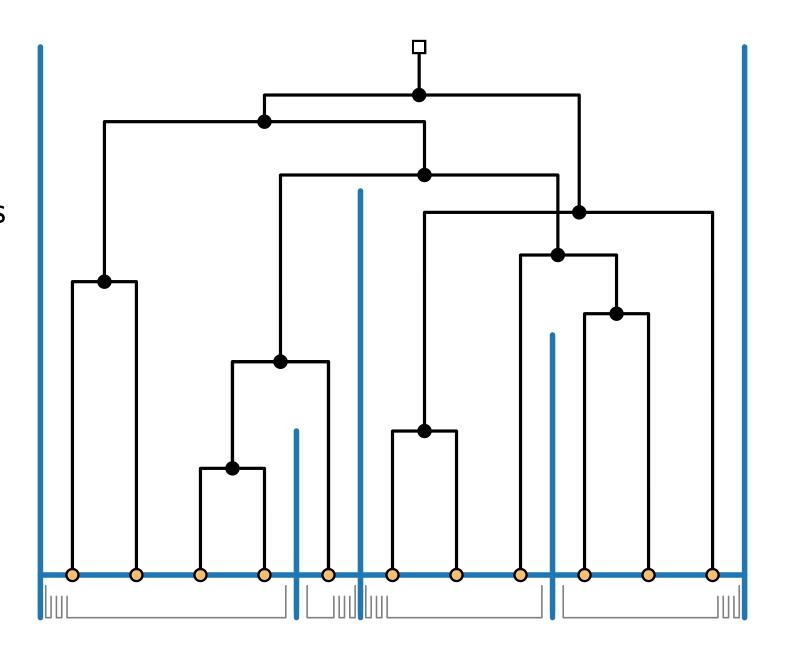
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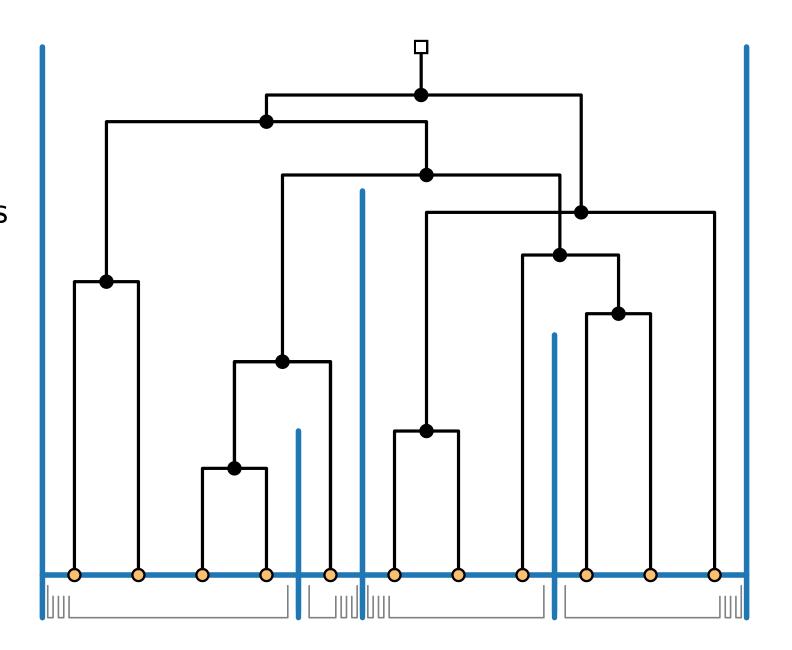


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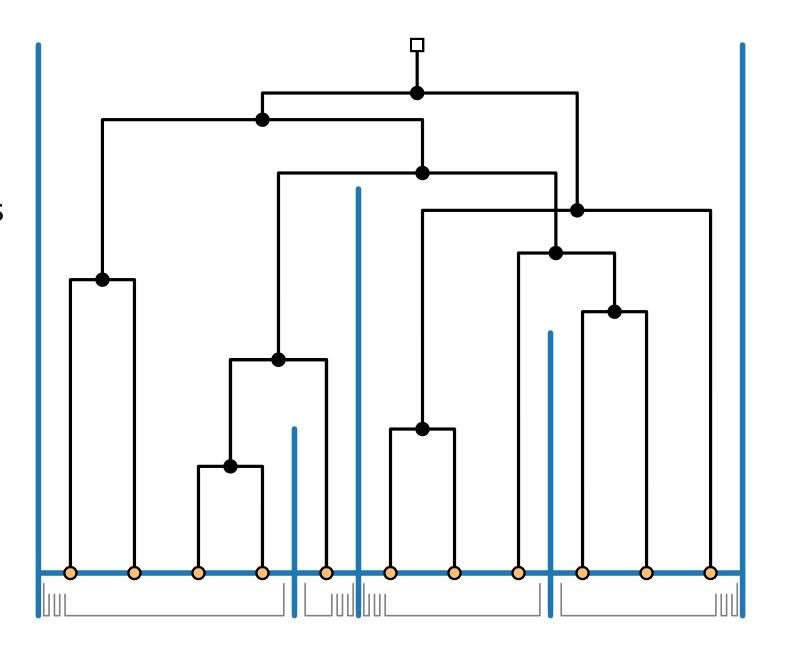
Done! :-)



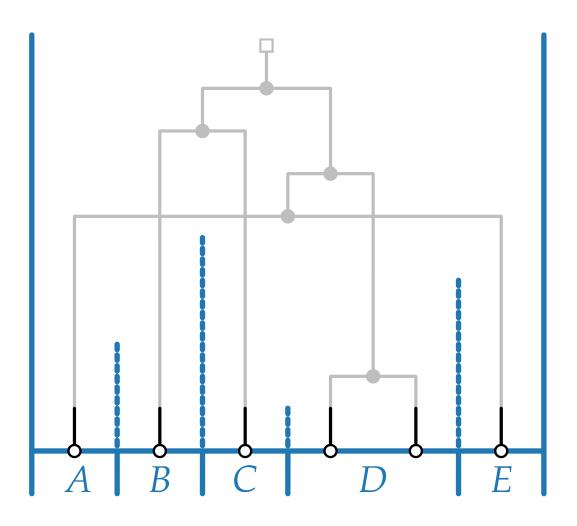
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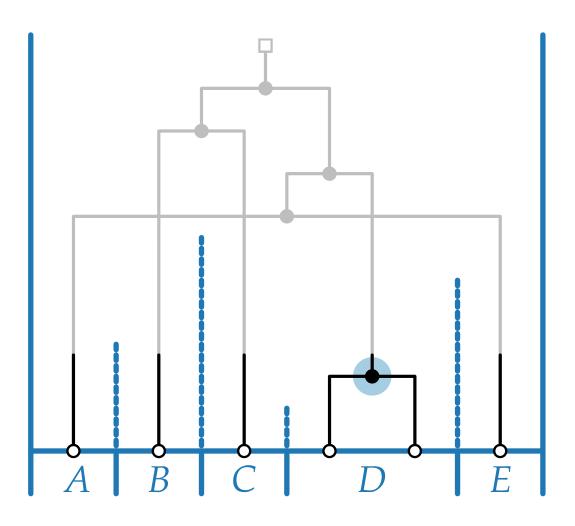
runs in linear time



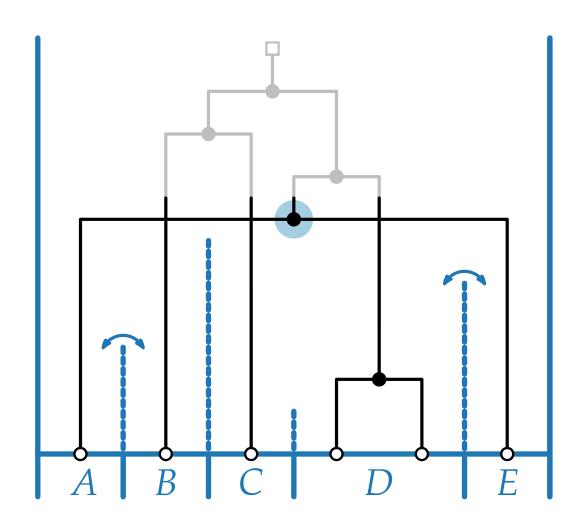
bottom-up



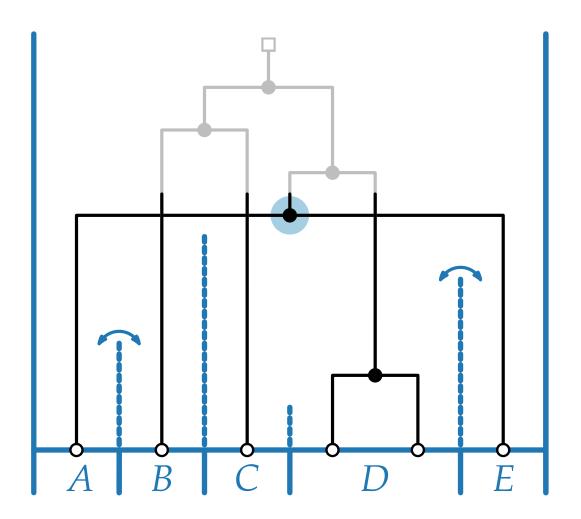
bottom-up



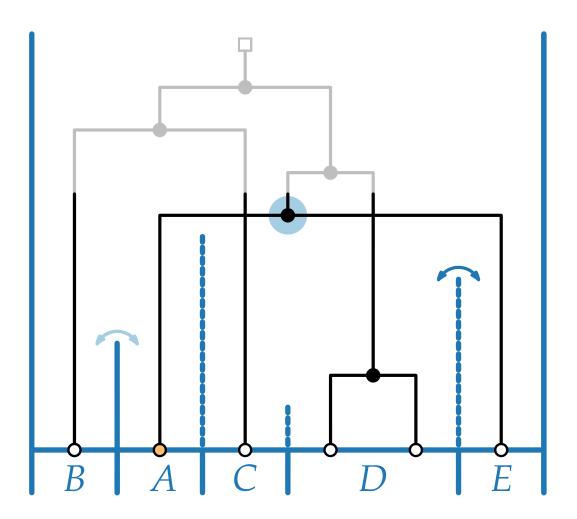
bottom-up



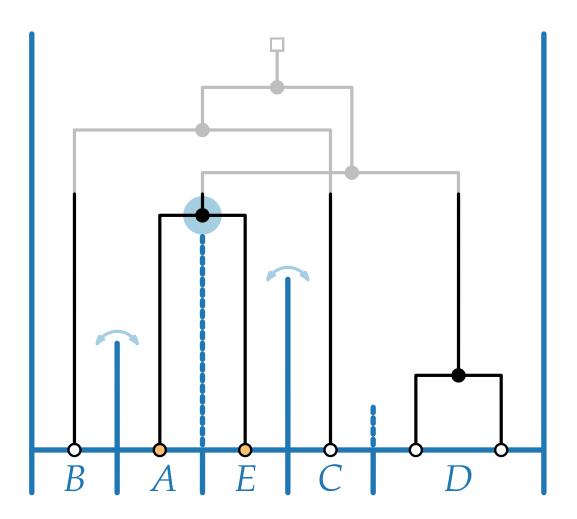
- bottom-up
- rotate species together, fix rotations



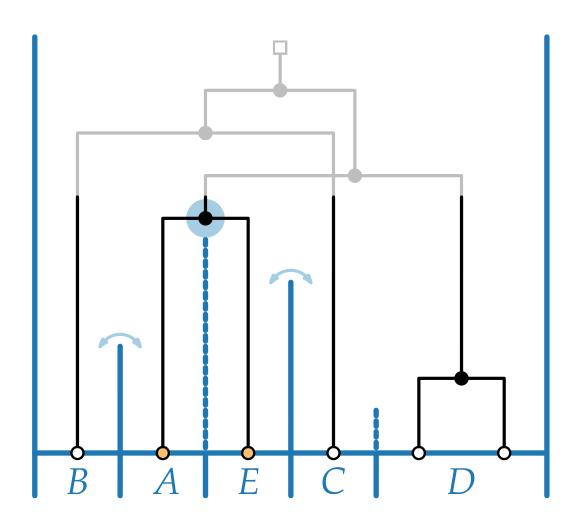
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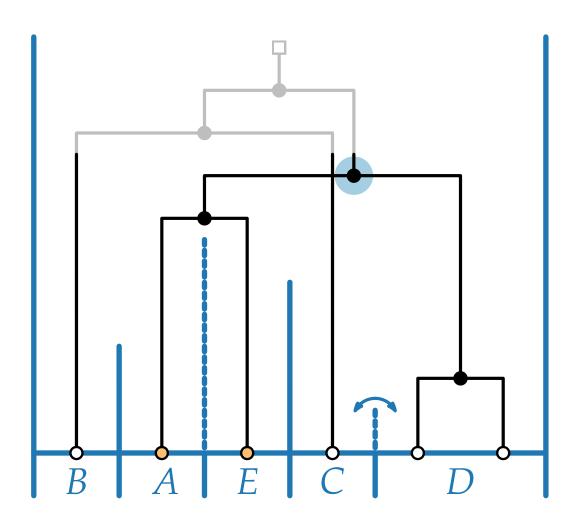
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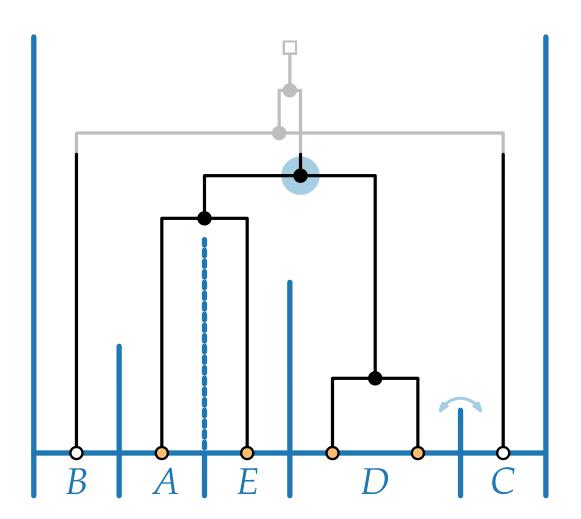
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- rotate species together, fix rotations
- then use previous heuristic on genes



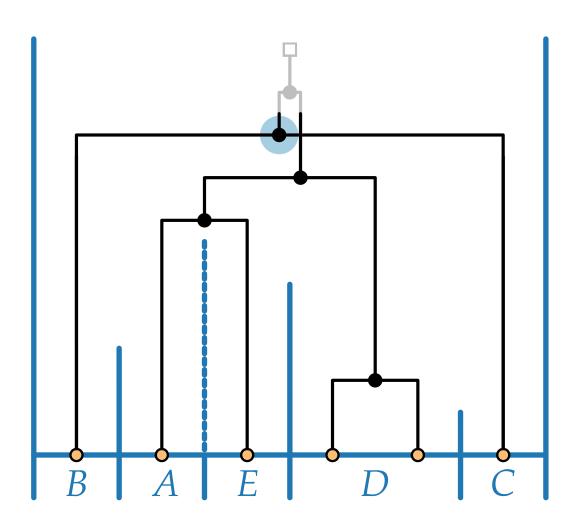
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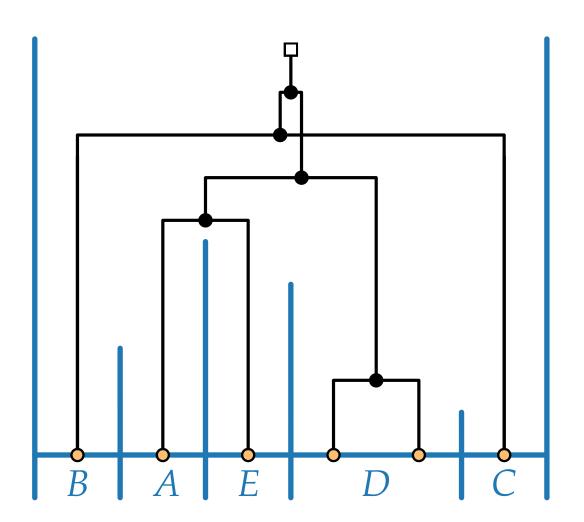
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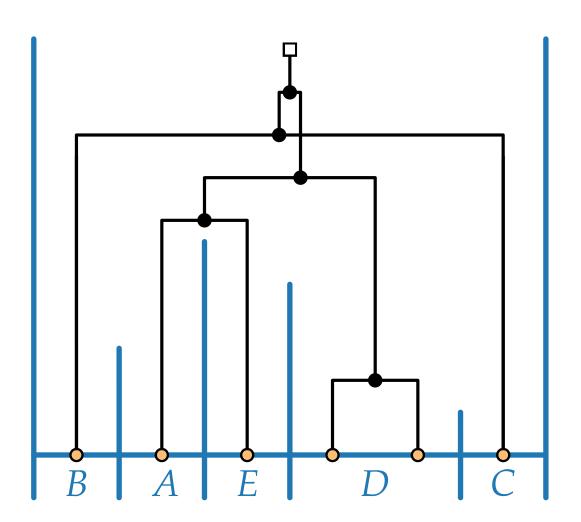


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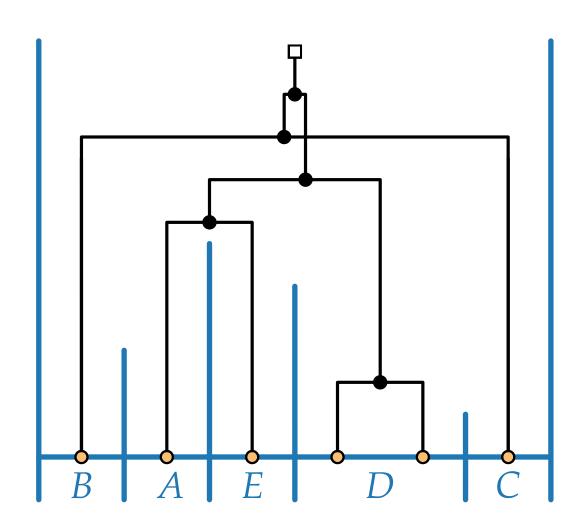
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quadratic running time



ILP

Integer variables encode the orders of the leaves of species and gene trees.

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- We need $O(n^2 + m)$ variables and $O(n^2 + n \cdot m)$ constraints, where n = |V(T)| and m = |V(S)|

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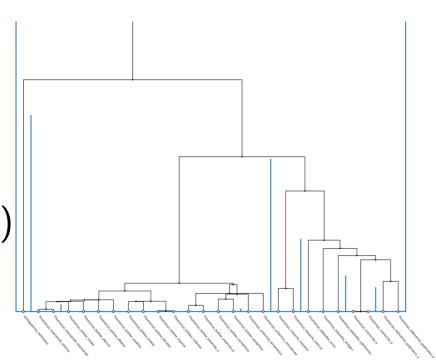
■ 10 random start embeddings per instance

Compare heuristics vs. ILP

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Data sets:

- 8 species, 26 genes, 1083 instances (different topologies)
- 21 species, 88 genes, 321 instances
- 36 species, 83 genes, 99 instances

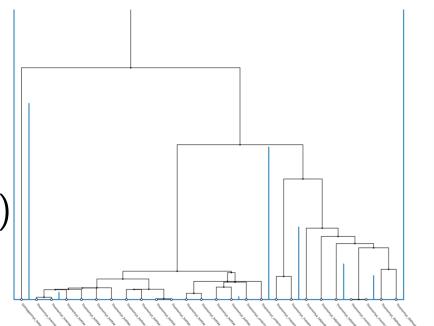


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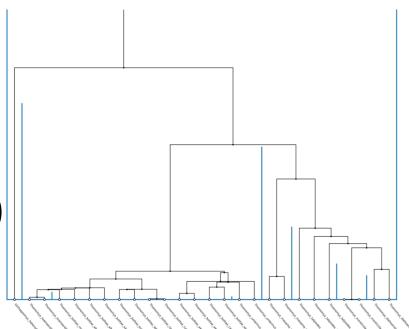
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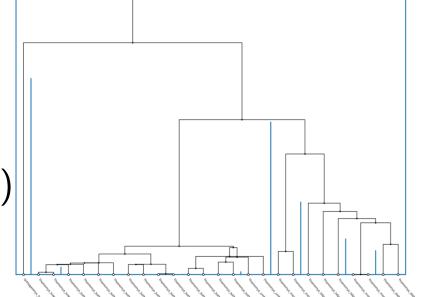
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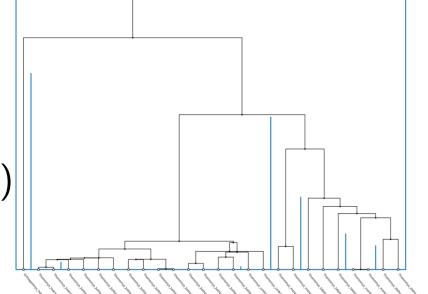
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Recommendation.

Try heuristics on random start embedding while improving; ILP only on small instances.

Summary

- Defined drawing style for multispecies coalescent trees.
- Planarity testing is easy.
- Crossing minimisation is NP-hard.
- Described simple heuristics and ILP.
- Recommend using heuristic on different start embeddings in practice.

