Summarizing Multiple Gene Trees Using Cluster Networks

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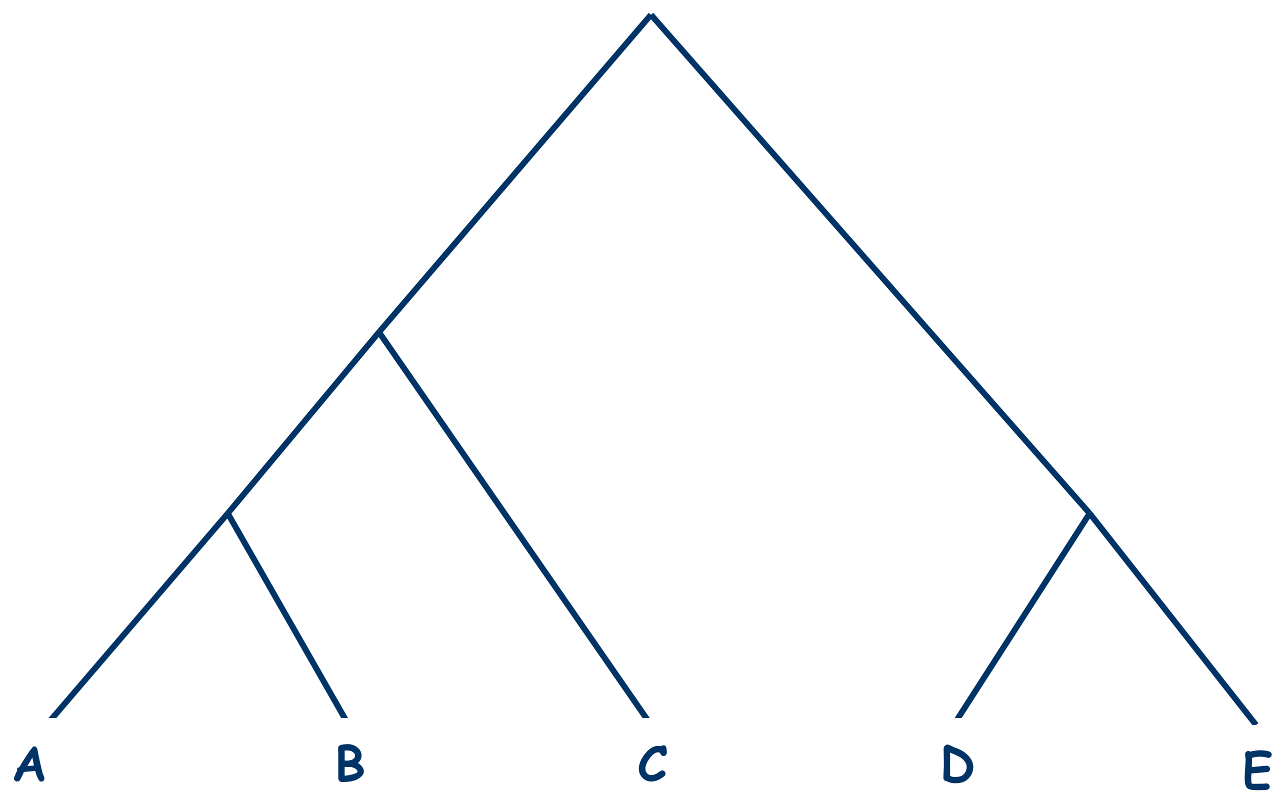
Eberhard Karls Universität Tübingen

Overview

- Trees, Clusters and Cluster Networks
- Hardwired vs. Softwired Networks
- Lowest Single Ancestor (LSA)
- LSA Consensus vs. Adams Consensus

Clusters on Rooted Trees

- Every edge of a rooted tree defines a cluster of the taxon set *X*:



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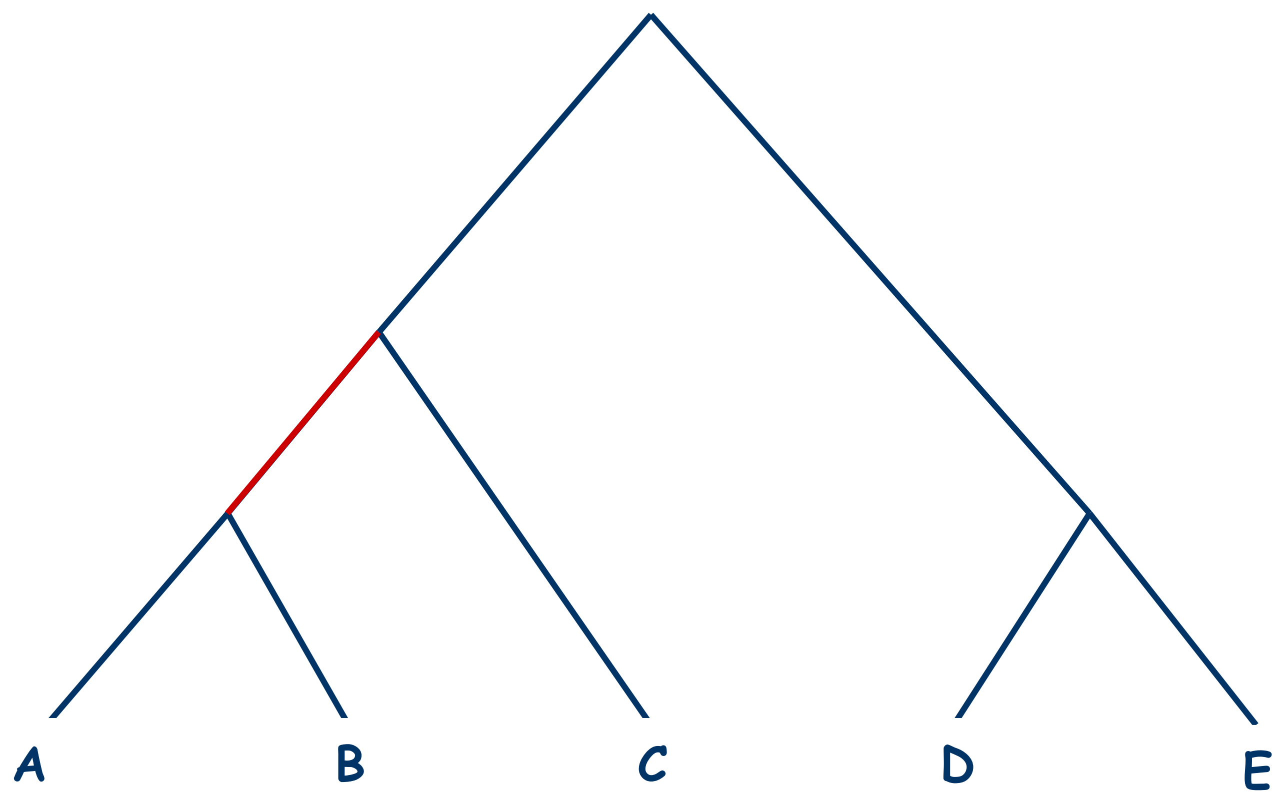

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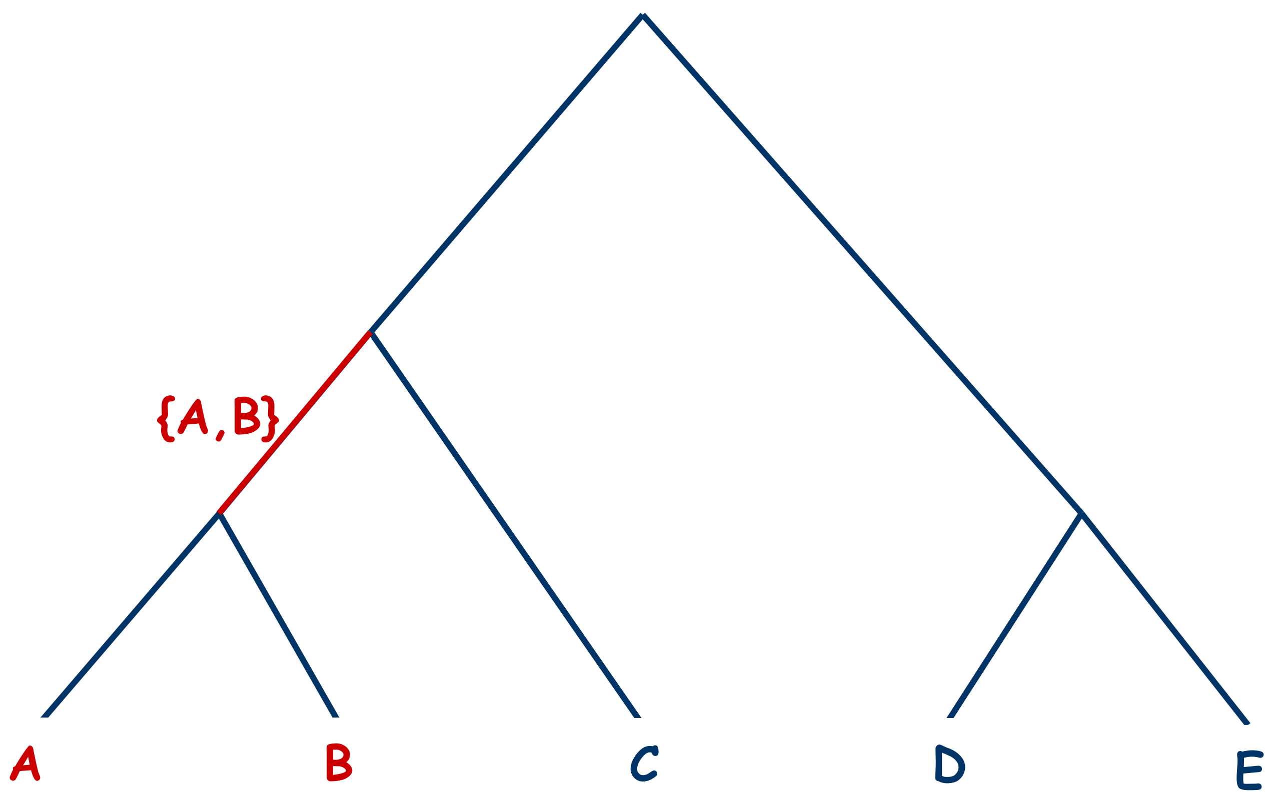
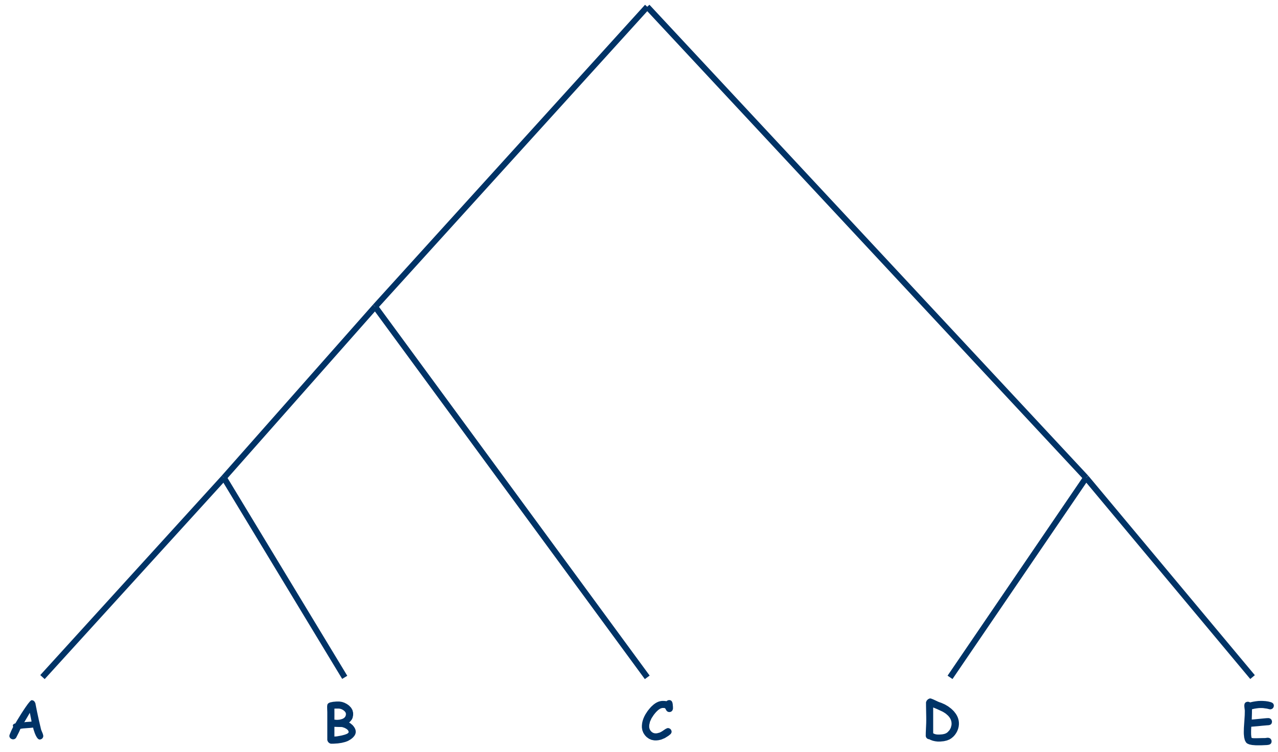


Compatible Clusters and Rooted Trees



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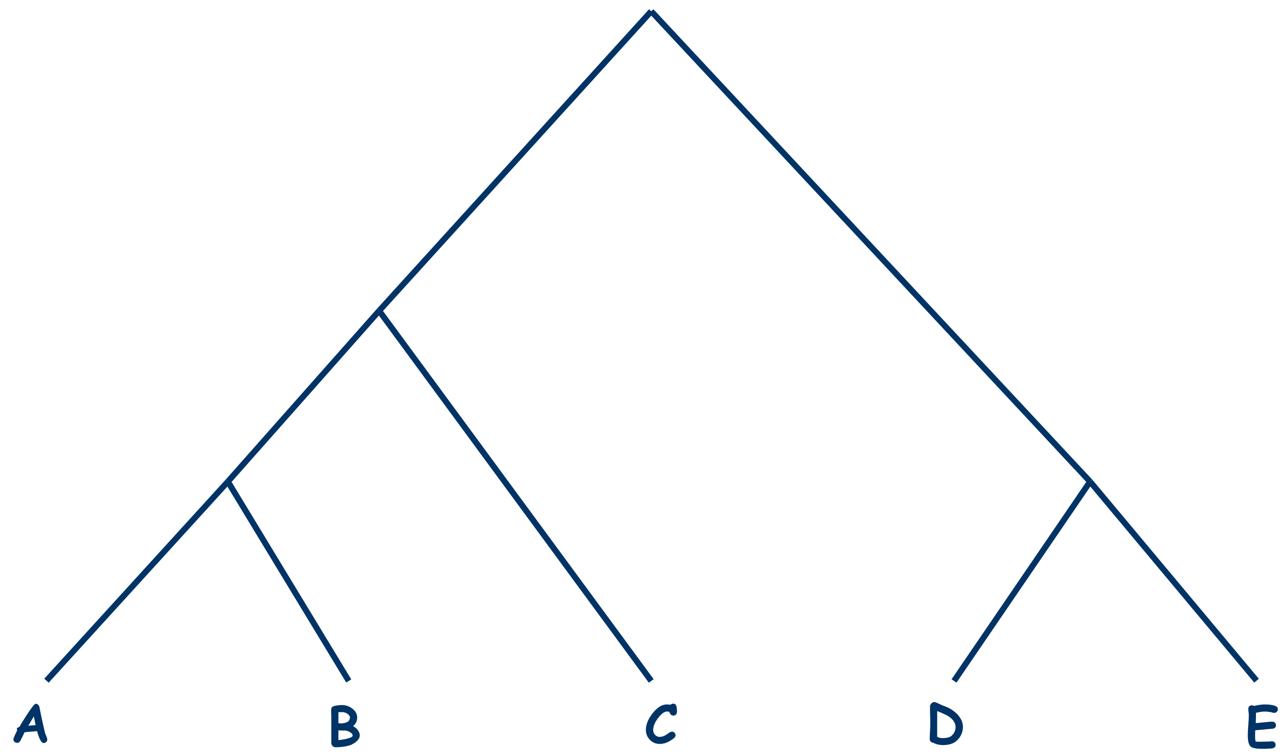

Rooted Tree -> Compatible Clusters

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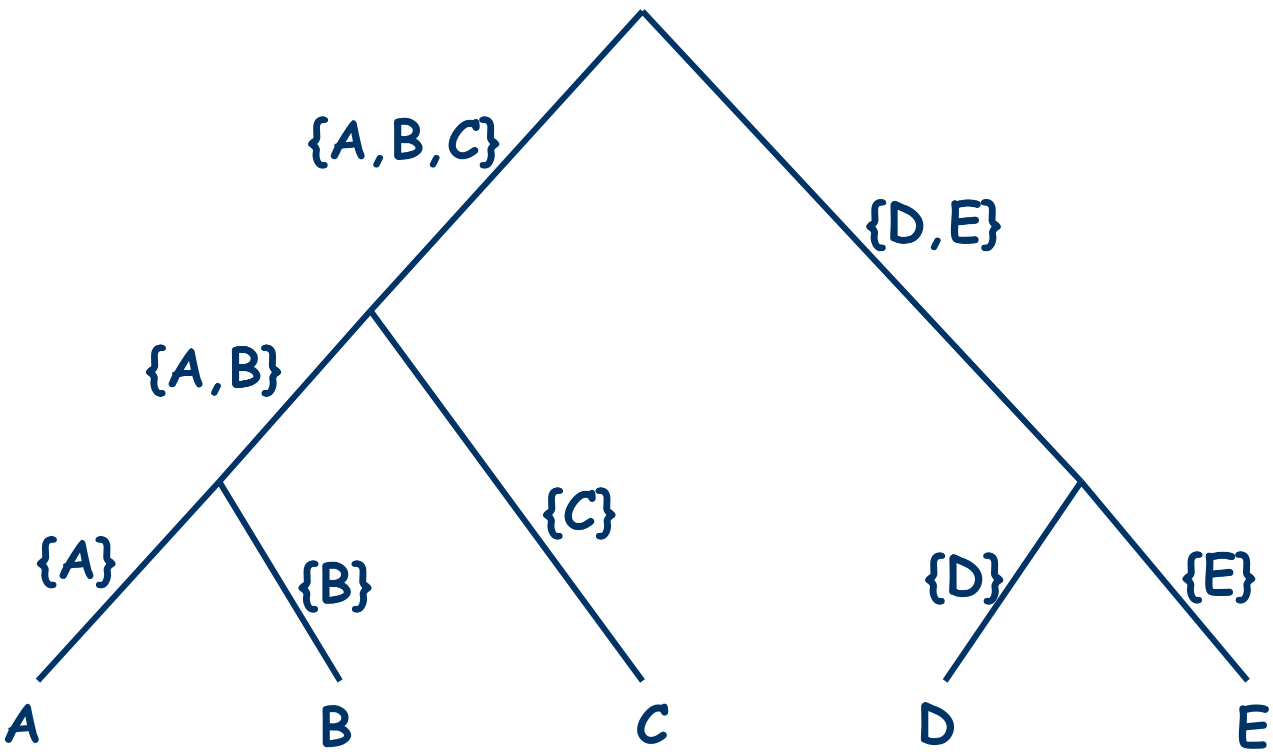

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Compatible Clusters and Rooted Trees

{A,B,C}

{D,E}

{A,B}

{C}

{A}

{B}

{D}

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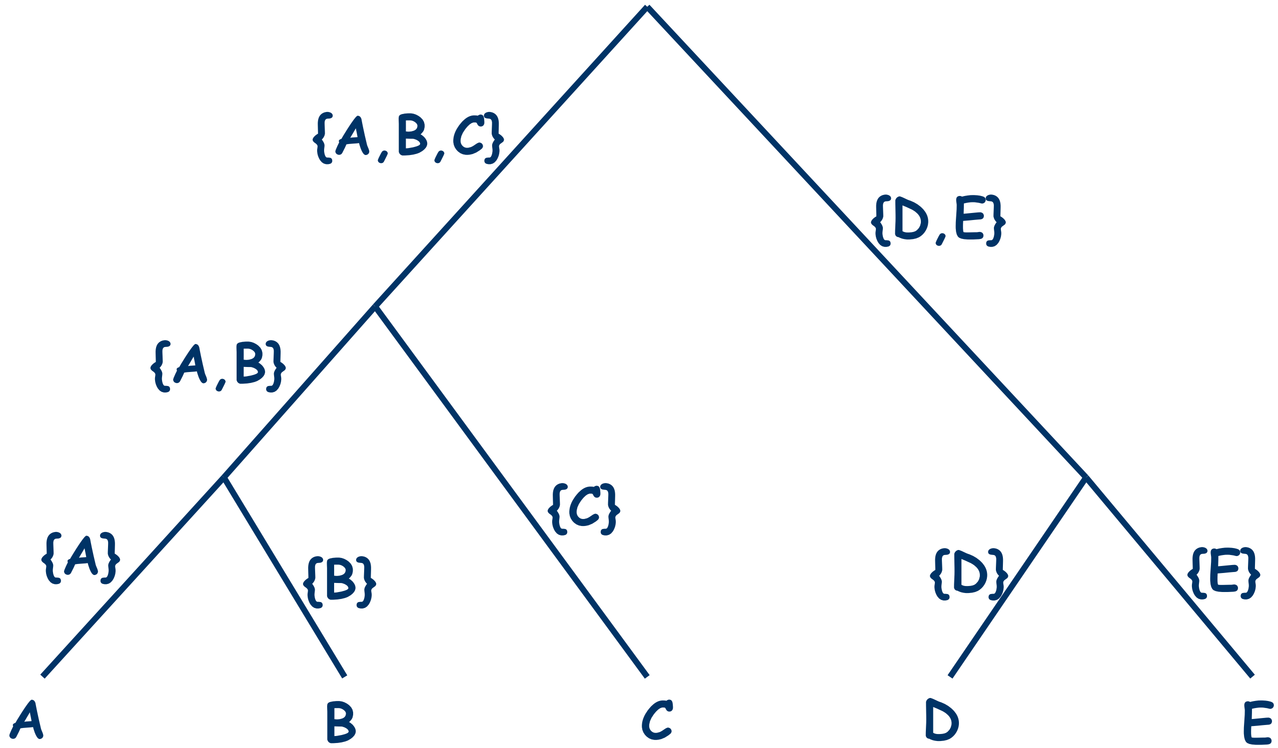

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Question:

How to represent *incompatible* clusters?

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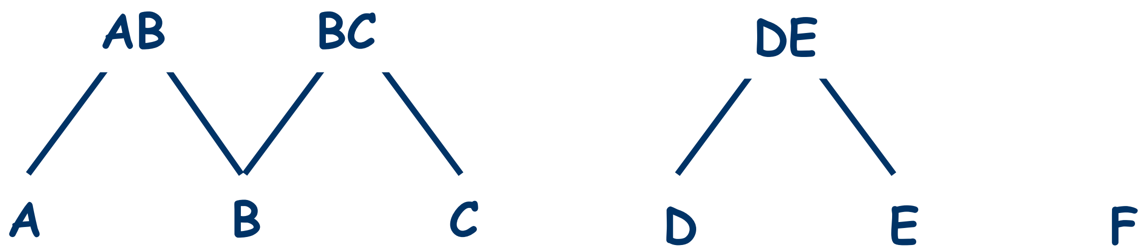

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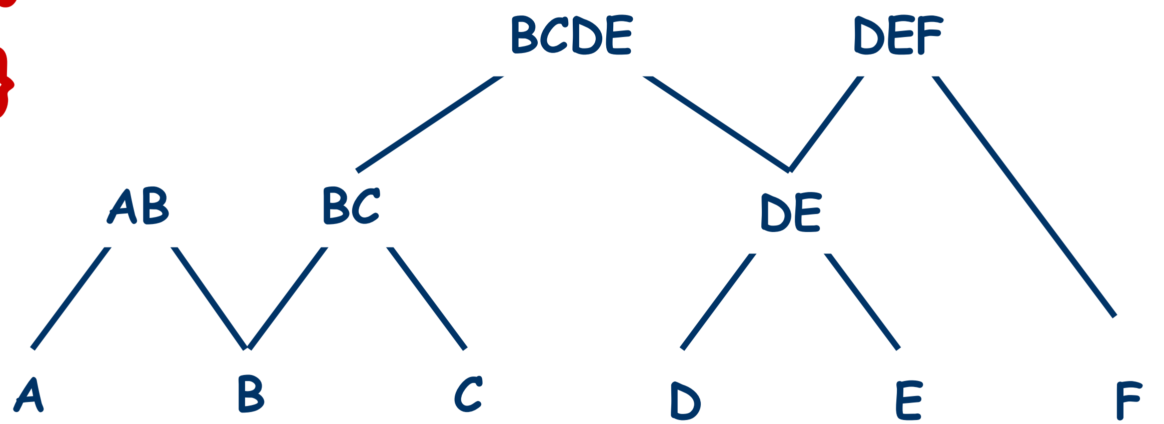

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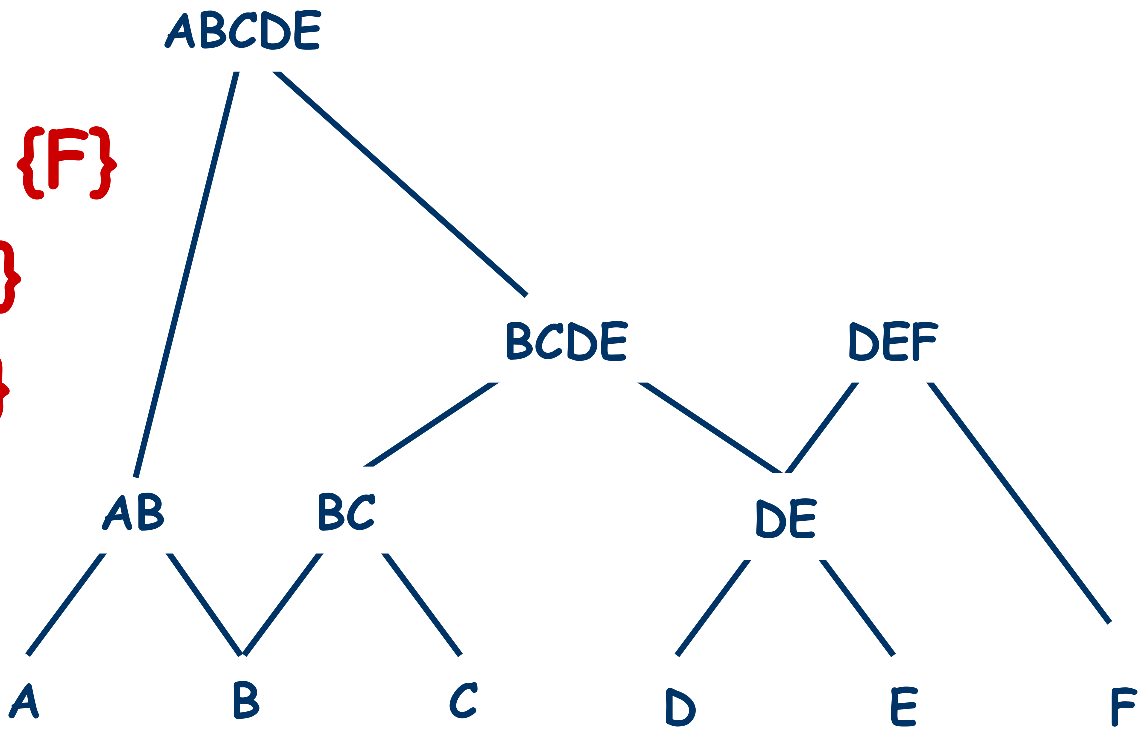

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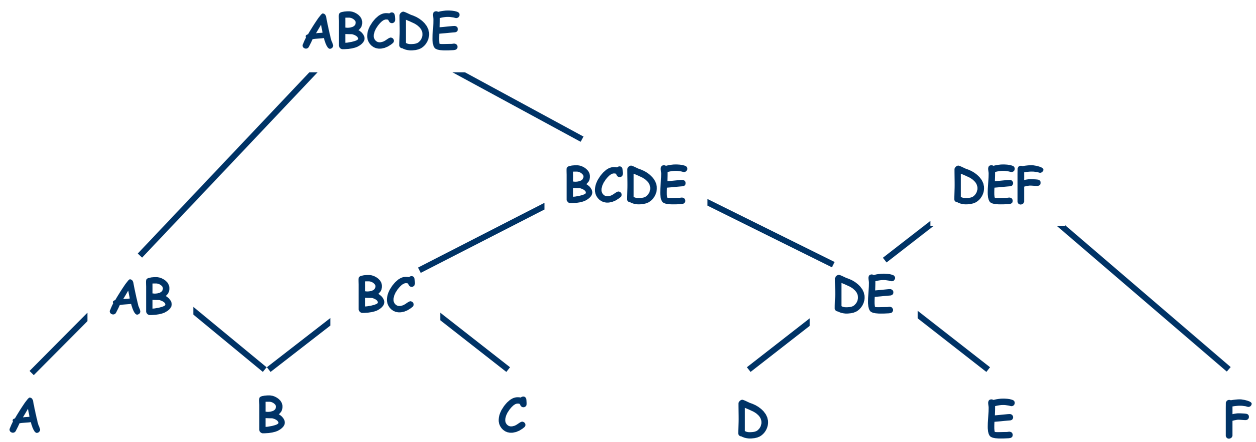

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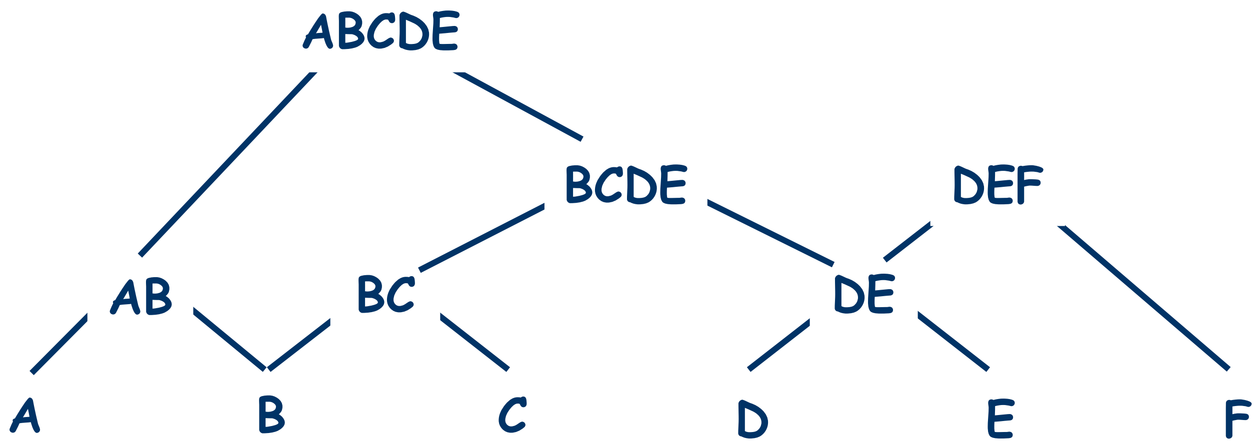

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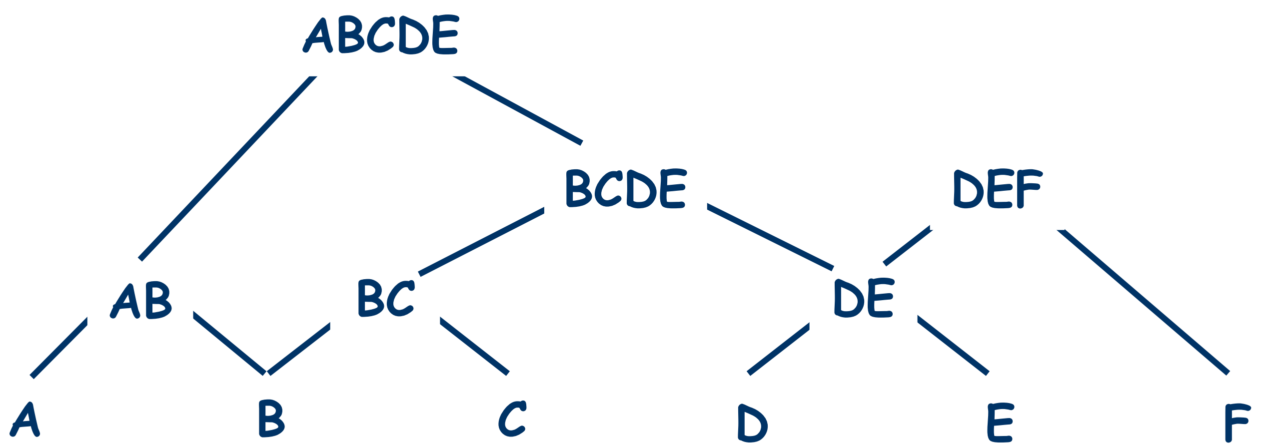

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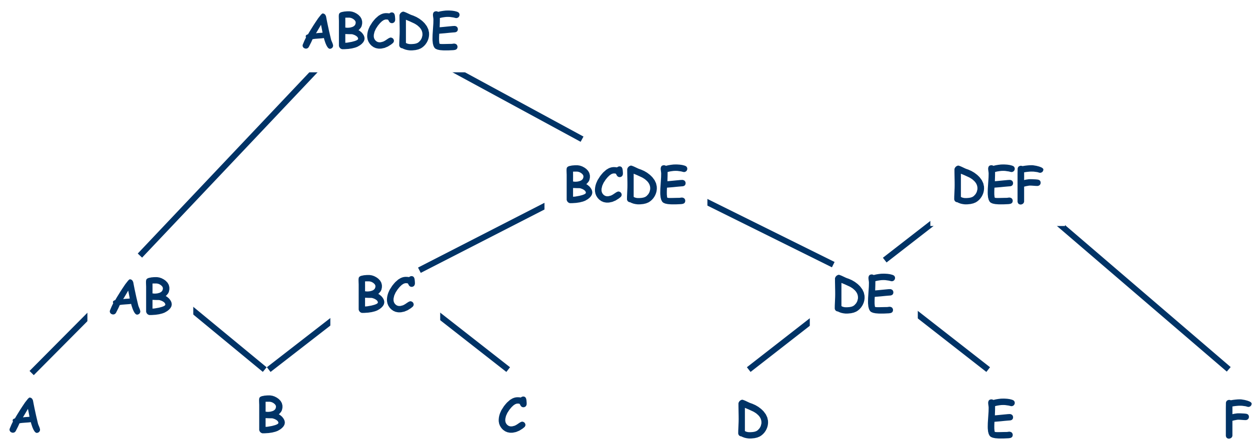

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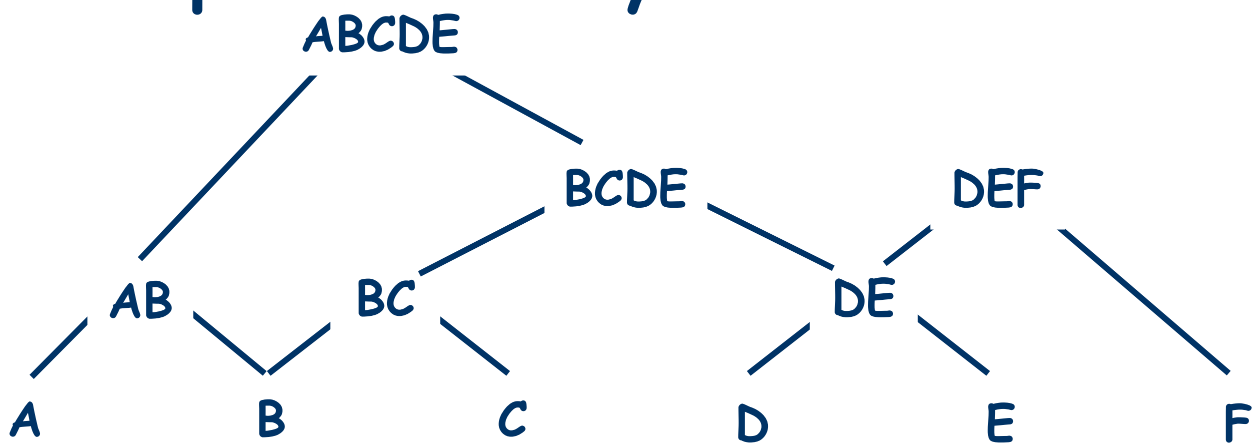

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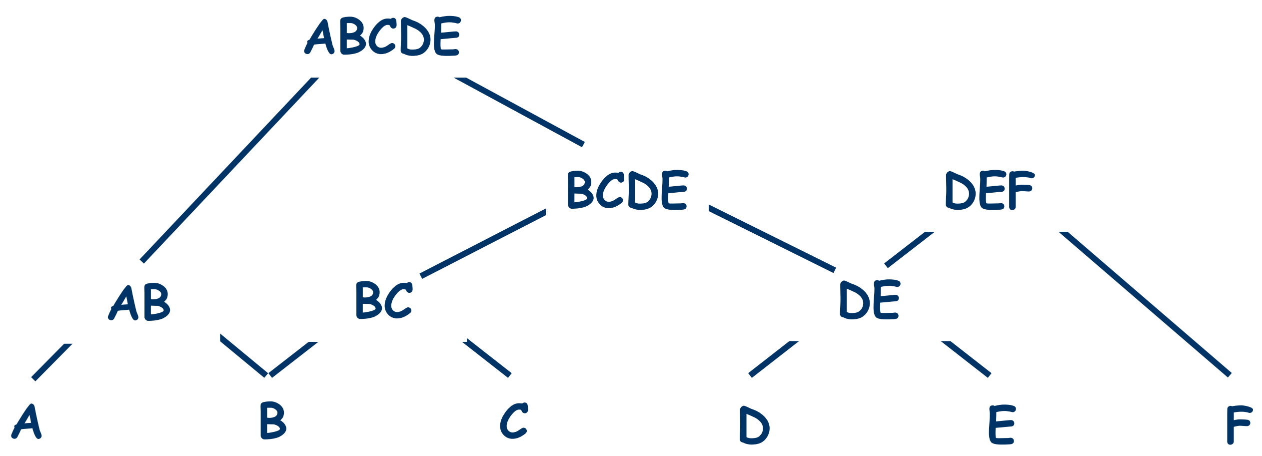

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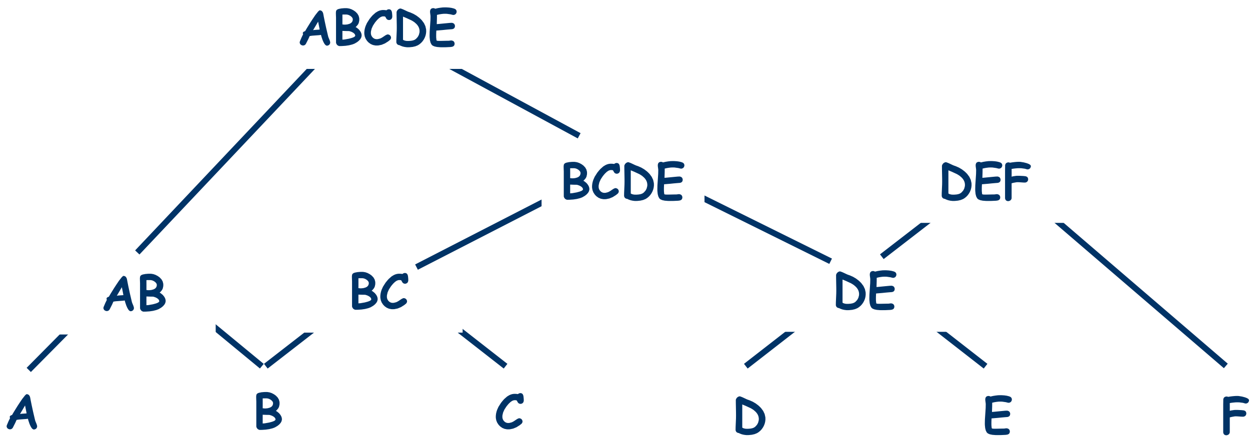

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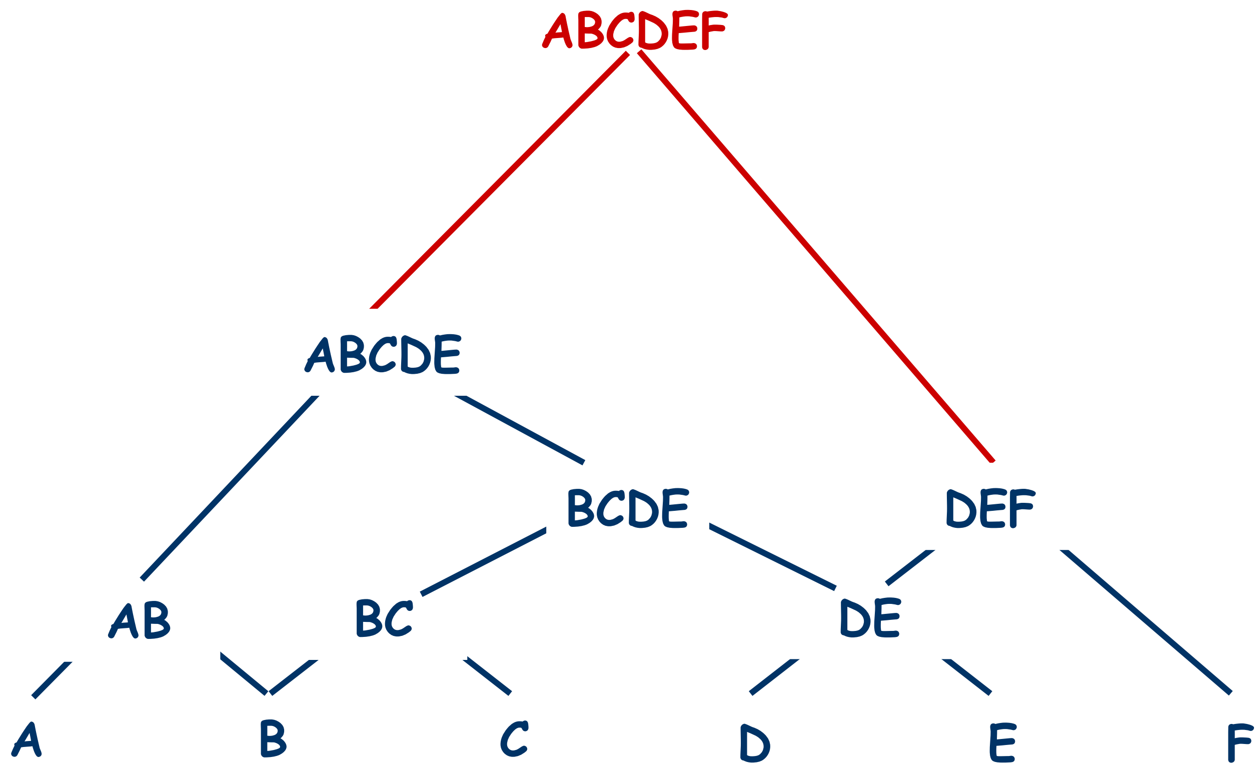

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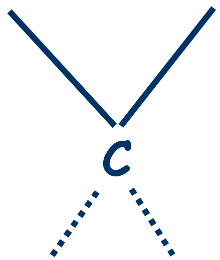

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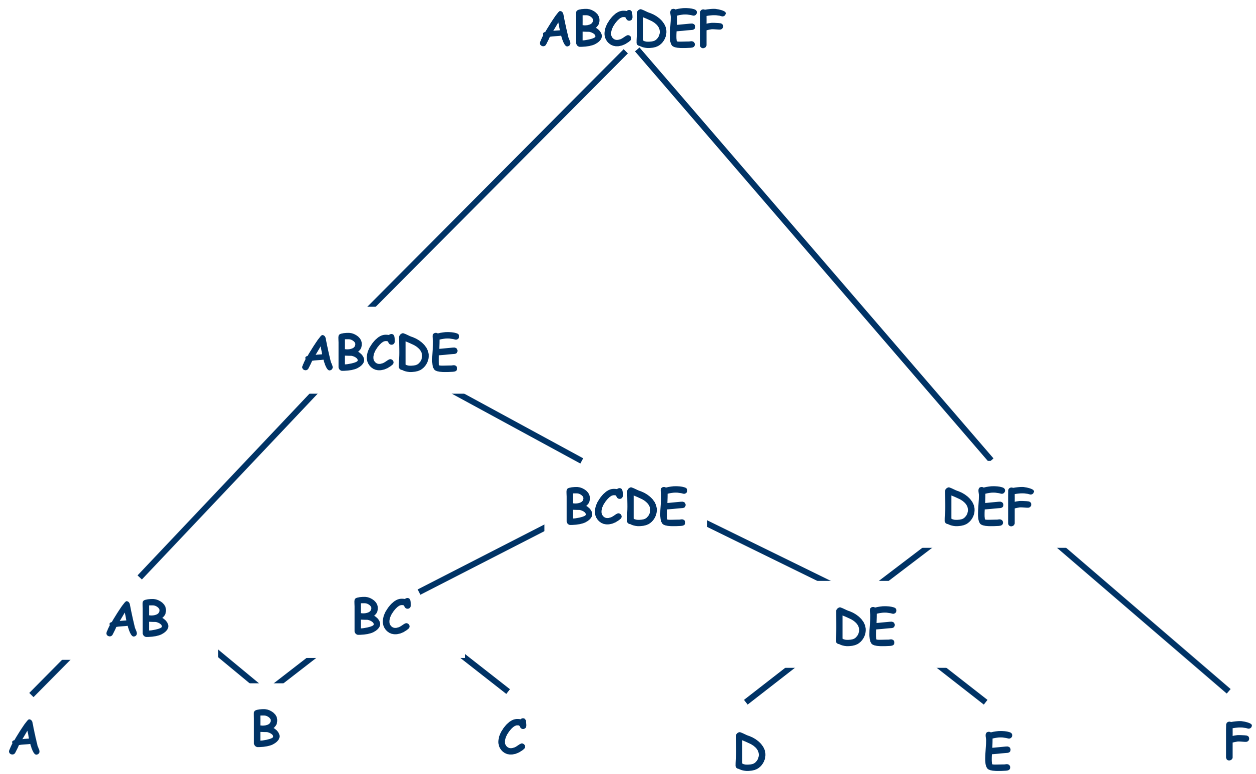
ABCDEF
ABCDE
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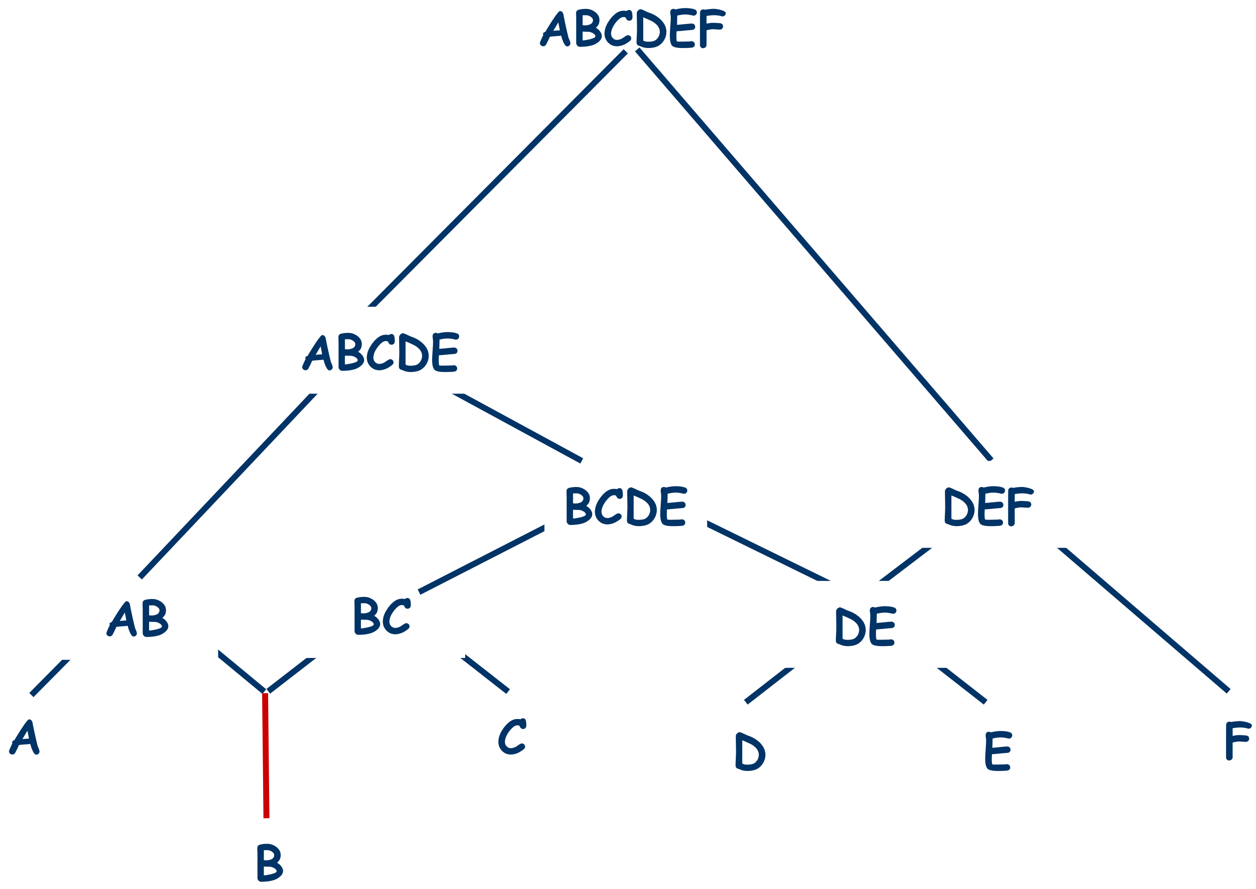
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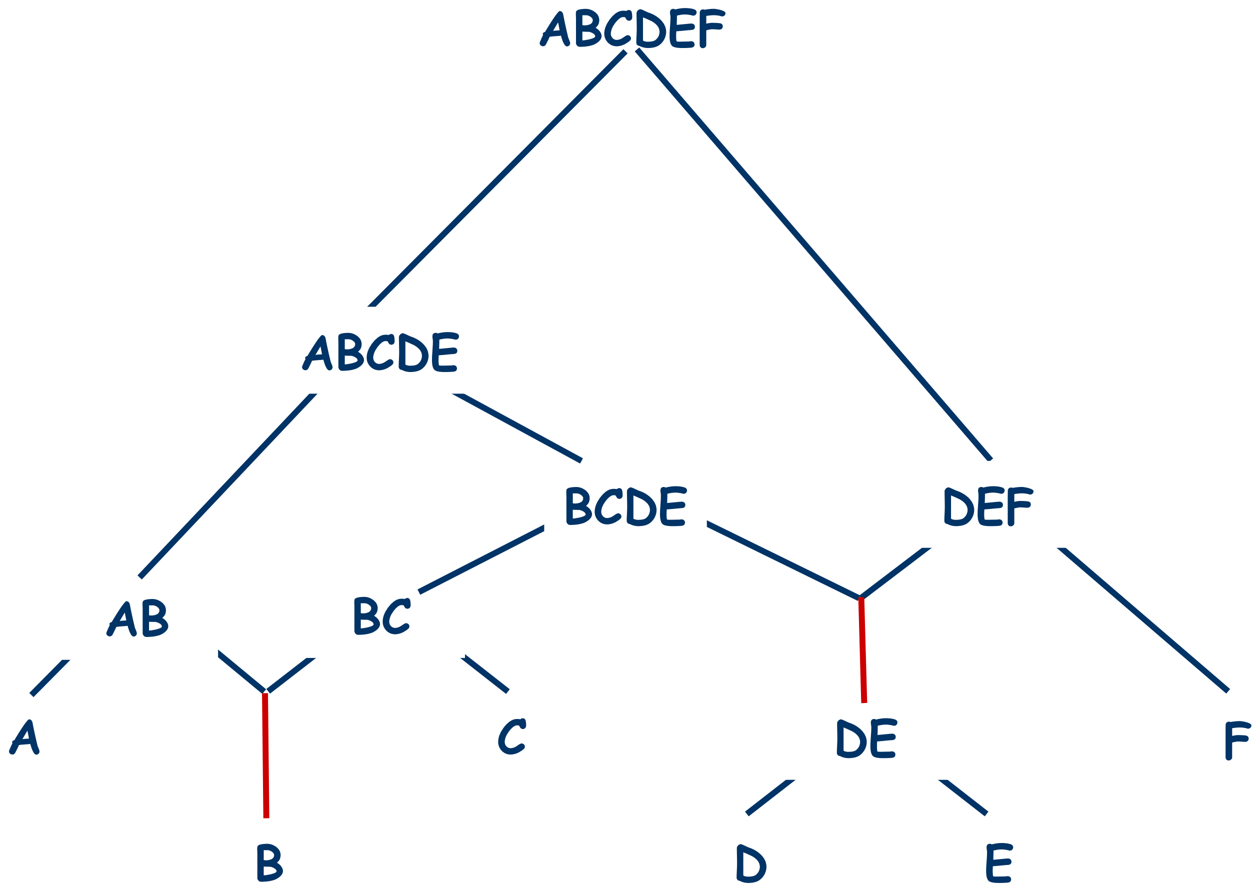
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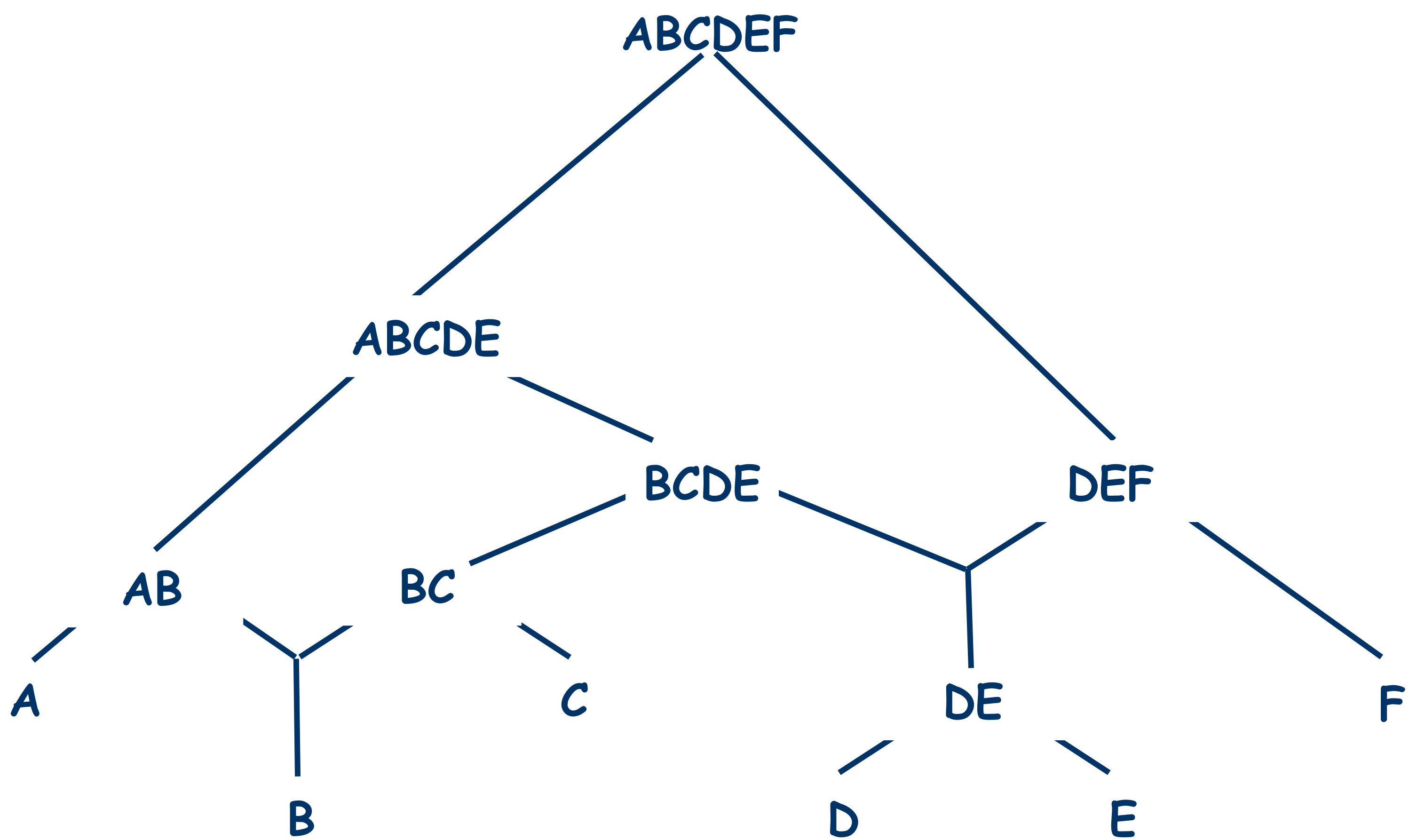
-> Represent every cluster by its in-edge
(which is unique now!)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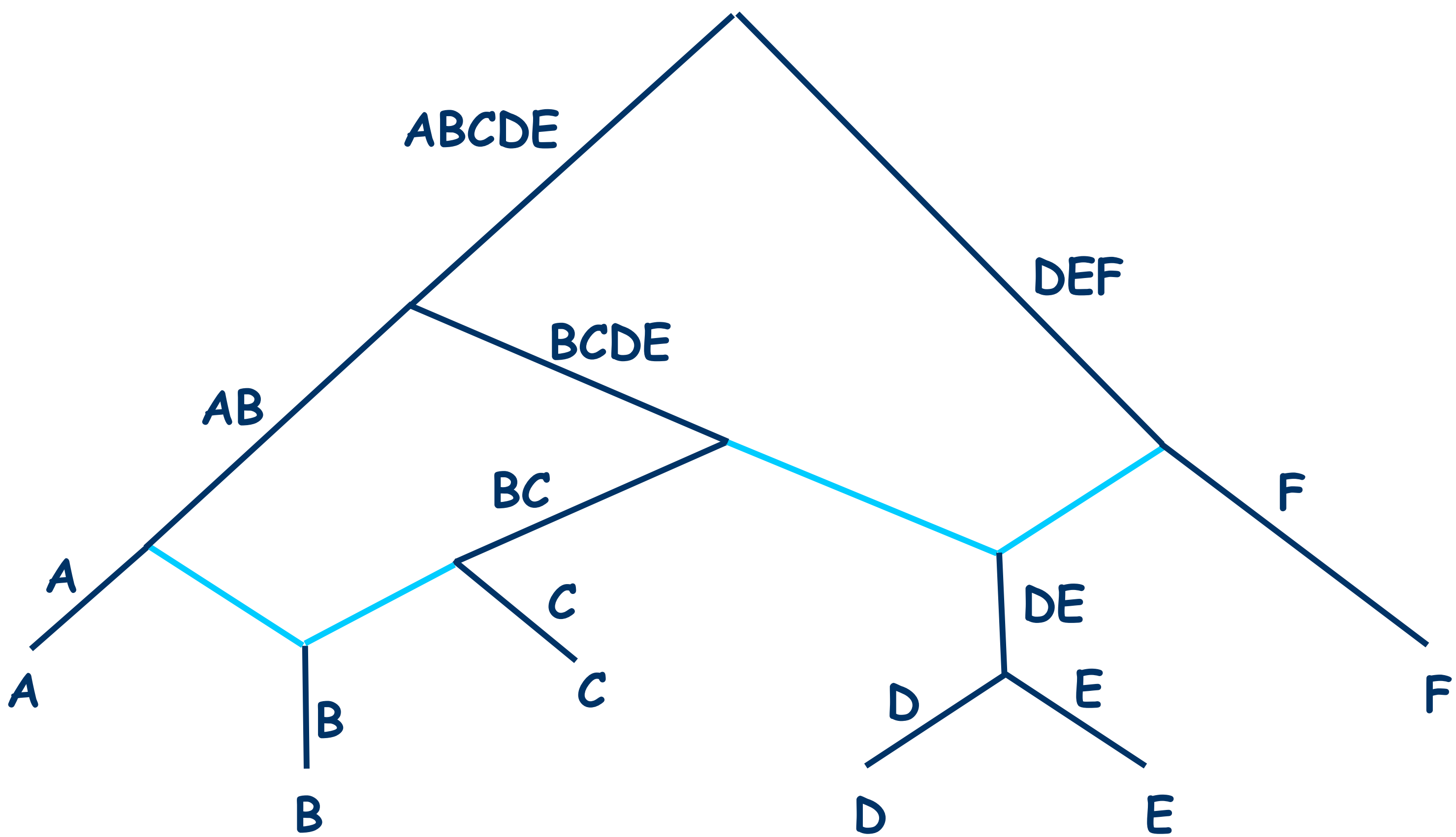
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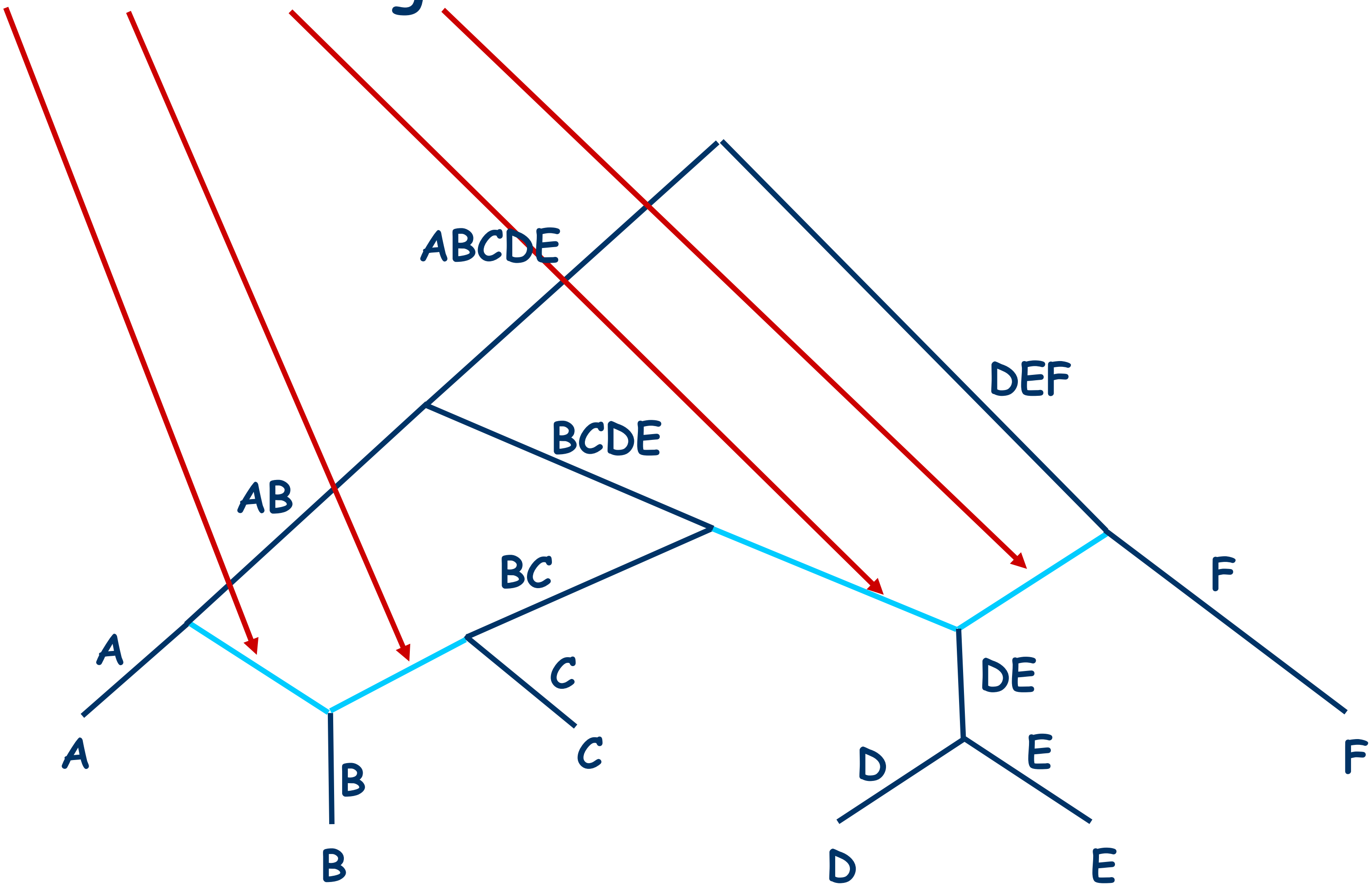
Reticulation edges



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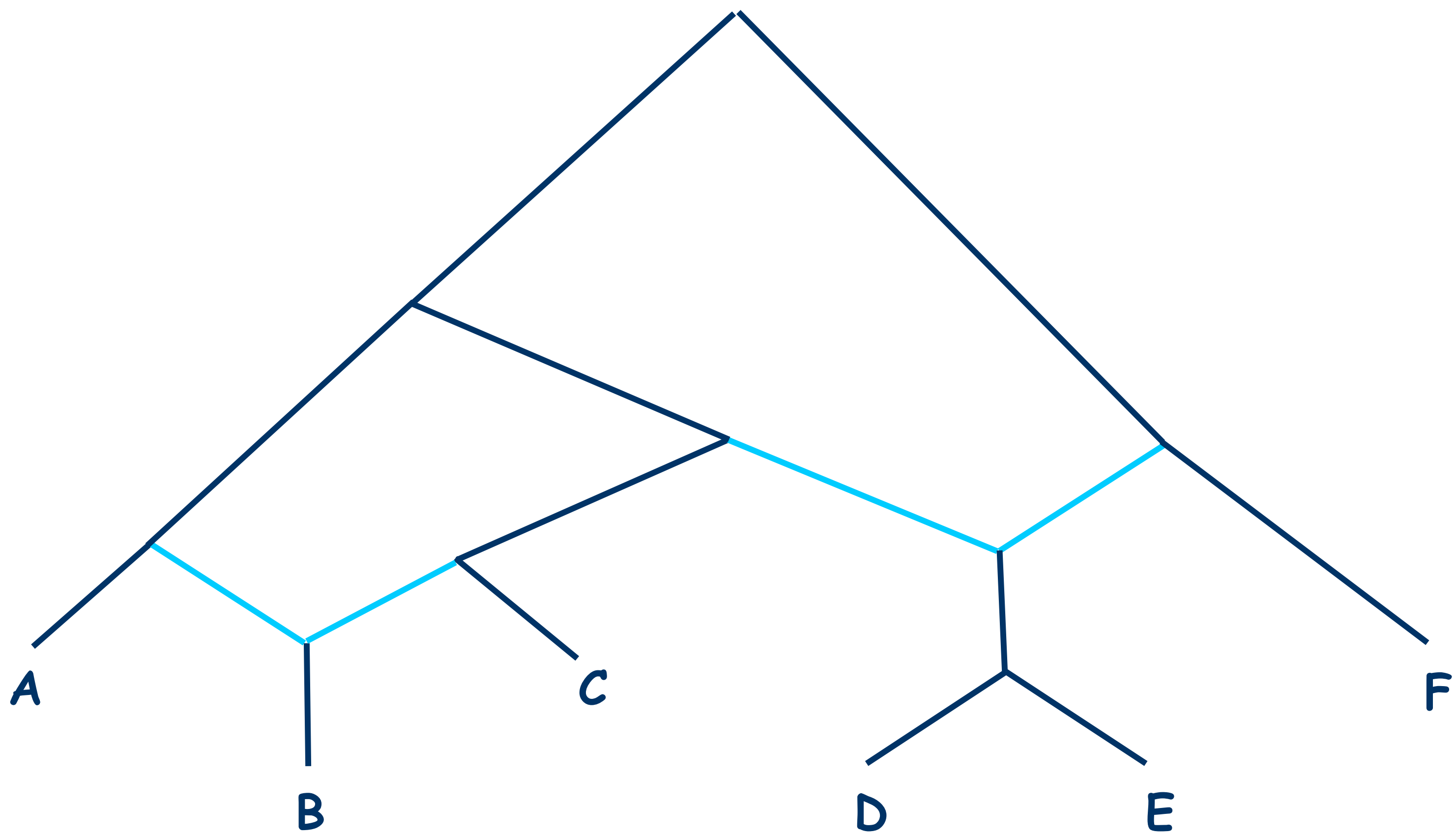

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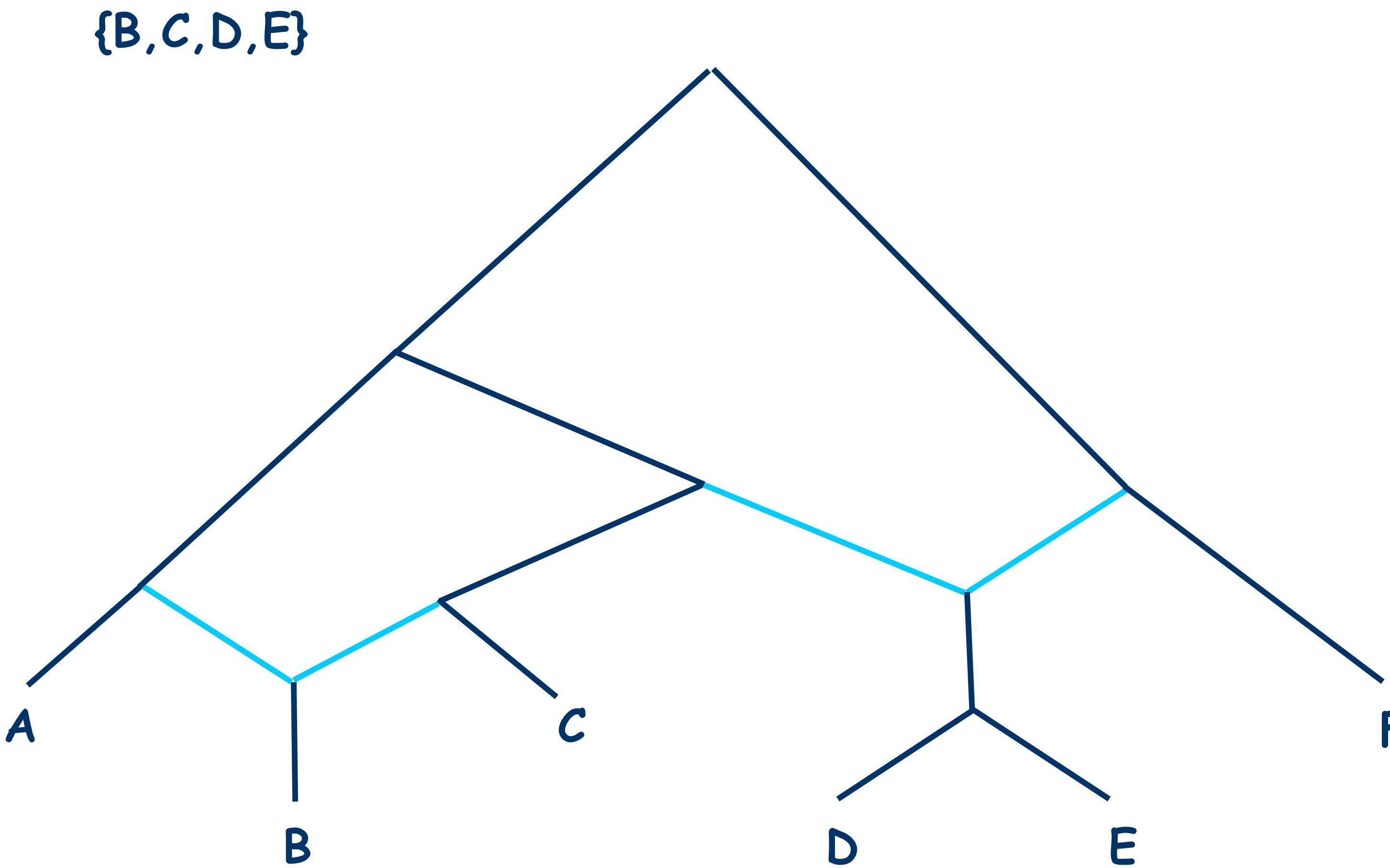

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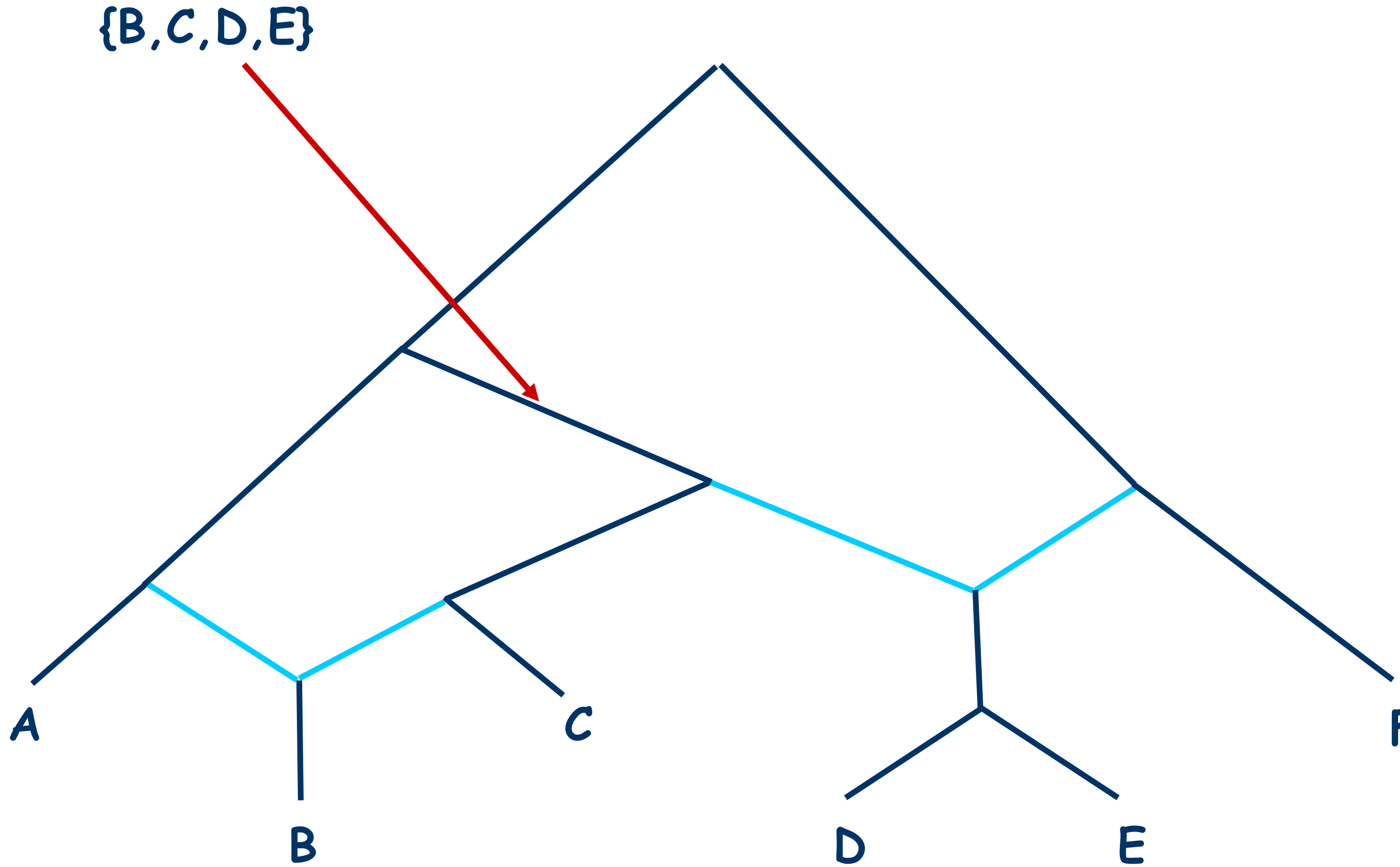
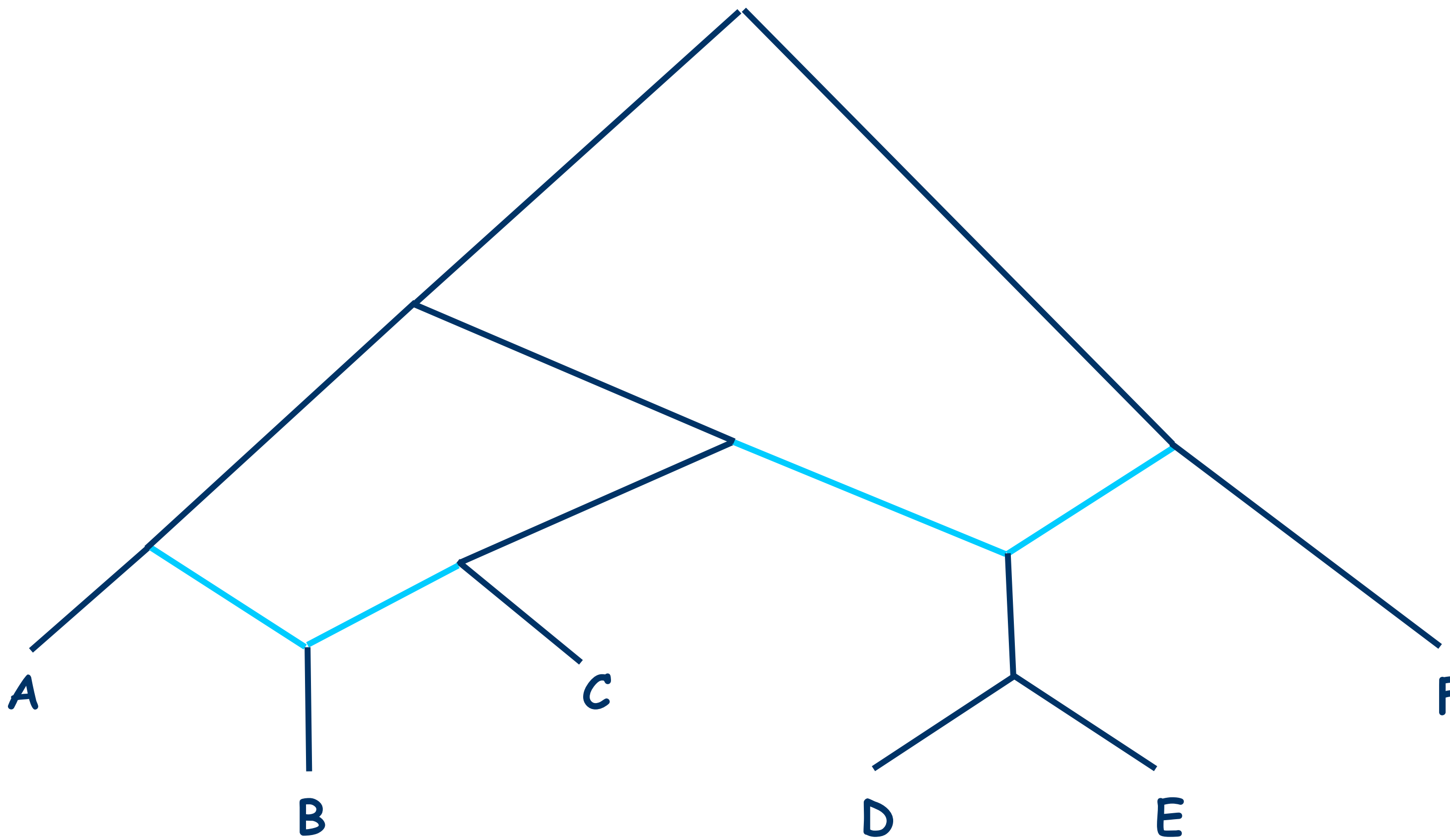
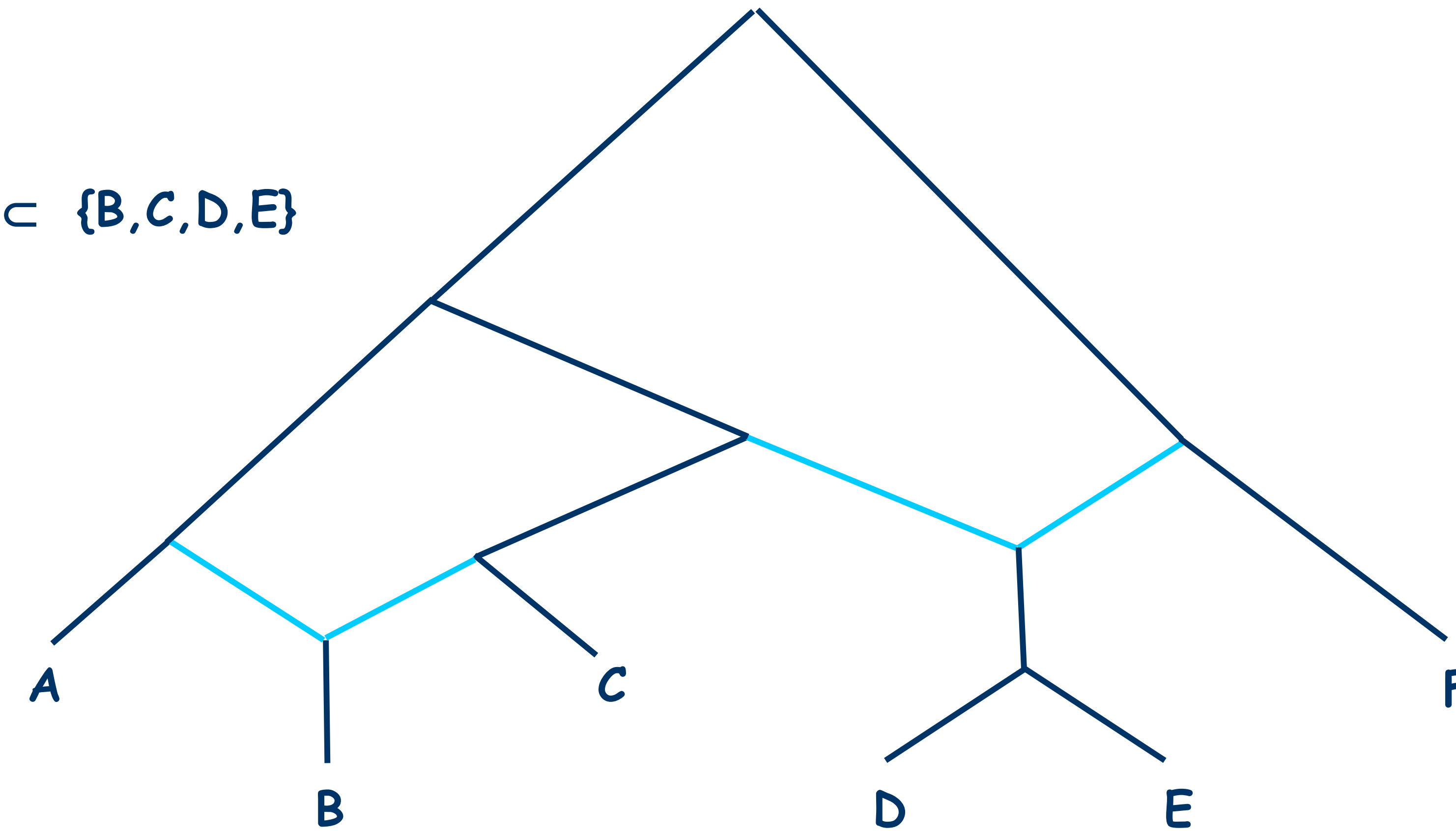


Nestedness



Nestedness

$\{B,C\} \subset \{B,C,D,E\}$



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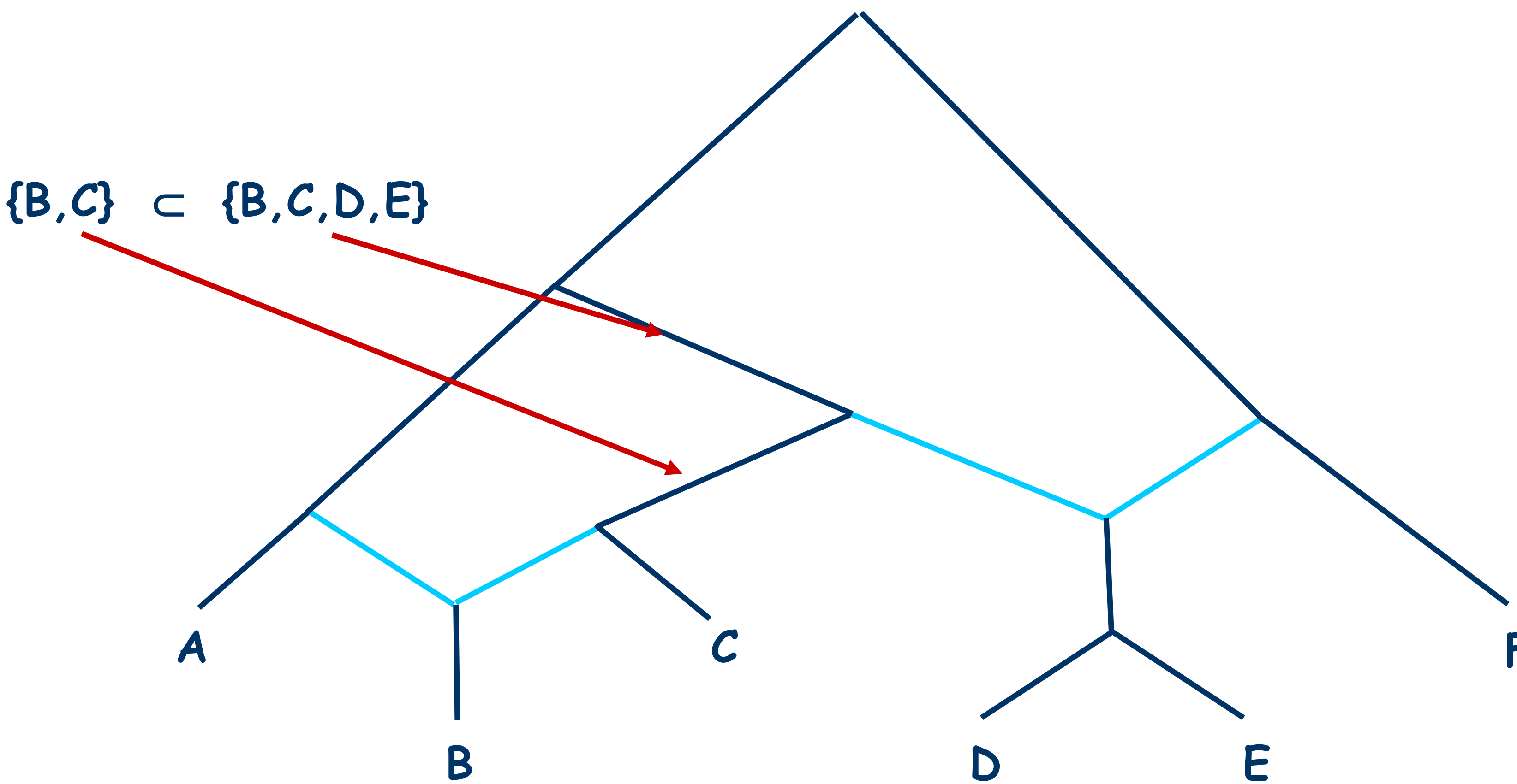
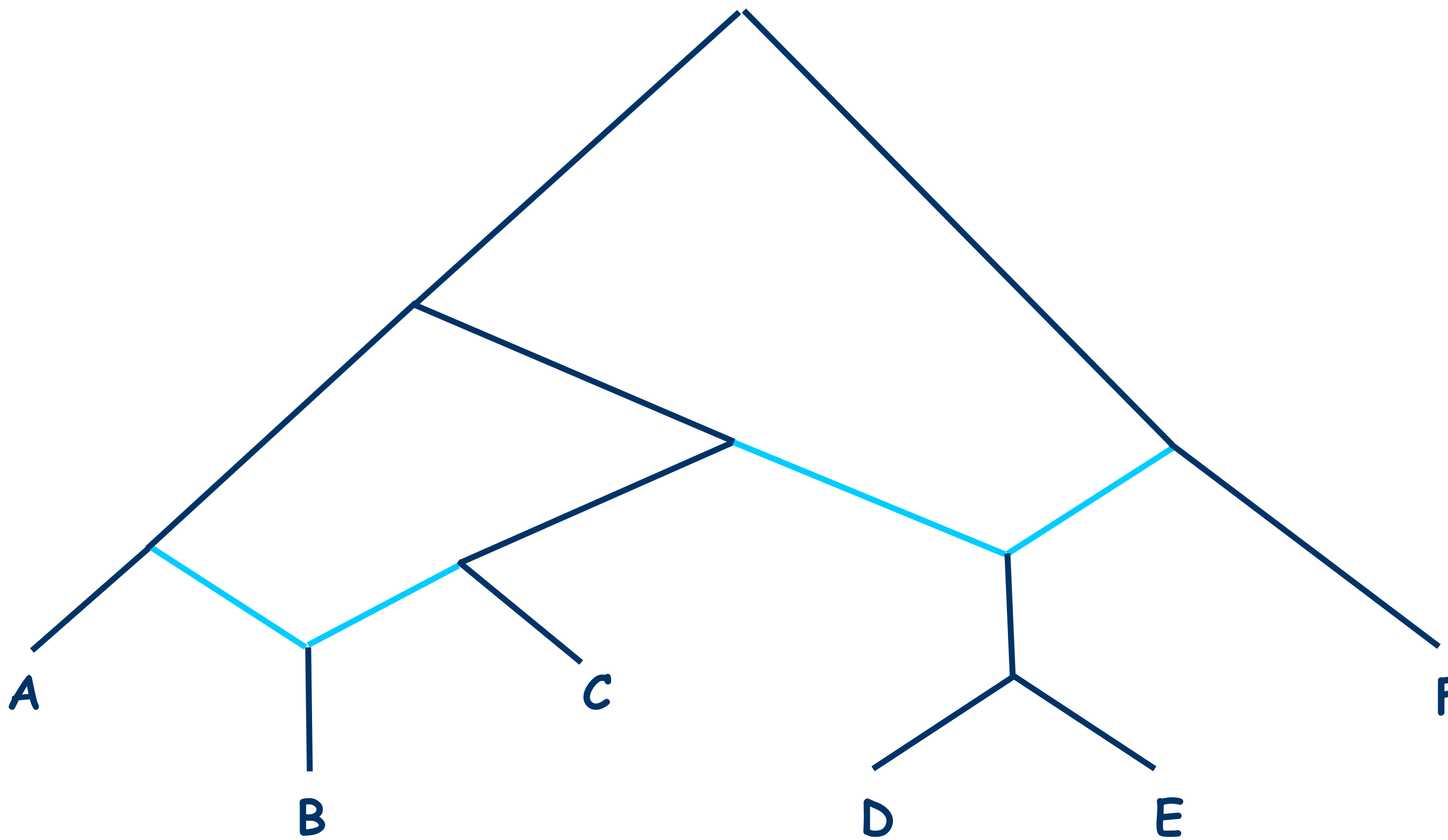


Reducedness



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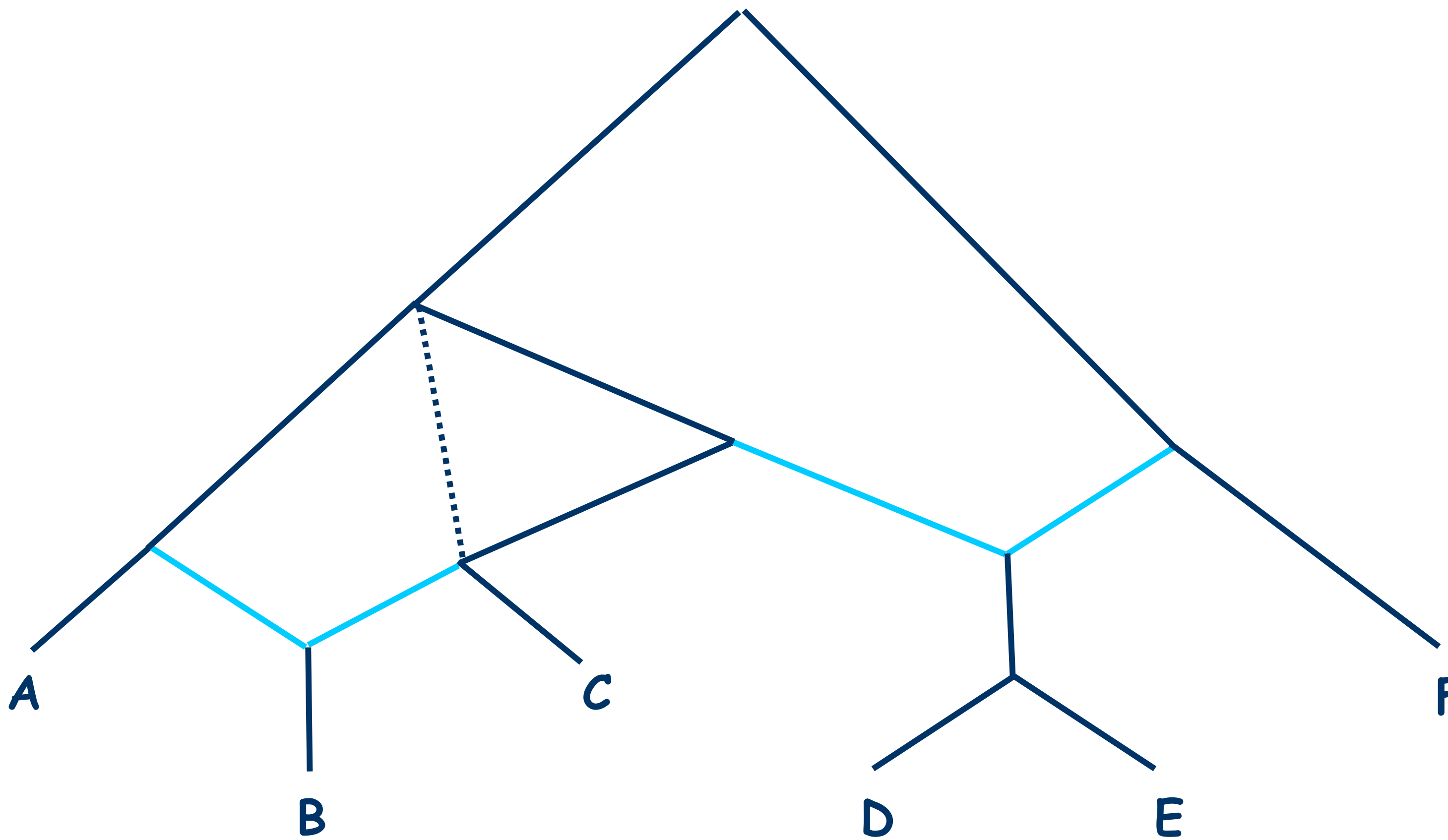

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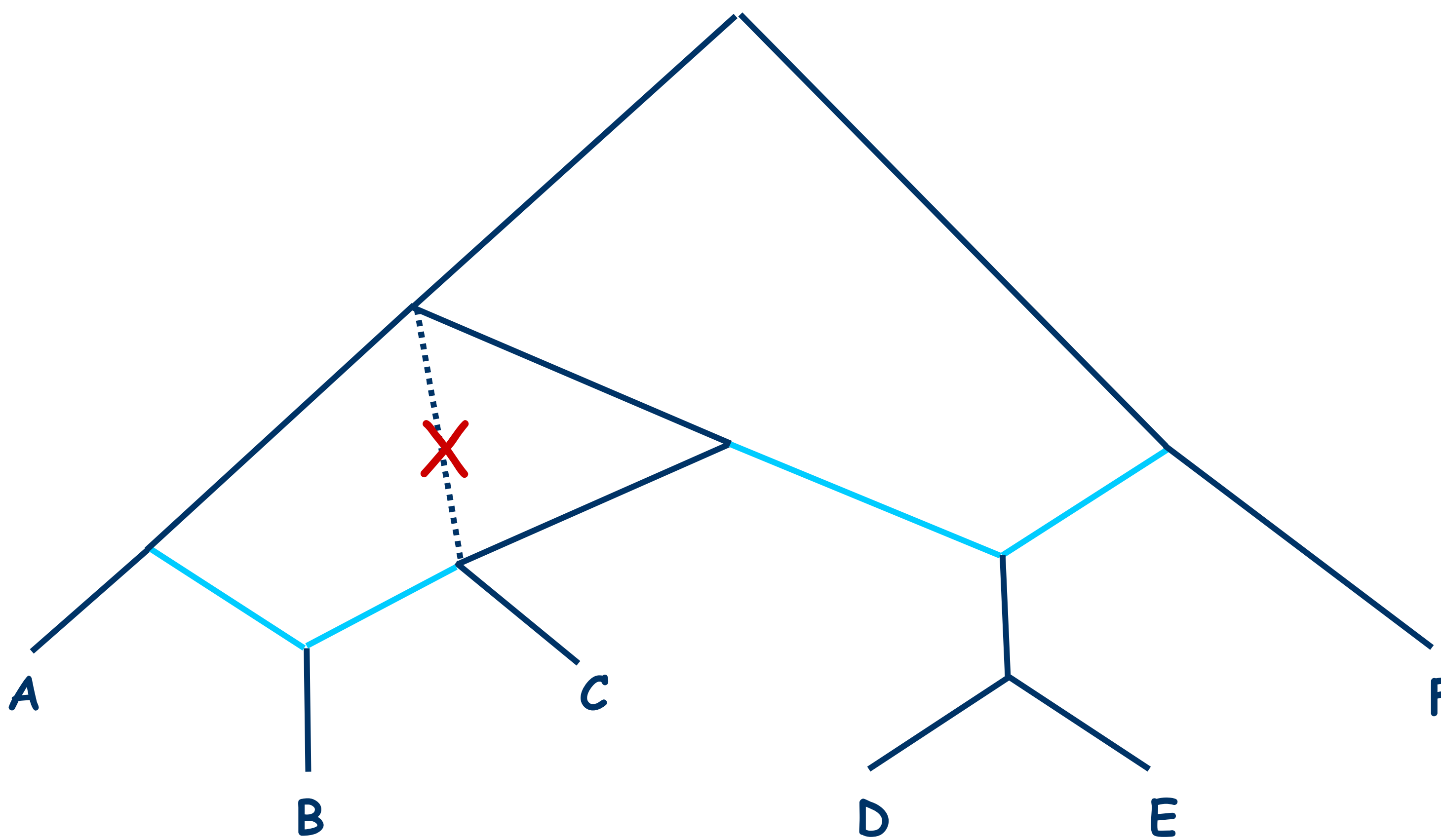

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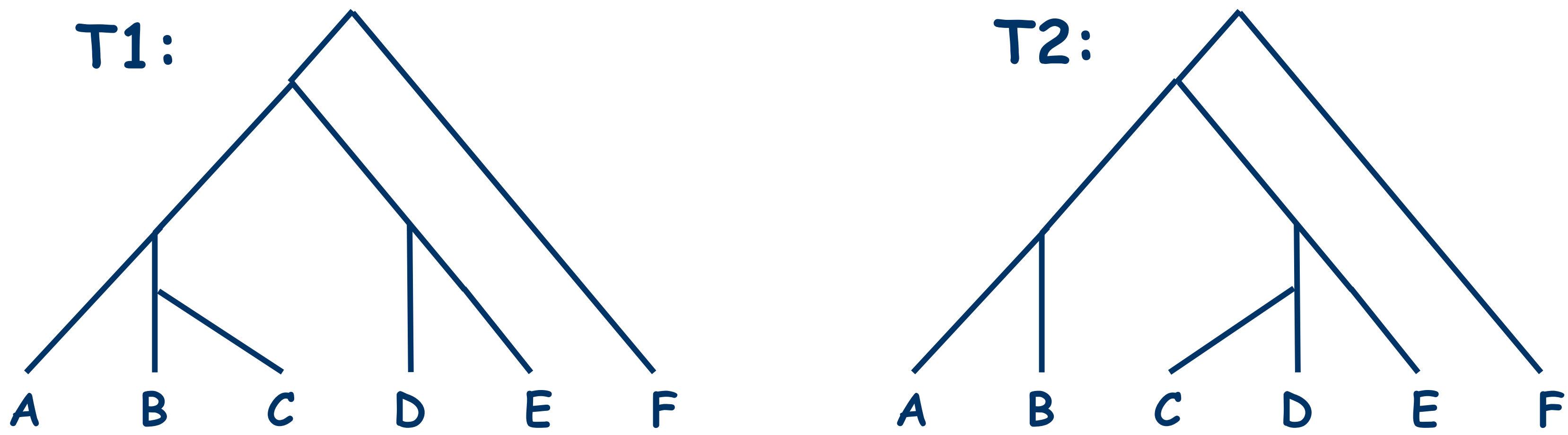
In contrast we define the „softwired interpretation" where we may switch reticulation edges on or off.

Hardwired / Softwired



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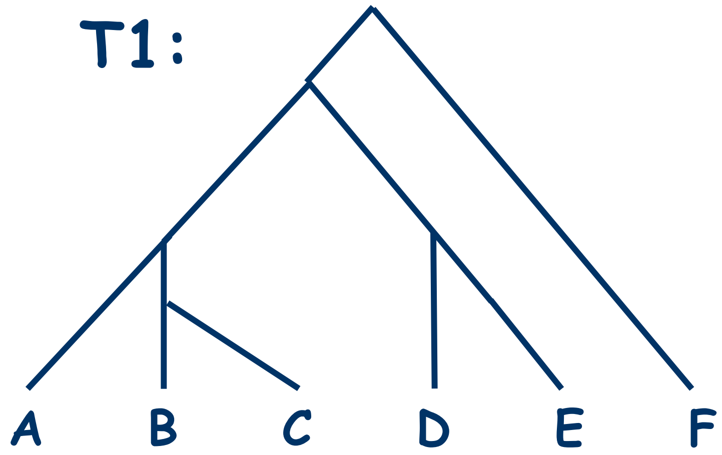

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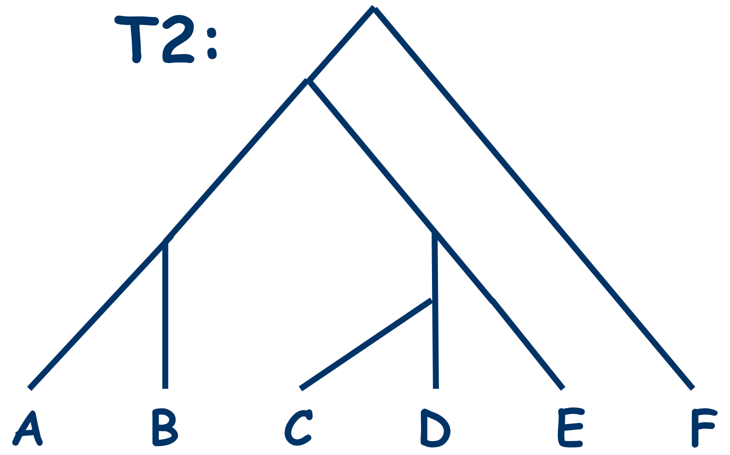

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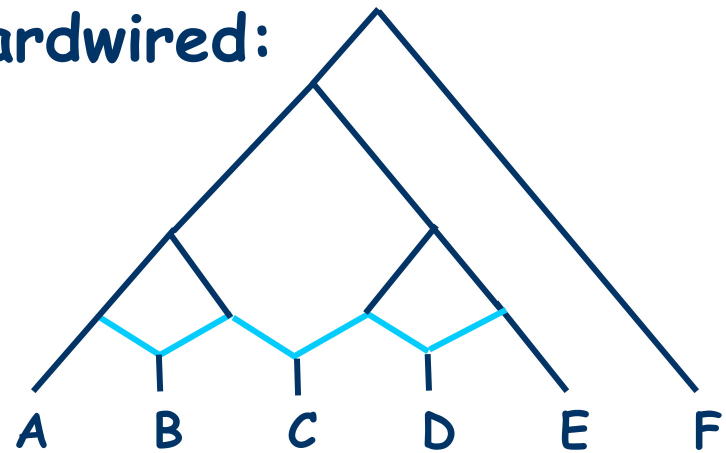

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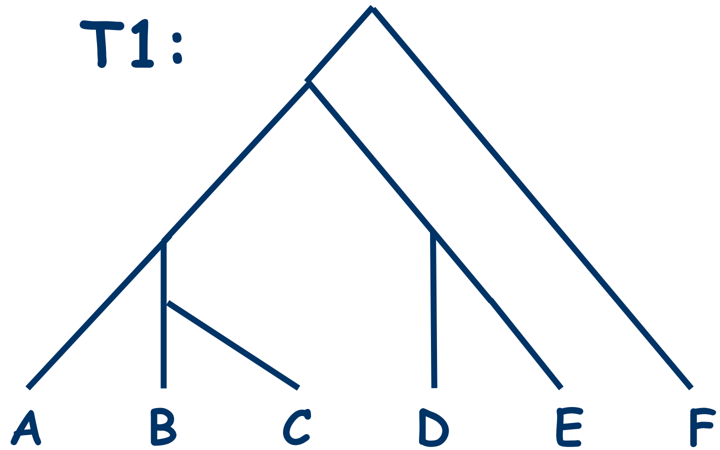

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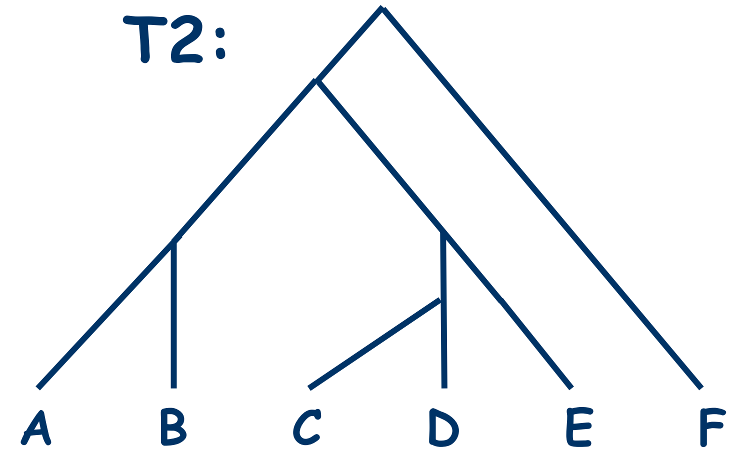

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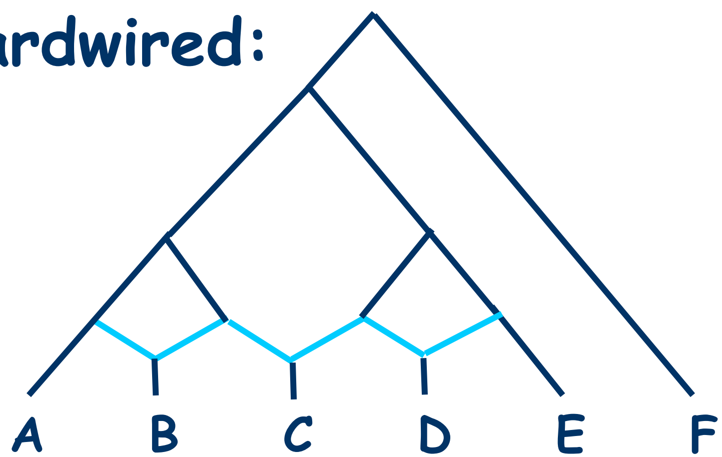

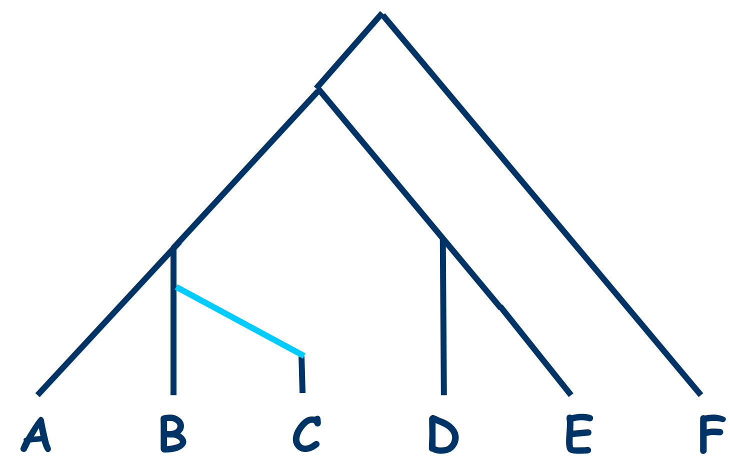

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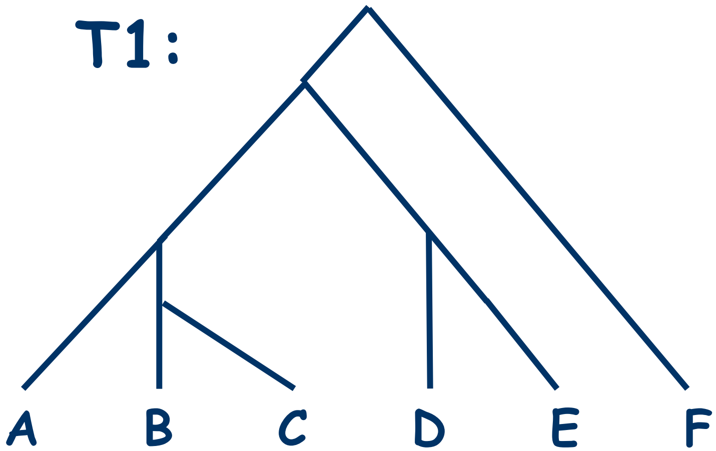

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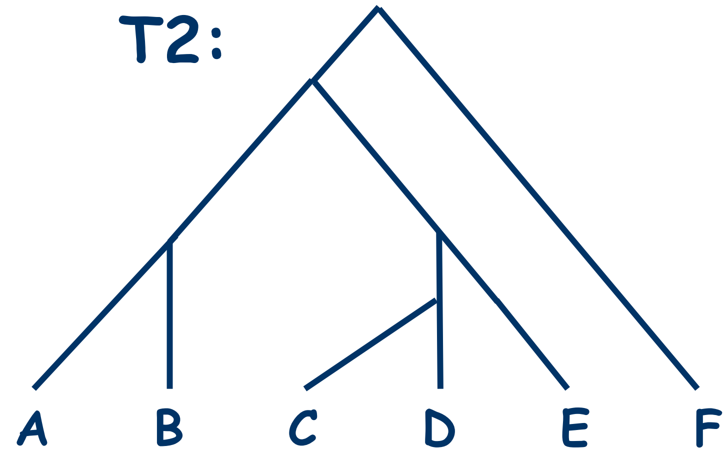

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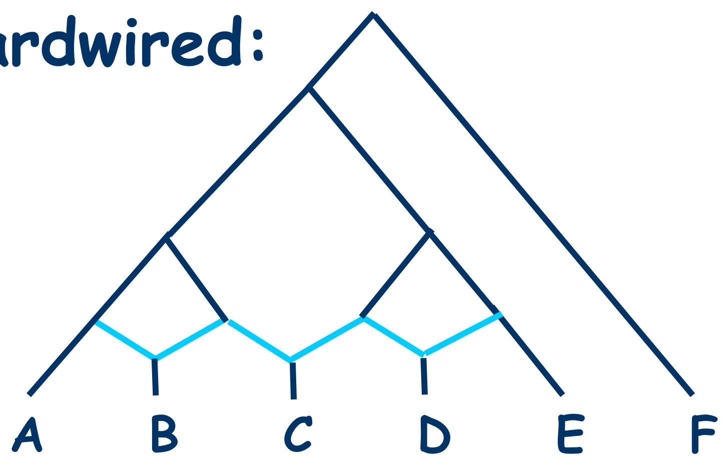

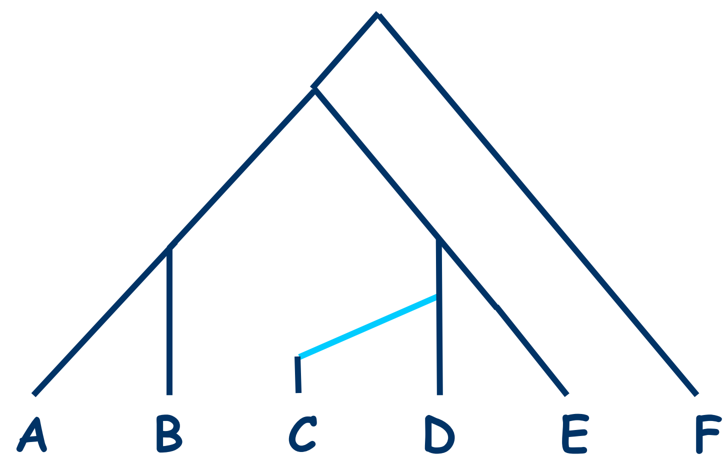

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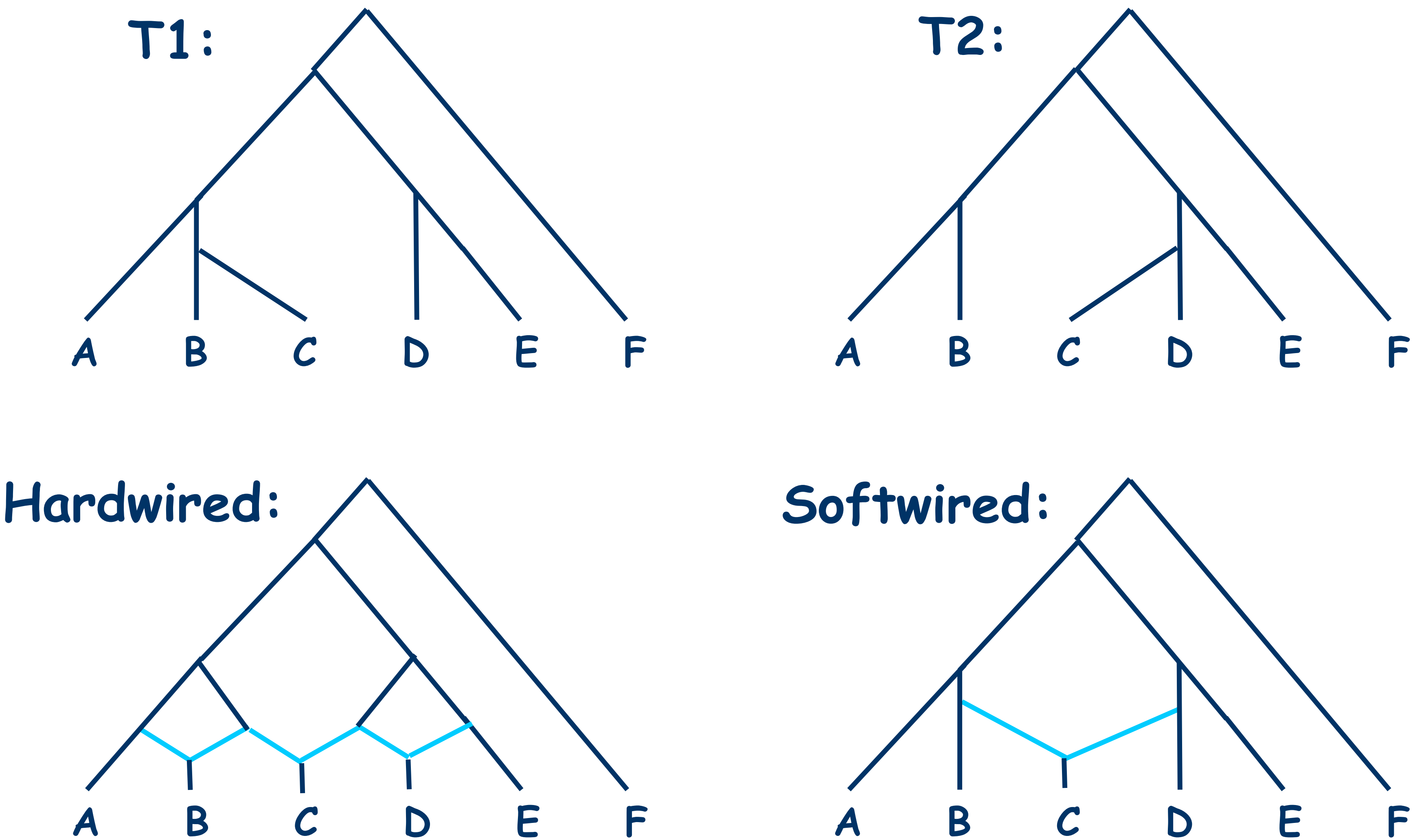

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  - More reticulations, "looks complicated"
  - Canonical network, computationally easy

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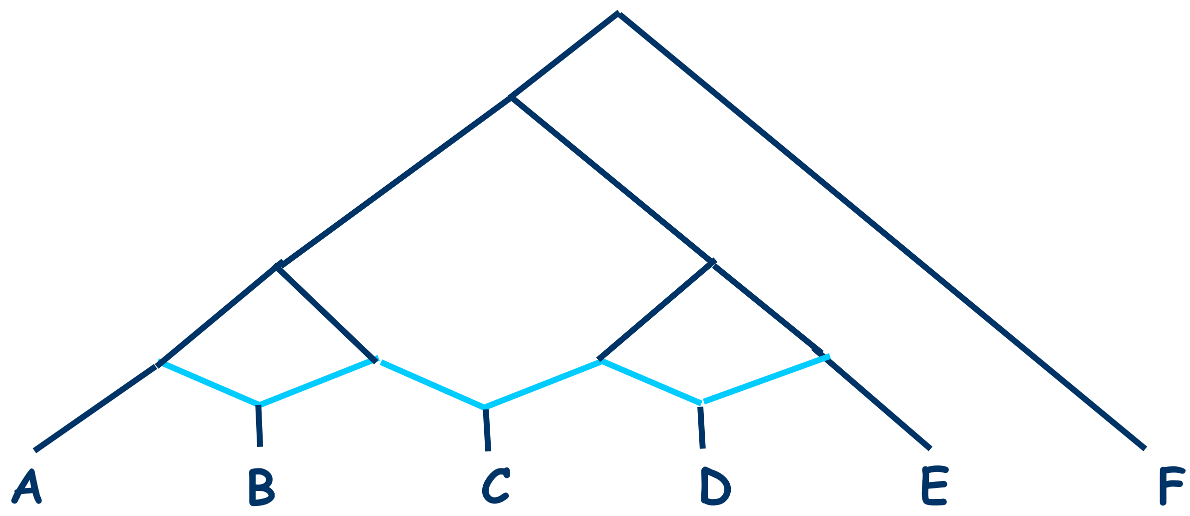
Lowest Single Ancestor: LSA



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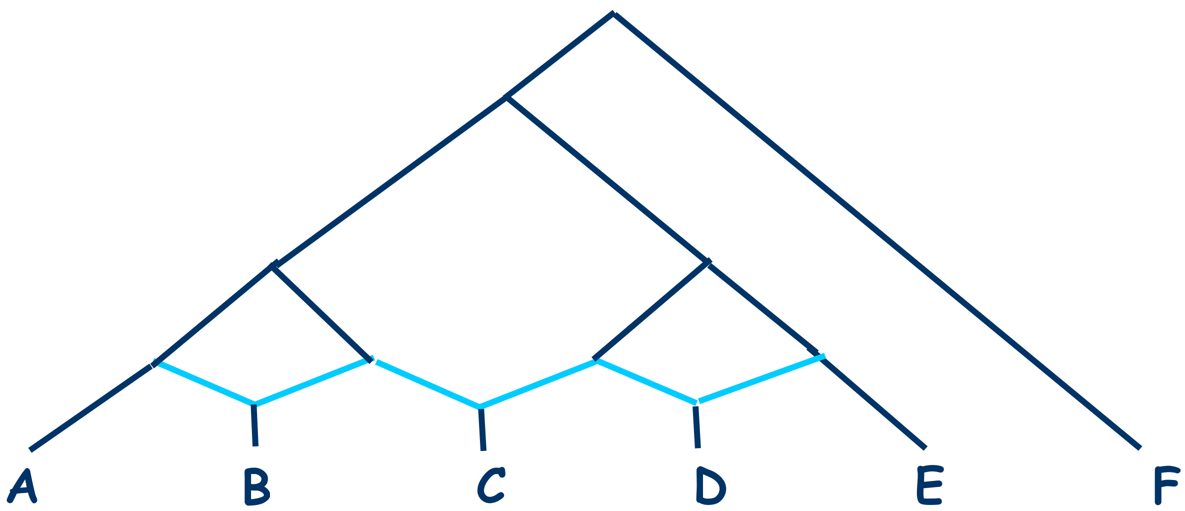
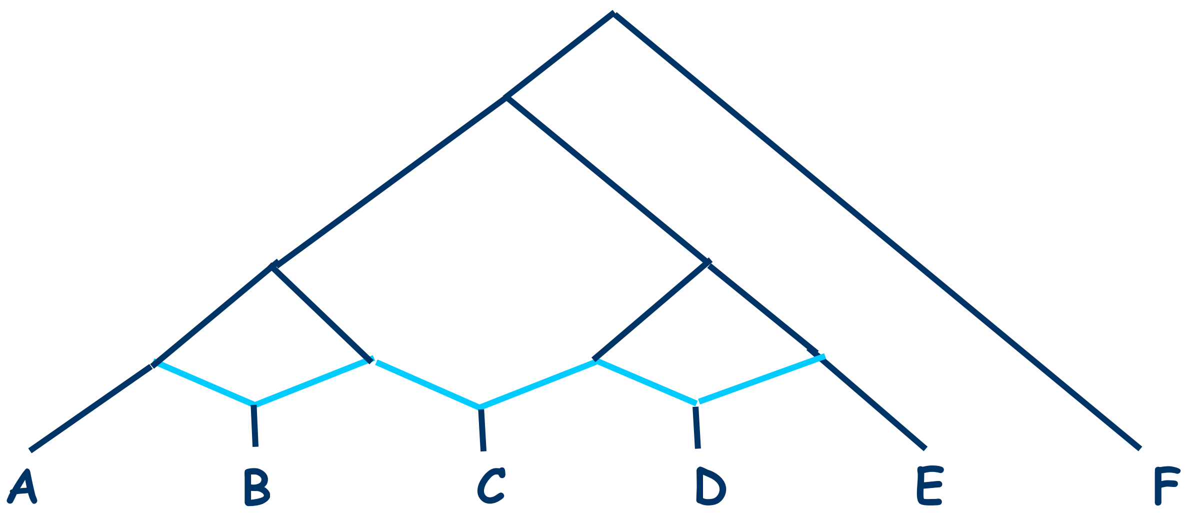
- In trees: LCA



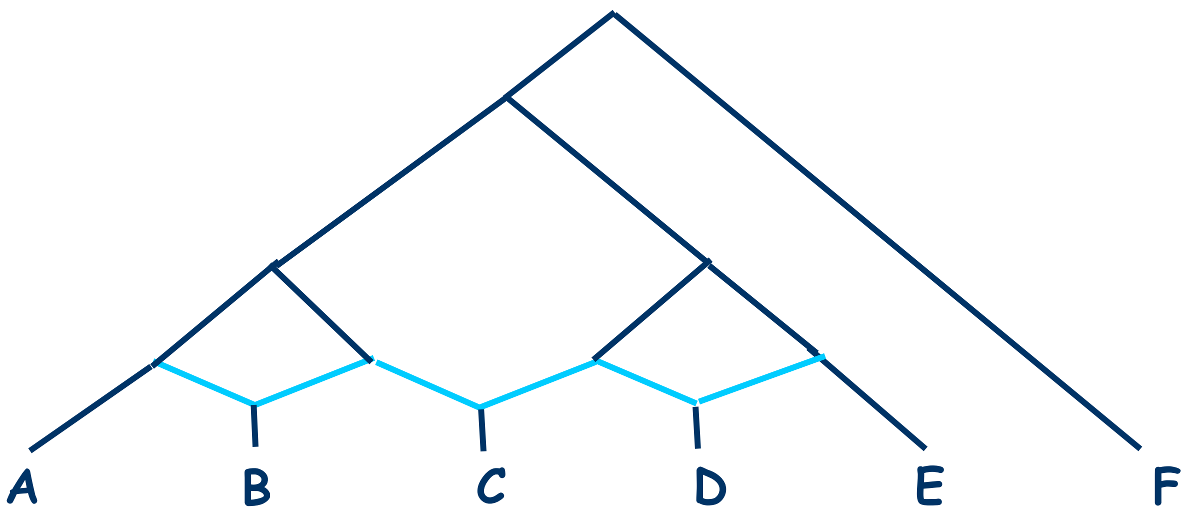
Lowest Single Ancestor: LSA

- In trees: LCA
- In cluster networks: LSA = Lowest Single Ancestor:



Lowest Single Ancestor: LSA

- In trees: LCA
- In cluster networks: LSA = Lowest Single Ancestor:
  LSA(S) = Lowest node that is on every path from the root to one of the nodes in S.



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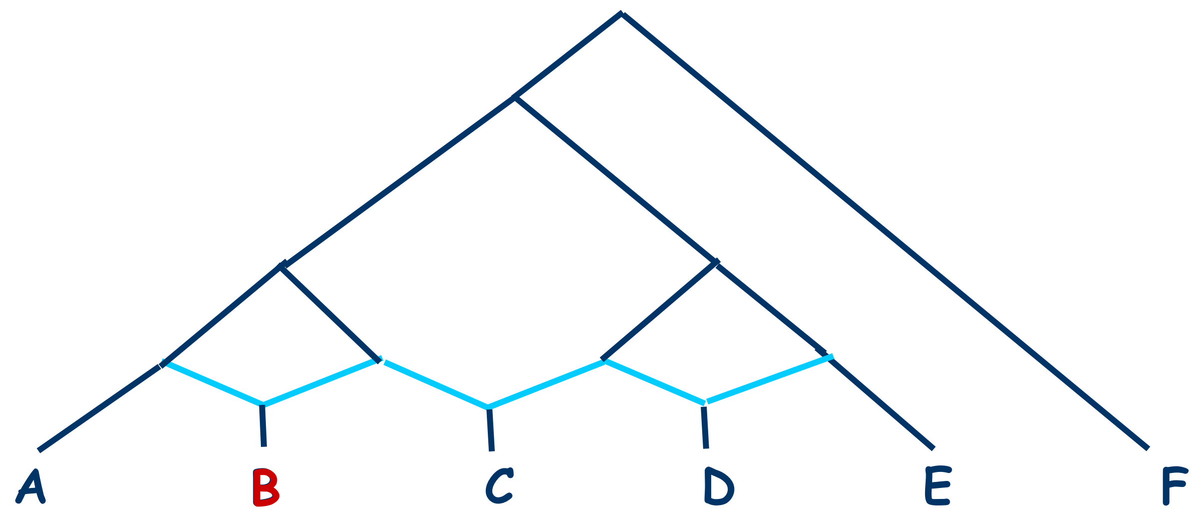

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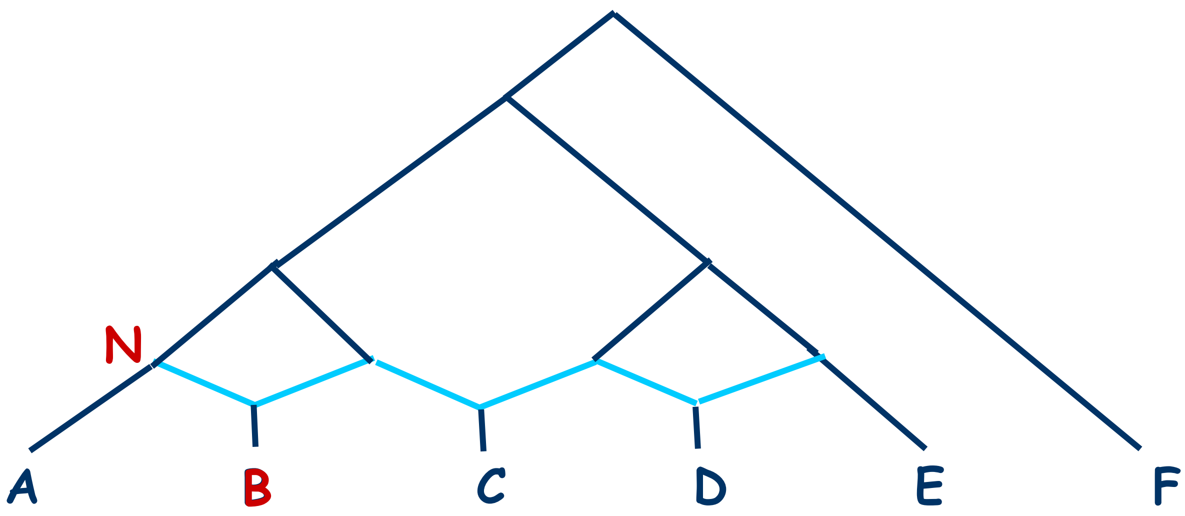

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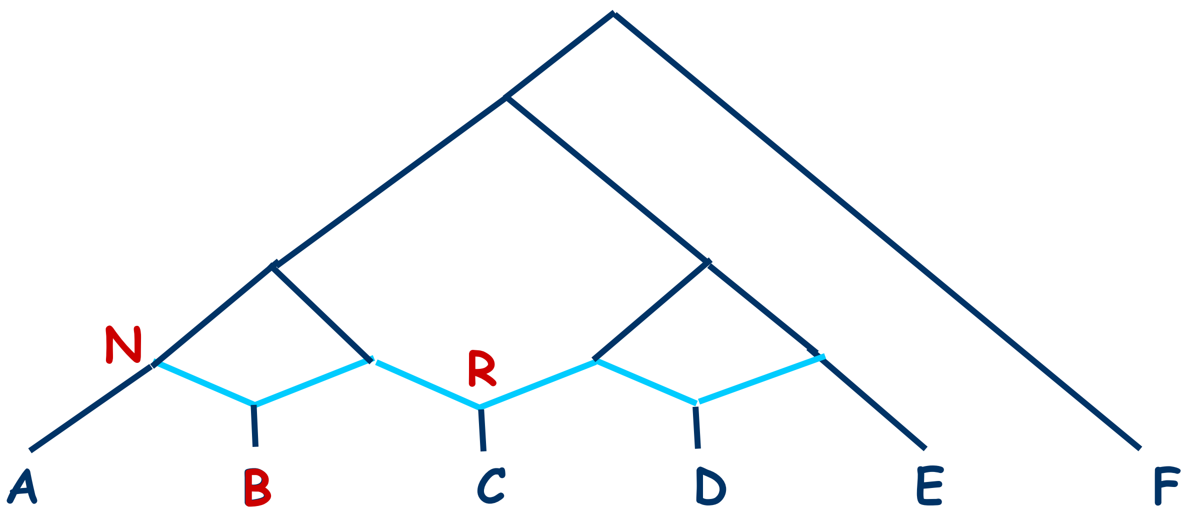

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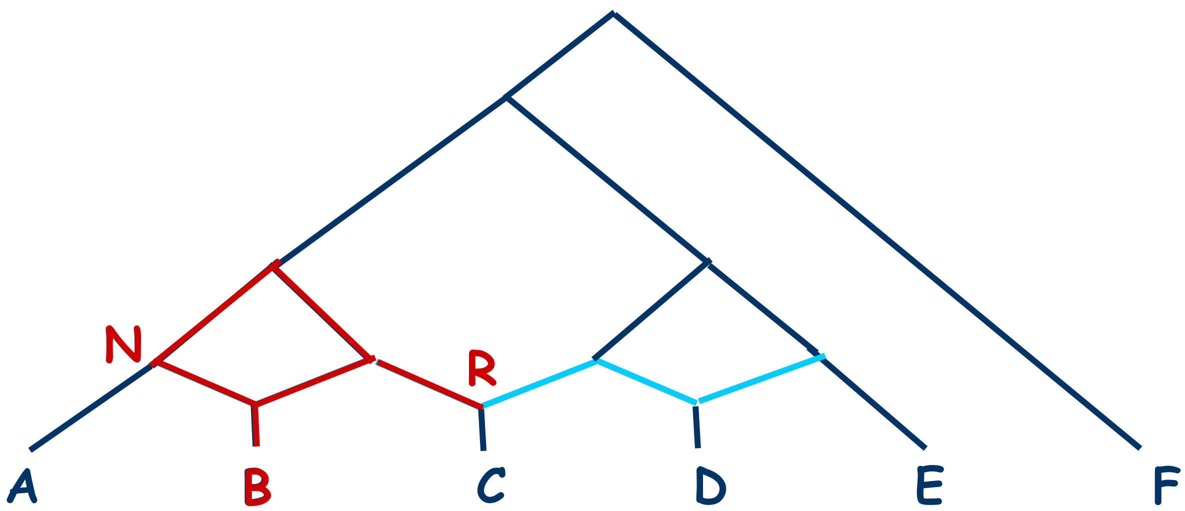

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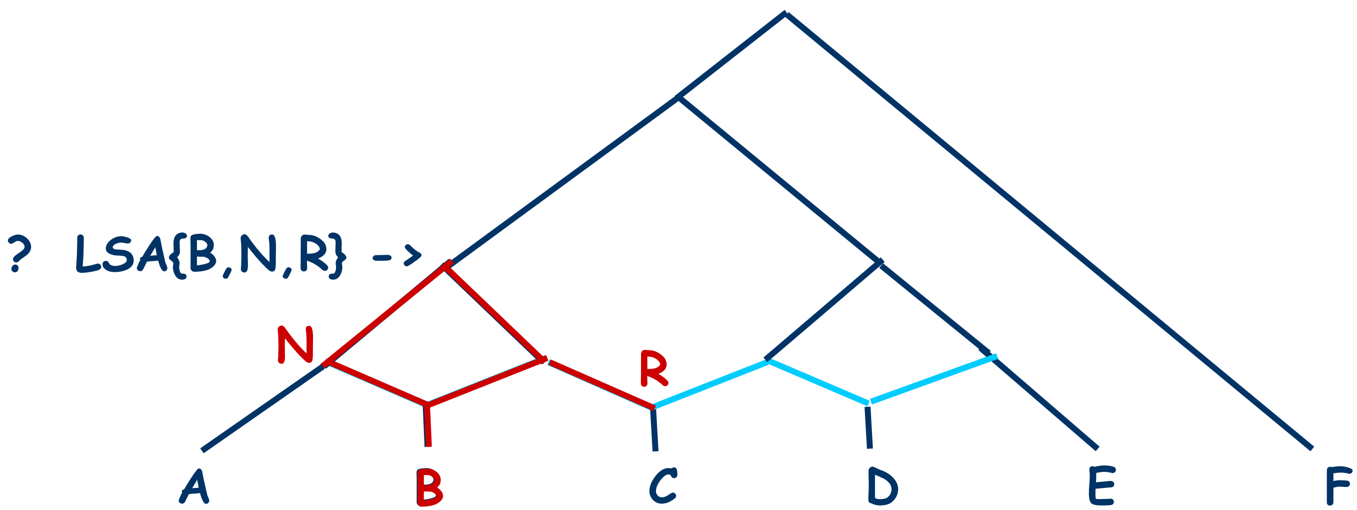

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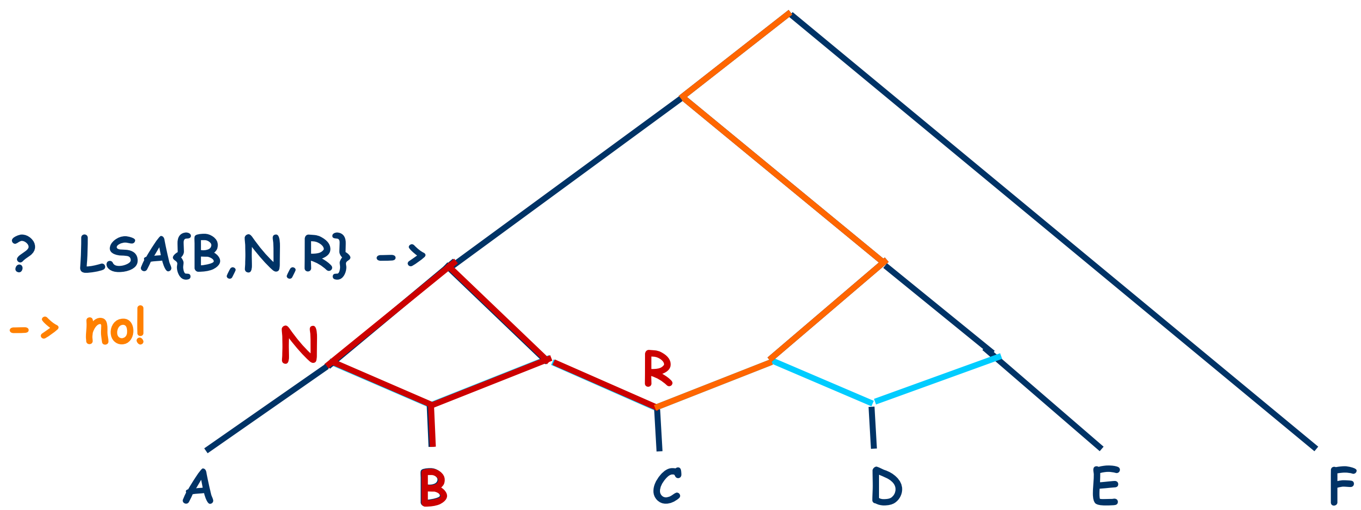

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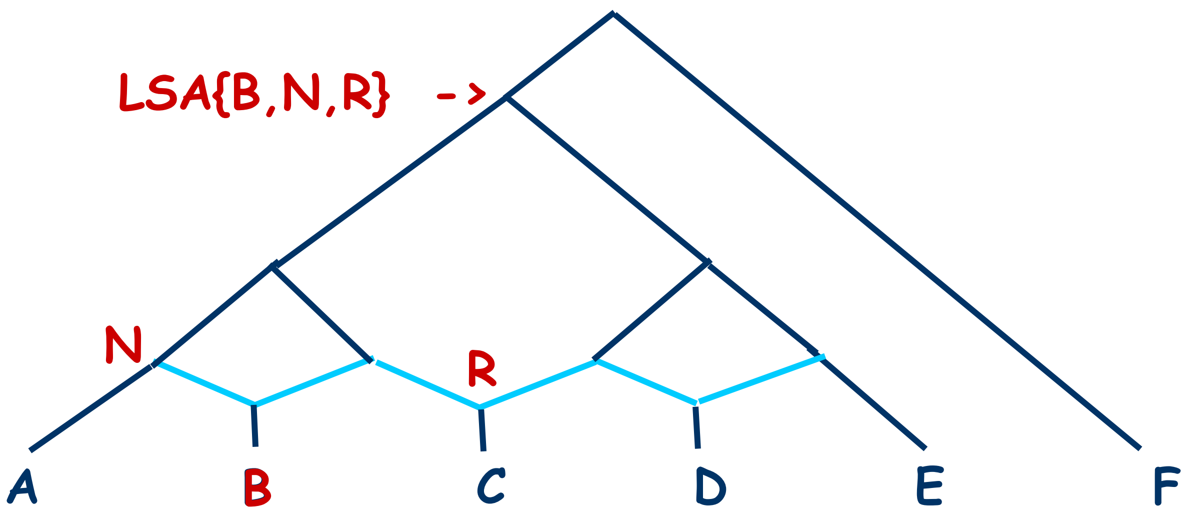
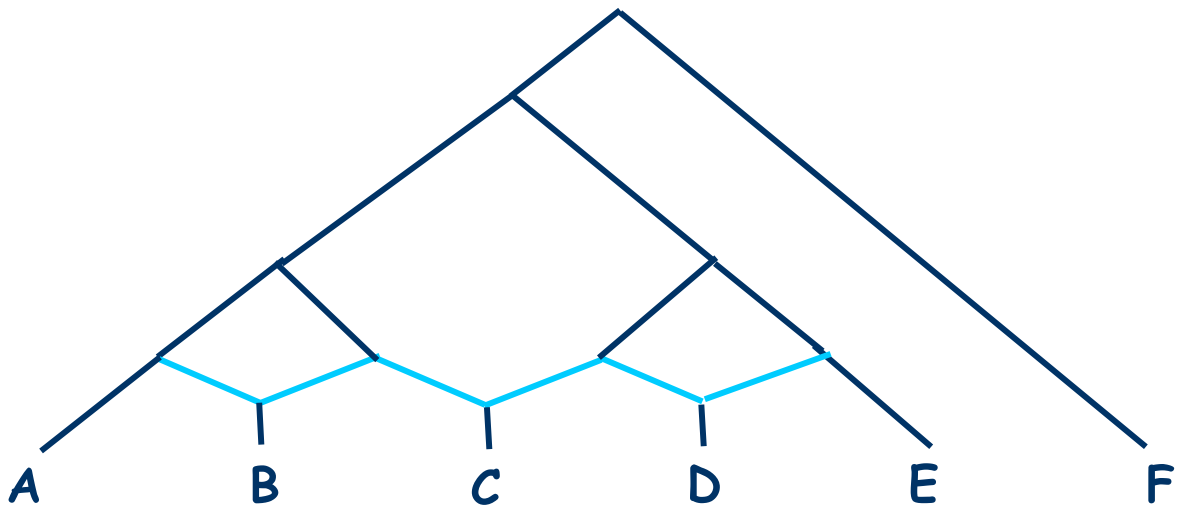


LSA consensus tree

LSA of a reticulation



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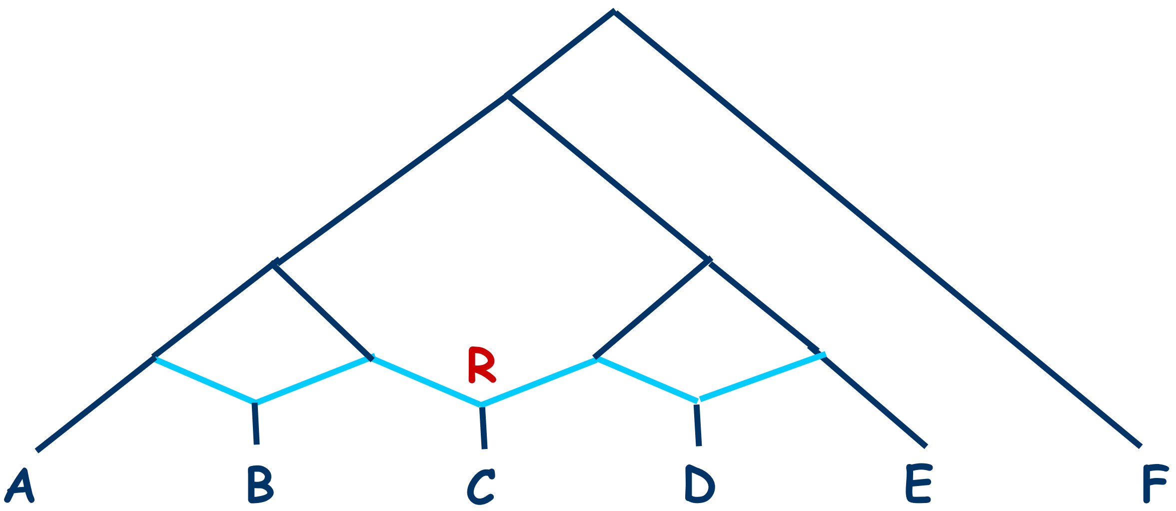

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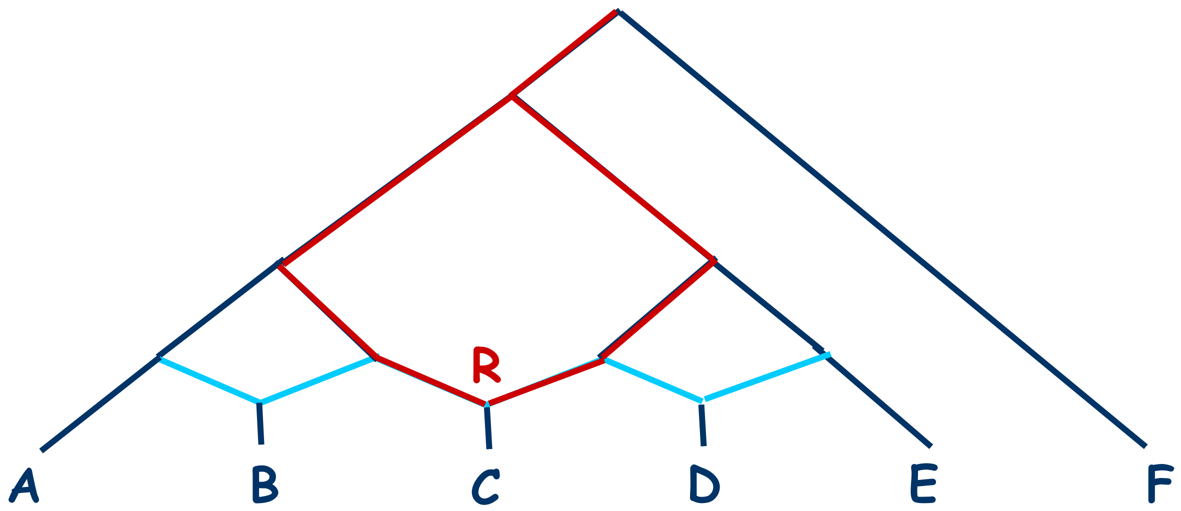

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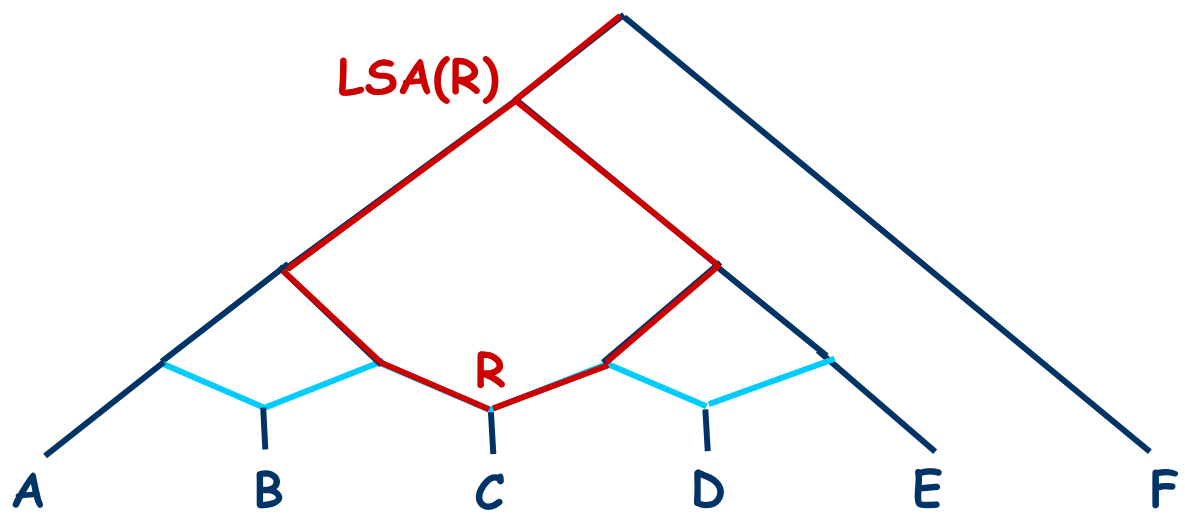

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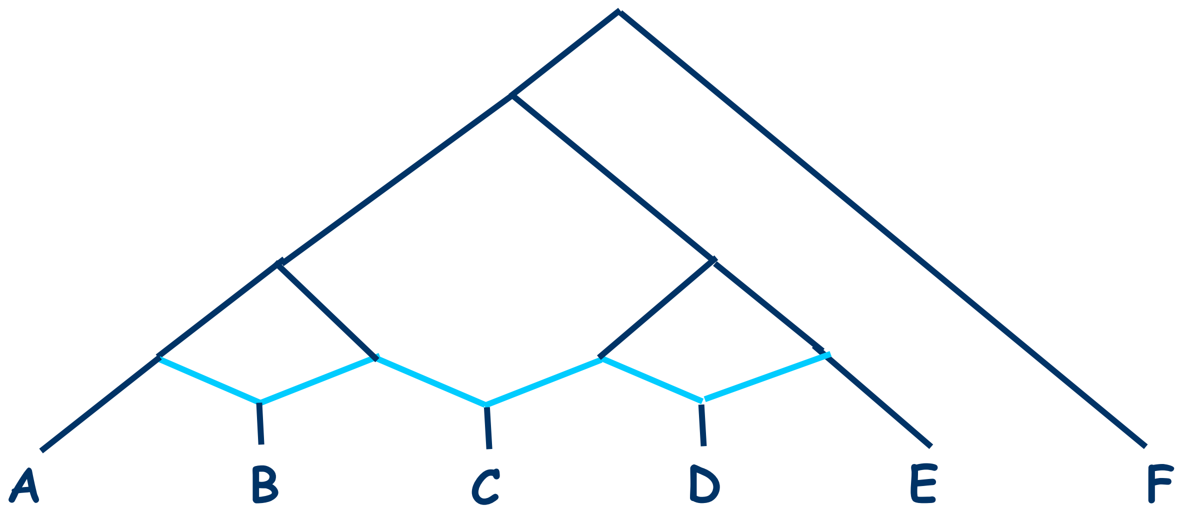

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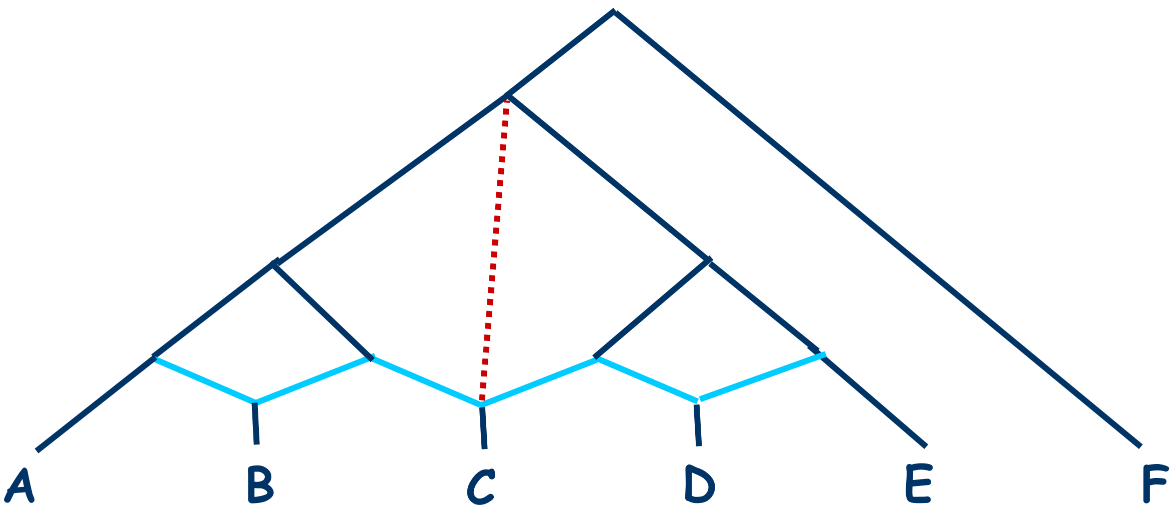

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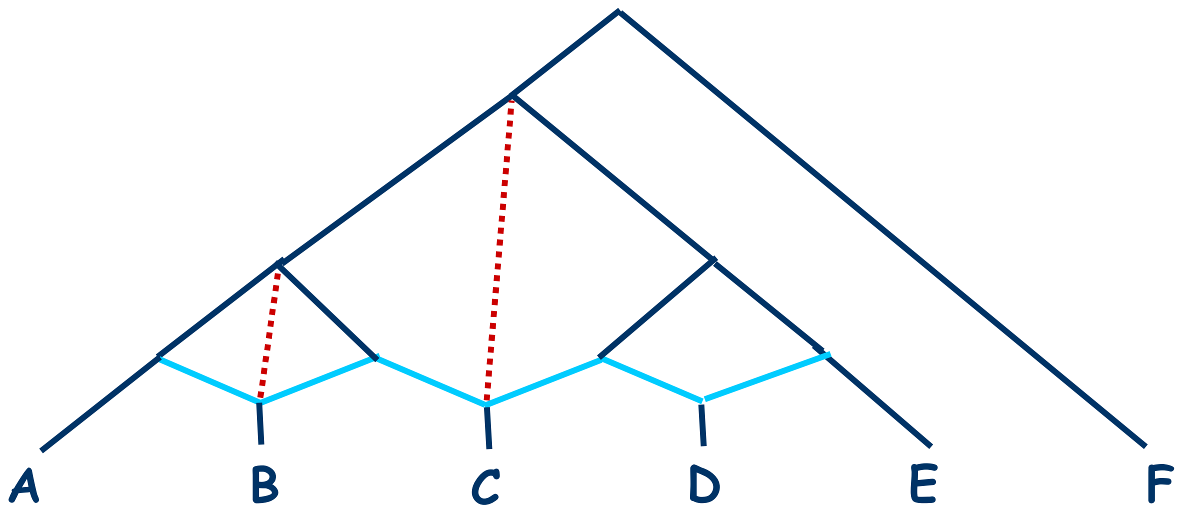

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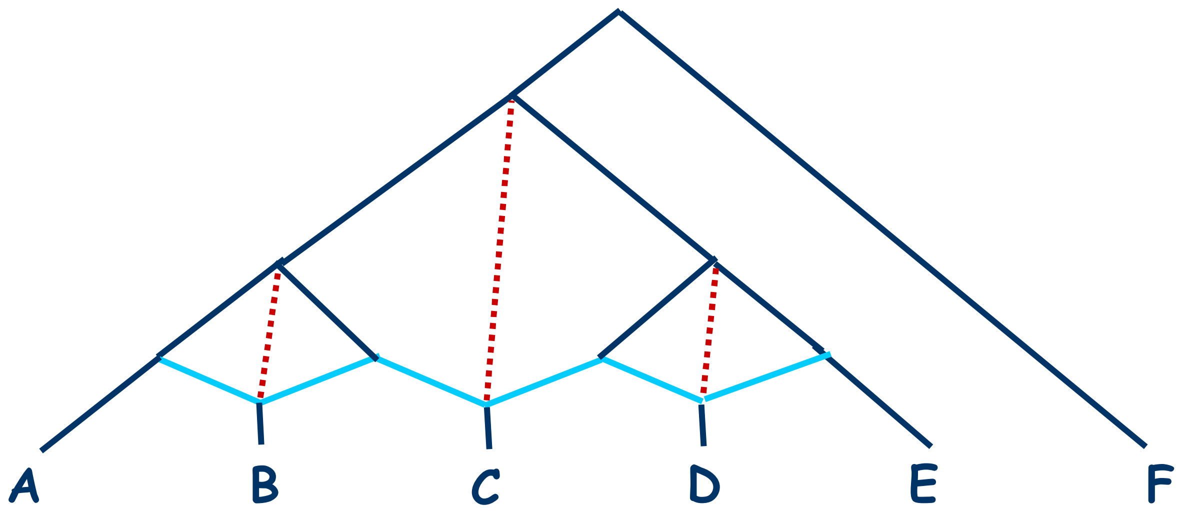

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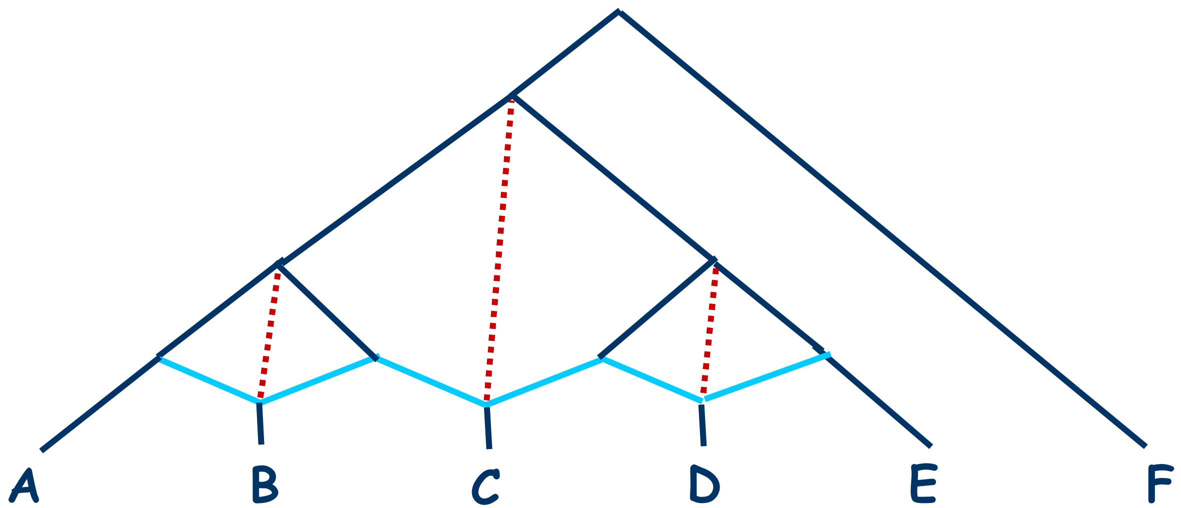
-> new consensus method!



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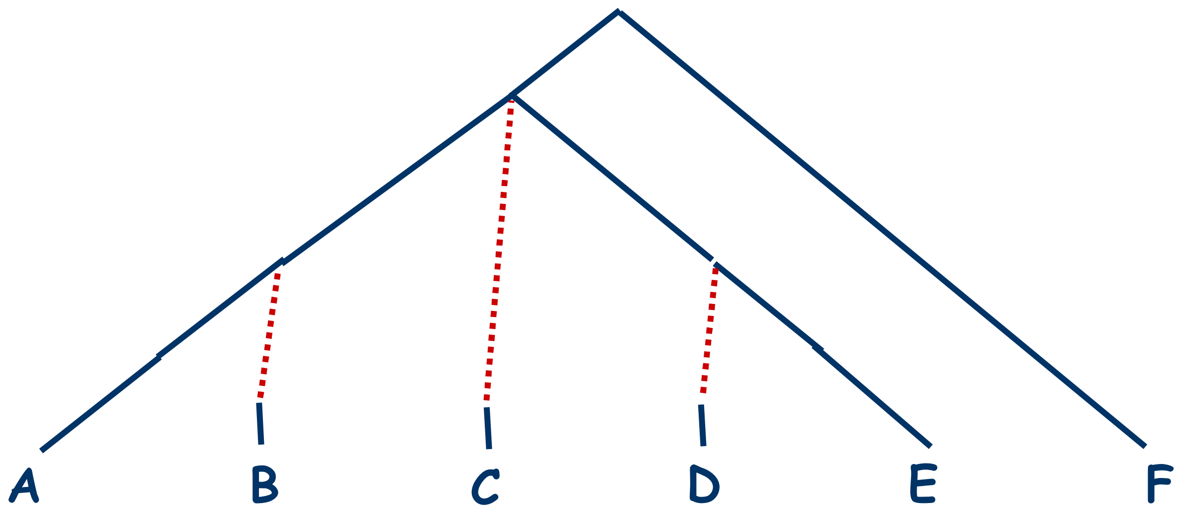

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- Restrict trees to maximal clusters of Adams consensus and repeat procedure recursively.

Adams vs. LSA

Question: LSA consensus = Adams consensus?

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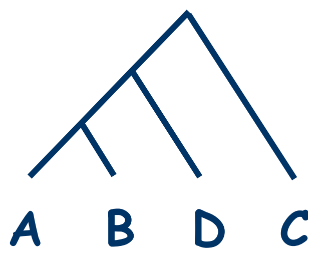

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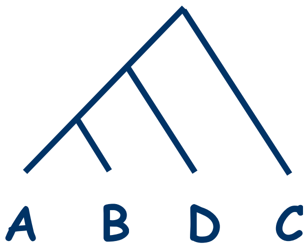

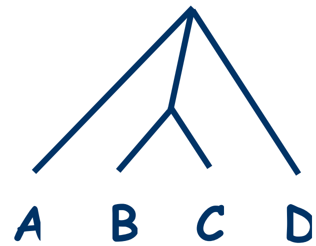

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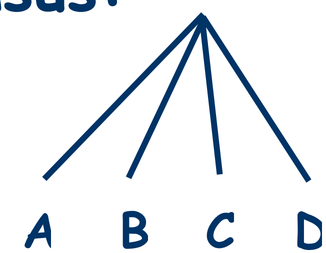

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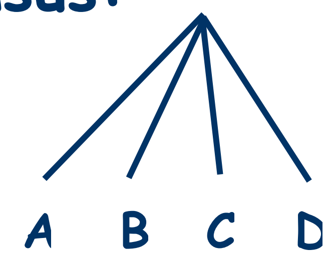

Cluster network:

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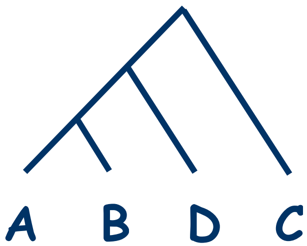

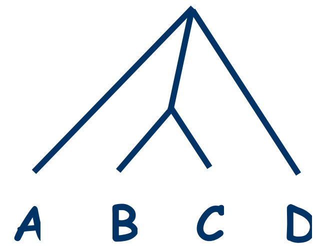

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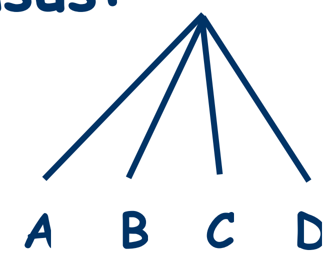

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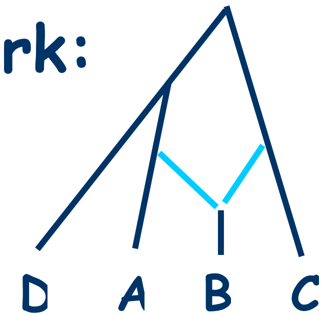

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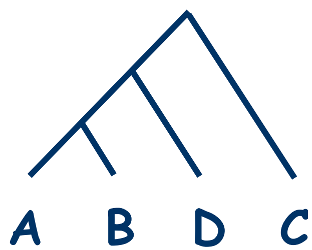

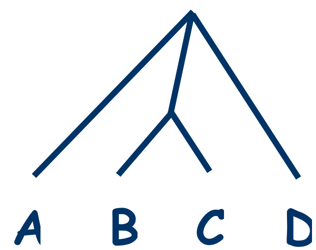

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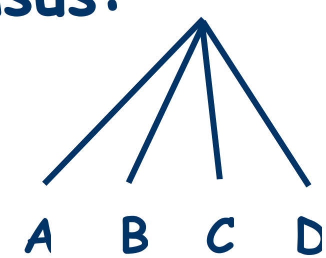

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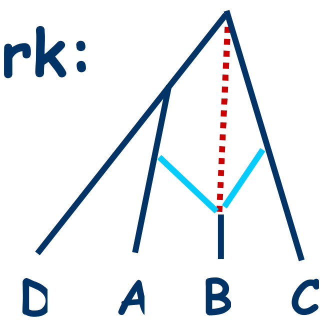

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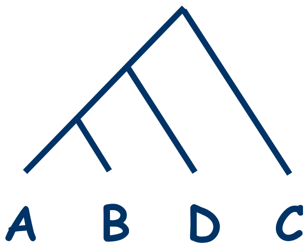

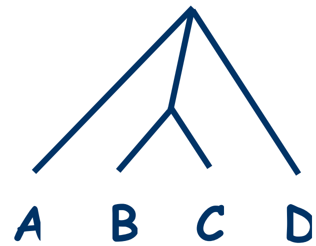

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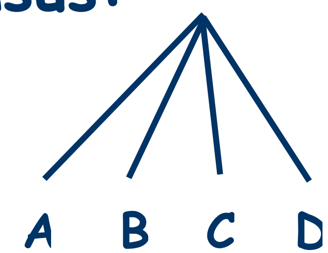

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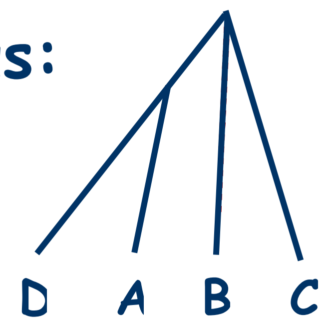

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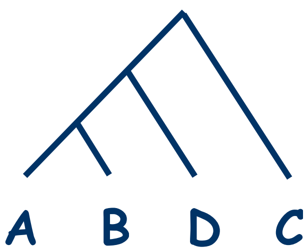

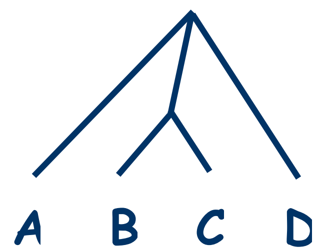

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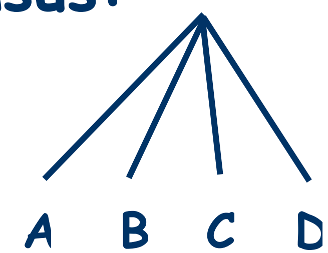

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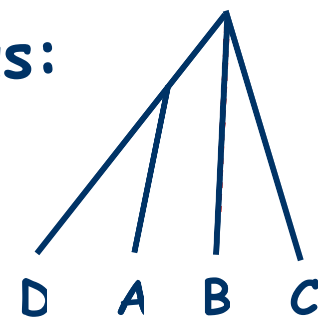

-> LSA consensus ≠ Adams consensus

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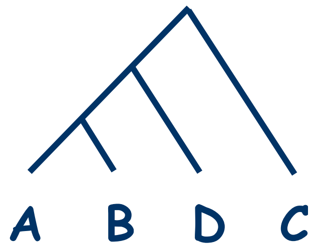

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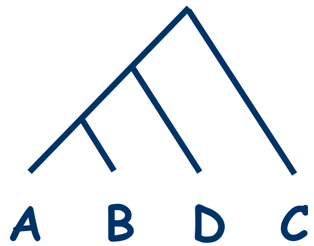

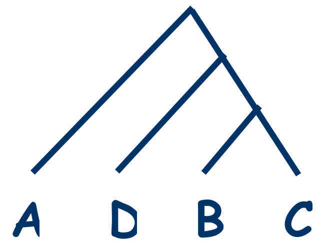

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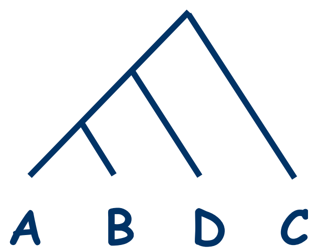

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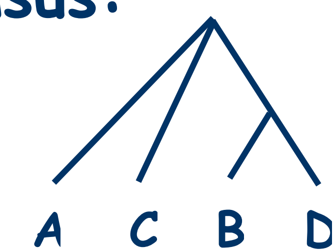

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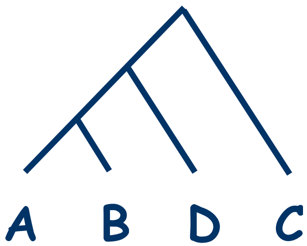

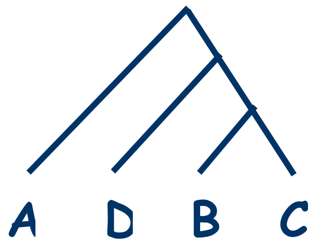

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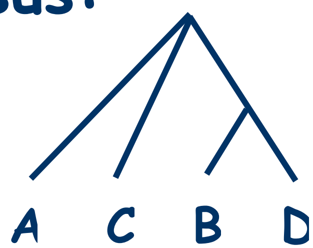

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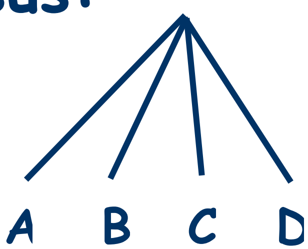

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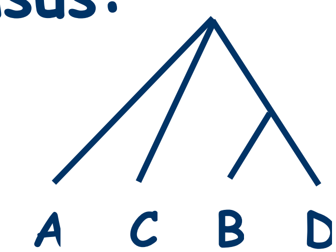

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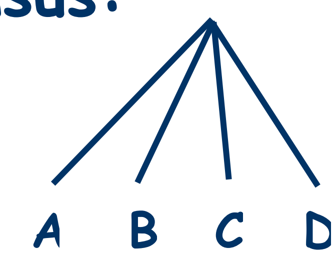

-> LSA not a refinement

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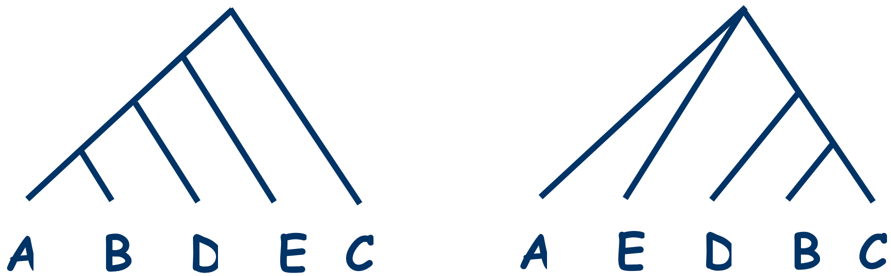

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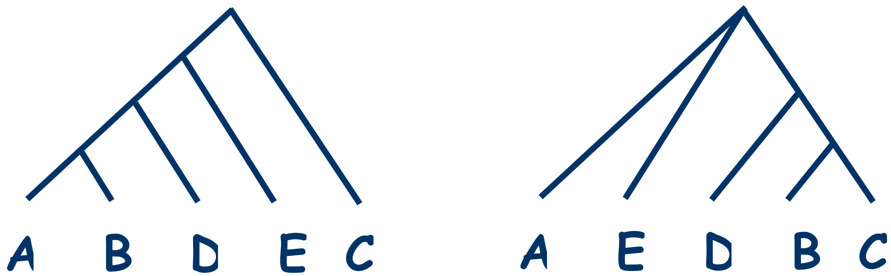

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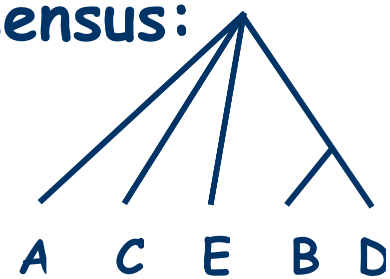

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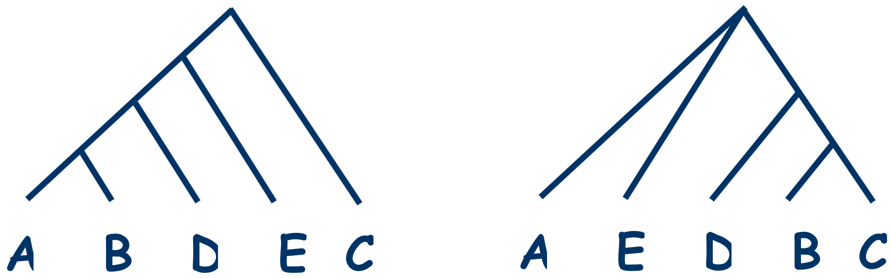

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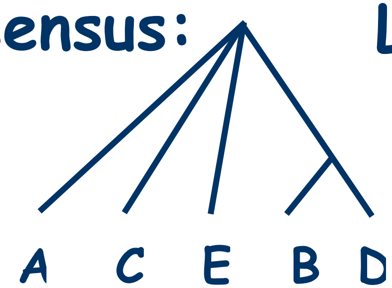

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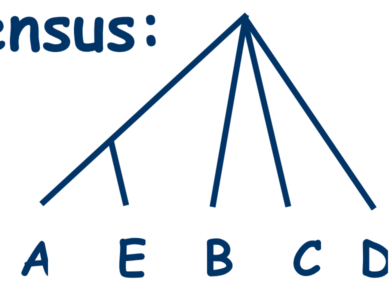

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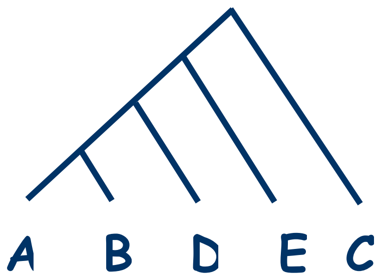

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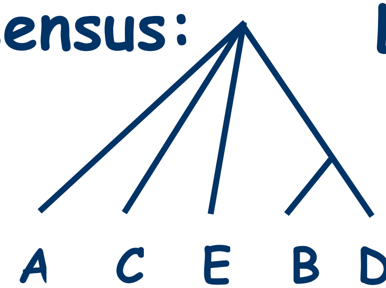

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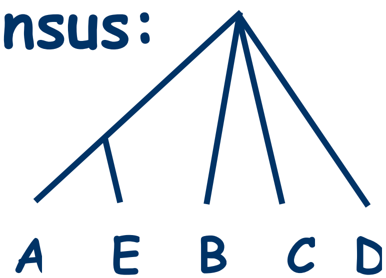

-> consensus trees are compatible

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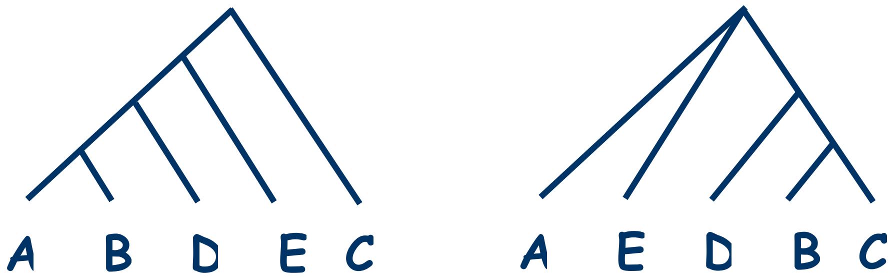

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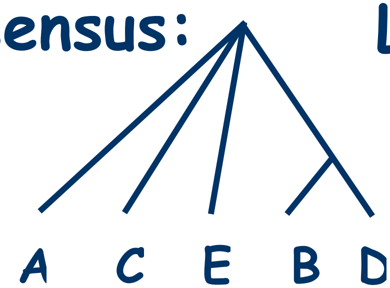

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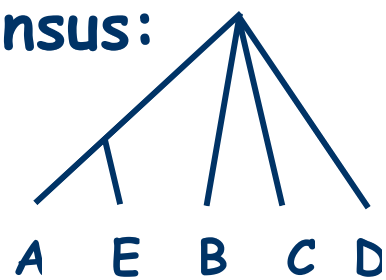

-> consensus trees are compatible

Is this always true? -> Open Question

Coming soon: Dendroscope 2.0

- Trees and networks
- Cluster networks
- LSA consensus

Dendroscope

by Daniel H. Huson

with contributions from Tobias Dezulian, Markus Franz, Christian Rausch, Daniel C. Richter and Regula Rupp

www-ab.informatik.uni-tuebingen.de/software/dendroscope