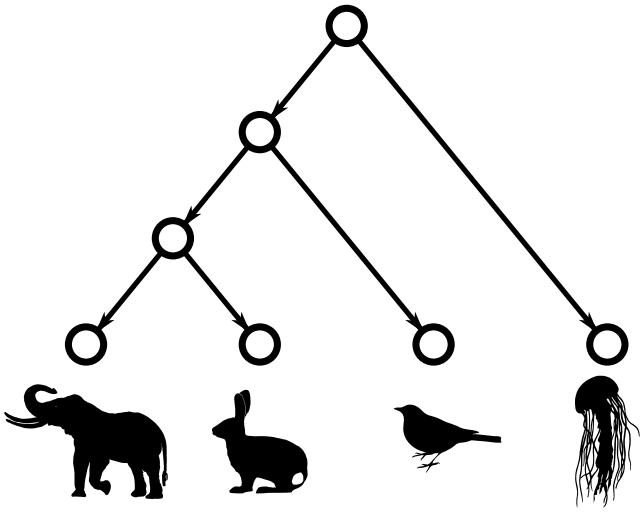
Stockholm University

LCA or no LCA:
A short story about simplifying networks

Anna Lindeberg
& Marc Hellmuth

Department of Mathematics
Stockholm University

Evolution: trees and networks



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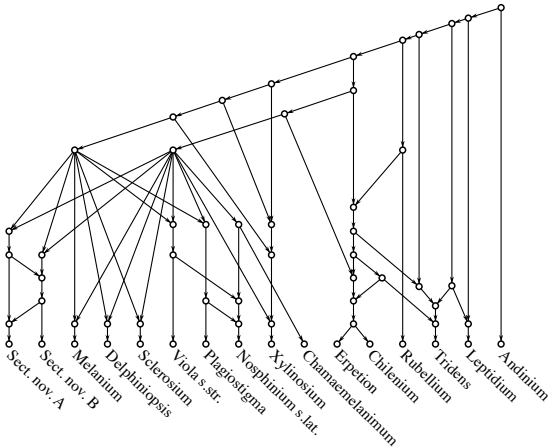

Network of groups of *Viola* flowers*

However. . . Some species are not too keen on evolving in a tree-like fashion.

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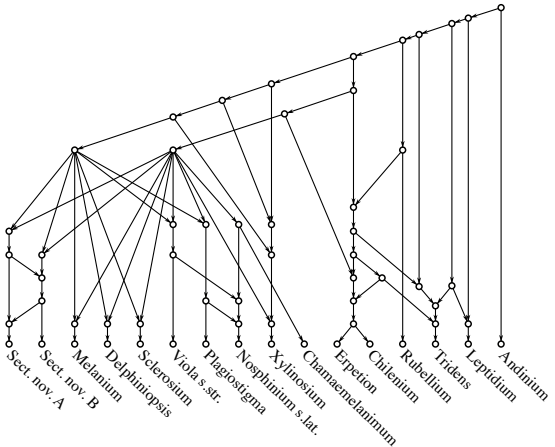

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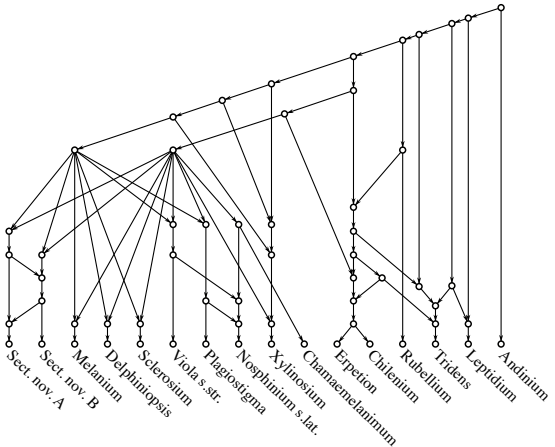

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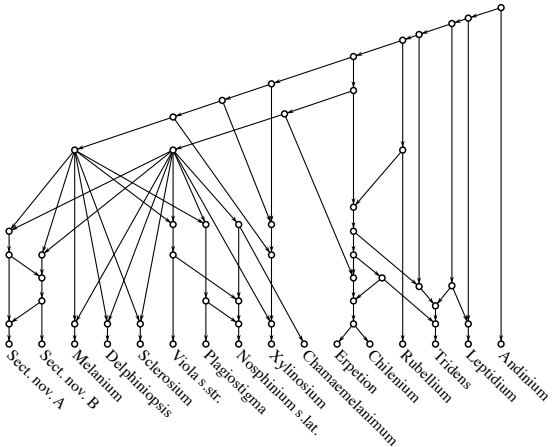

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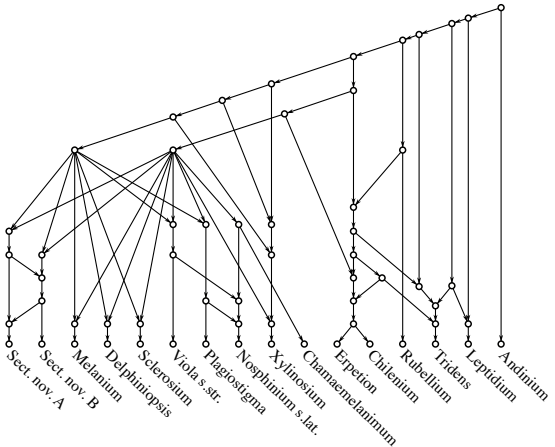

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The evolutionary history is network-like!

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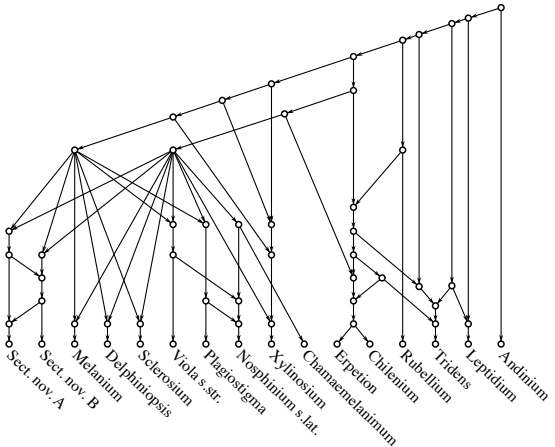

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How to obtain such networks?

Start with observable data

= genomic sequences of extant taxa

= set $L(N)$ of leaves in network N

Based on observable data, infer† the network N

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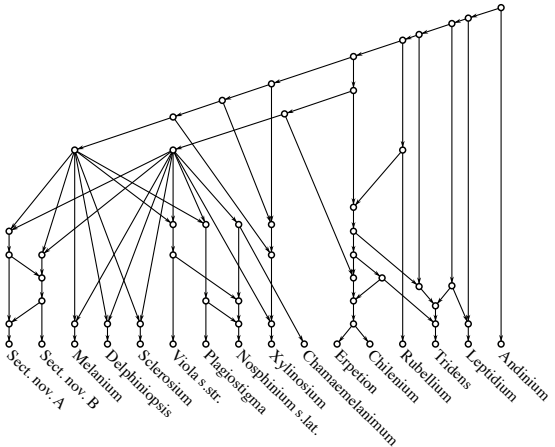

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Networks inferred from genomic data can . . .

. . . be highly complex and tangled

. . . contain information that is not supported by "observable data"

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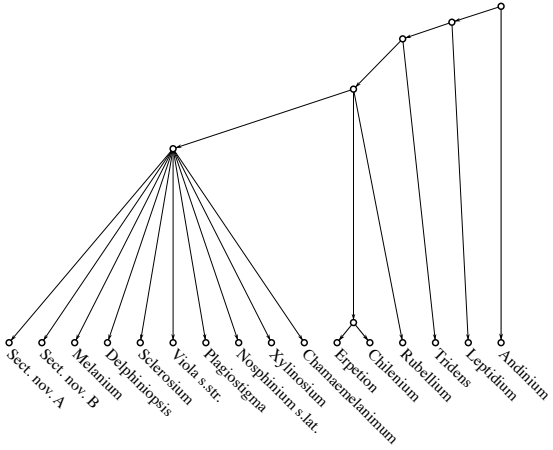

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Aim: methods to simplify networks while keeping main structural features

Lowest Stable Ancestor (LSA) tree to show "trend of evolution"[‡]

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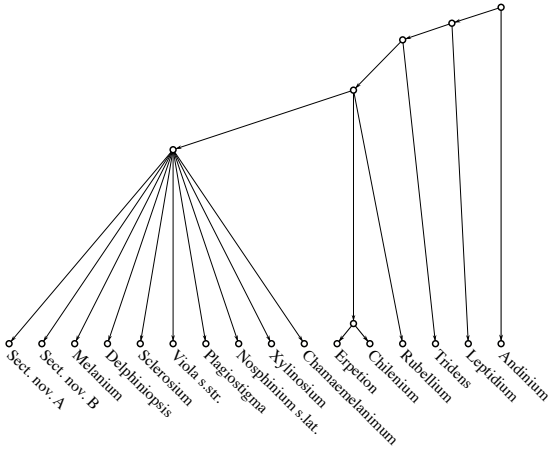

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The method we propose aims to simplify by eliminating vertices that are not supported by "observable data"

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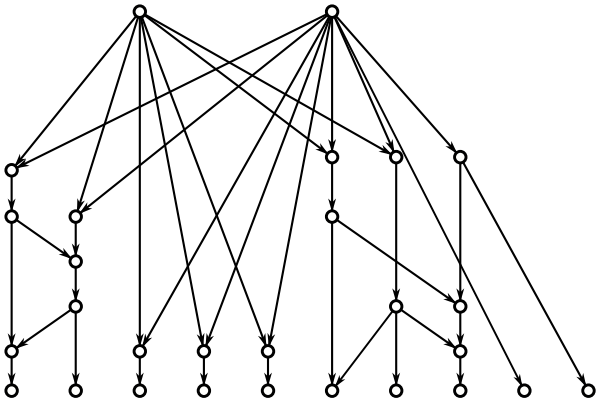
Absolutely necessary definitions



Directed Acyclic Graph, known as a DAG. The vertices are $V(G)$.

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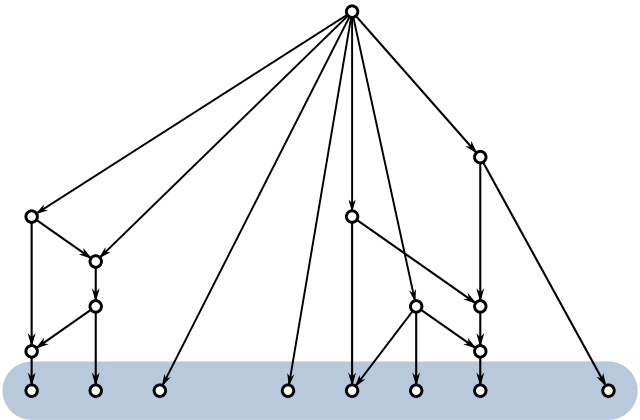

A network N is a DAG with a unique root (= source).

$L(N)$ denotes all leaves.

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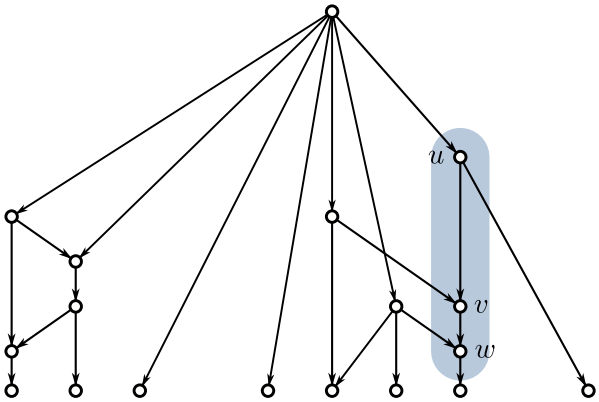

Ancestor and descendant: joined by directed path. Denoted $w \preceq u$.

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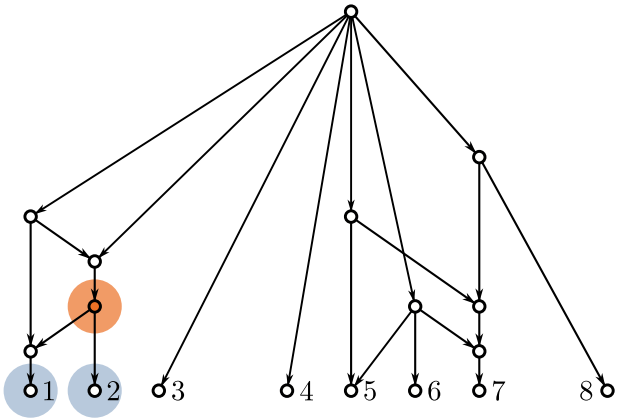

Least Common Ancestors: for $A \subseteq L(G)$, the set $\mathrm{LCA}(A)$ comprise all $\preceq$-minimal vertices that are ancestors of all leaves in A

$\mathrm{LCA}(\{1, 2\})$

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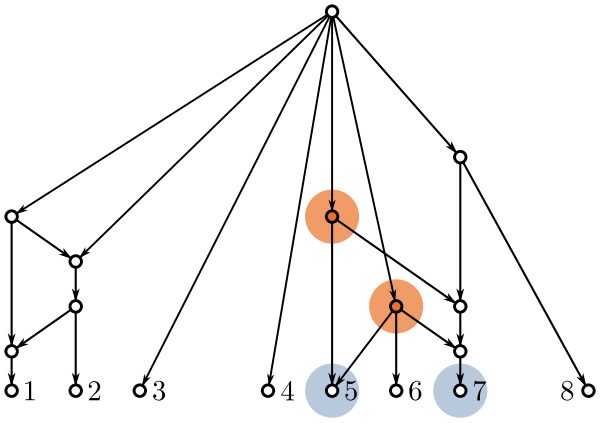

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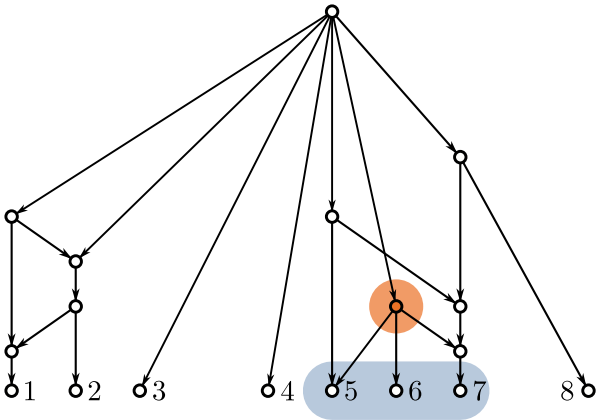

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We aim to **simplify** by removing vertices not supported by data.

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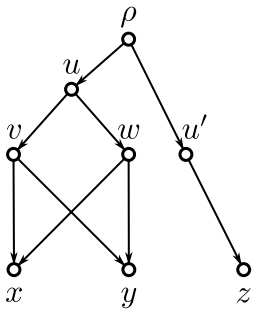
A DAG G is LCA-Relevant if every vertex is an LCA-vertex.



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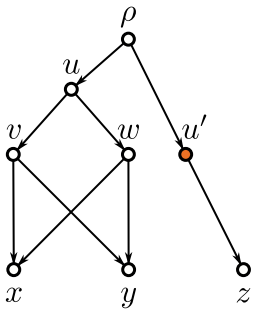

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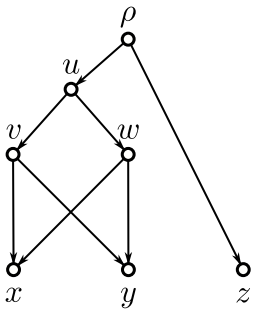

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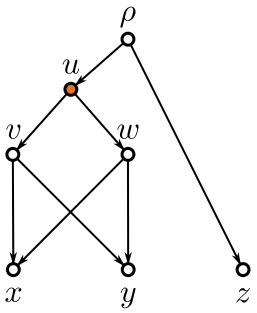

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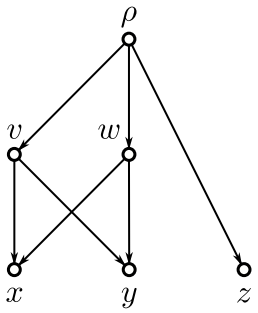

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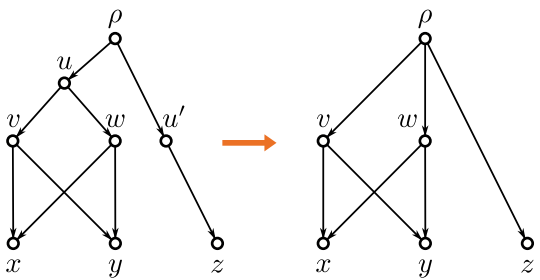

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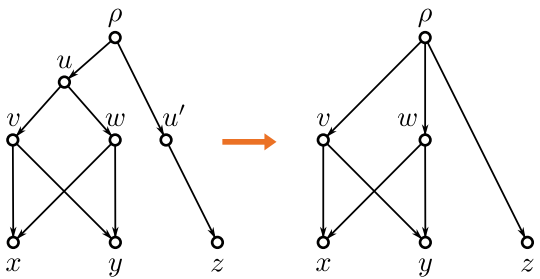

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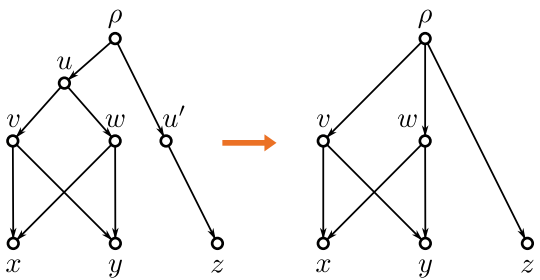
- Can we characterize LCA-Relevant DAGs?



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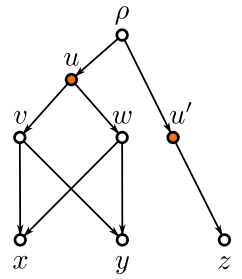
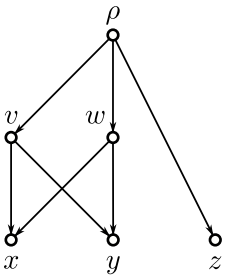


not LCA-Relevant



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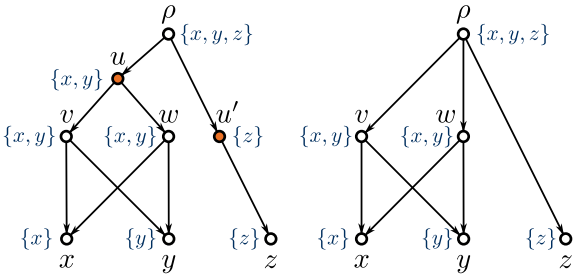

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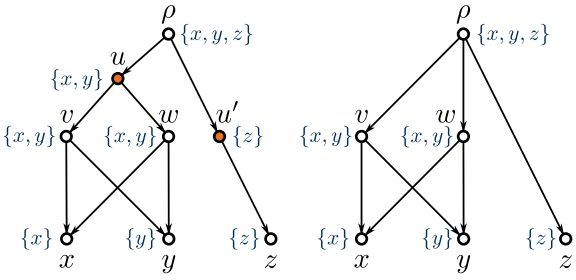
All non-LCA-vertices can be determined in polynomial time.



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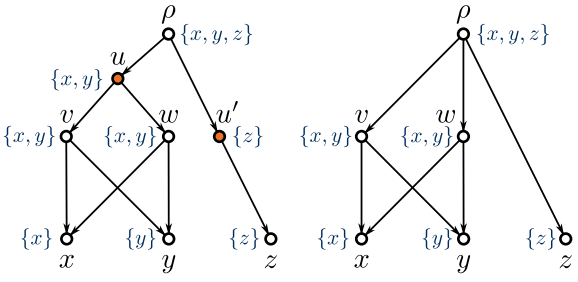
A DAG G is LCA$-$RELEVANT $\iff$ no two adjacent vertices of G have the same cluster



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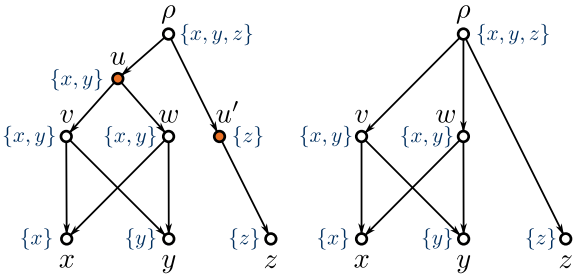

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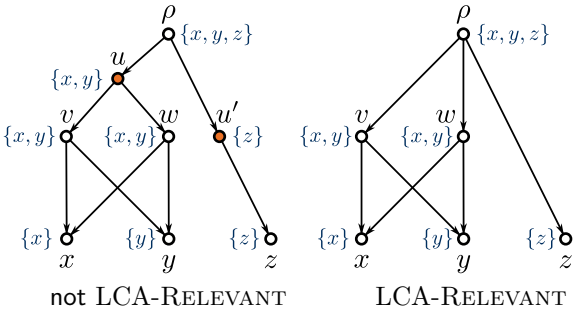

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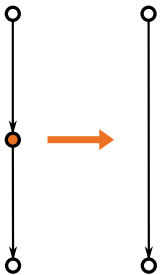

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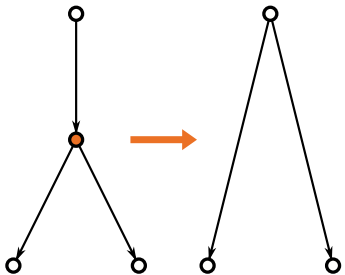

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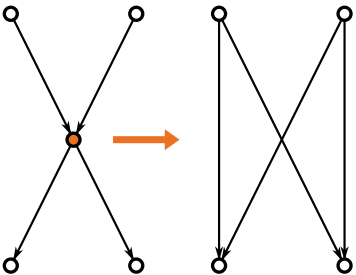

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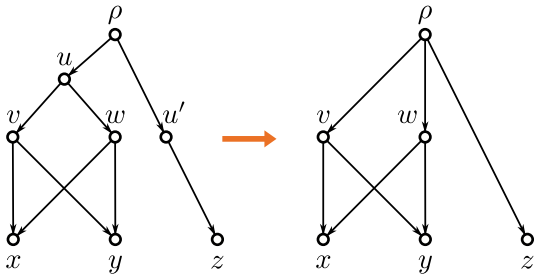

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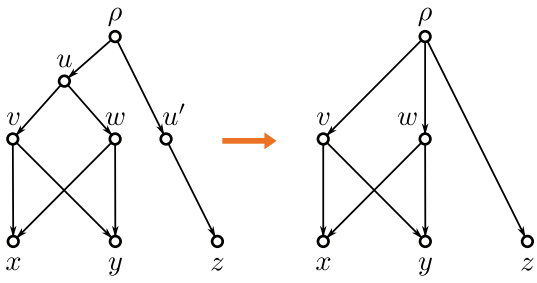

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If W is the set of all non-LCA vertices of G, then $G \ominus W$ is LCA-RELEVANT and satisfy

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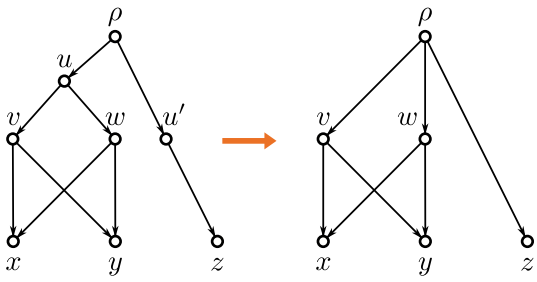

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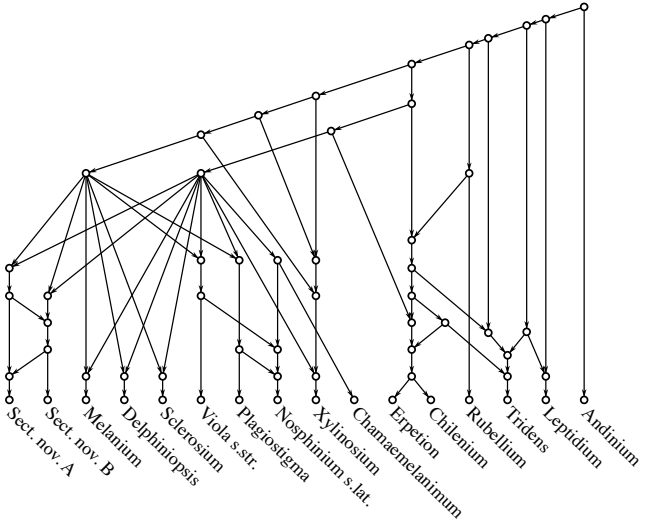
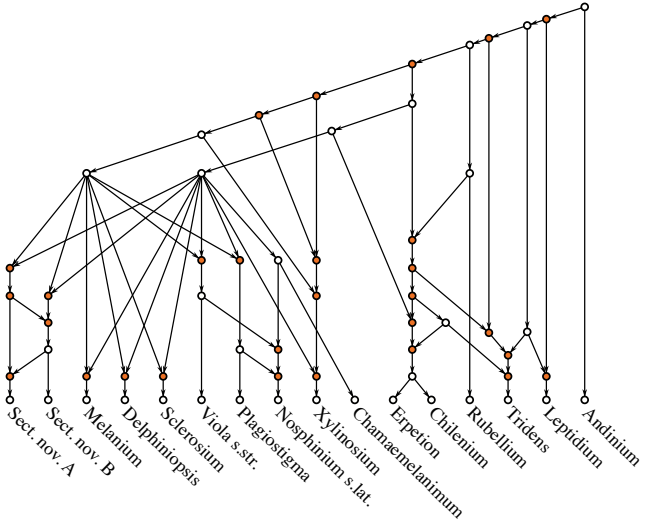
Well... a long list of appealing properties of what structure of G is kept

Bigger example



Network N

Bigger example



Network N with non-LCA-vertices highlighted

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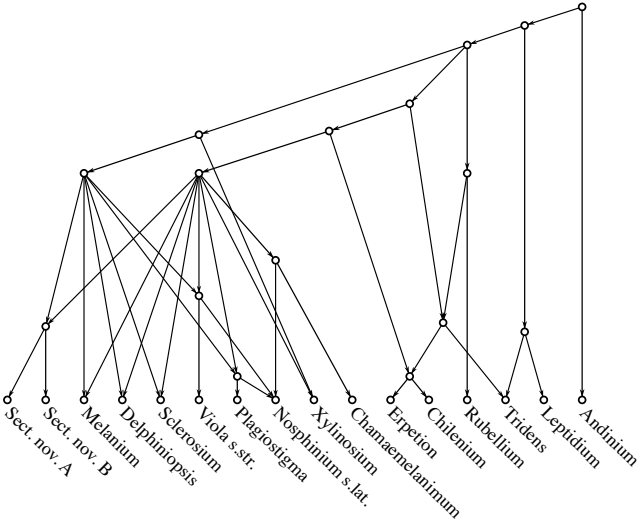

LCA-RELEVANT version $N \ominus W$ of N

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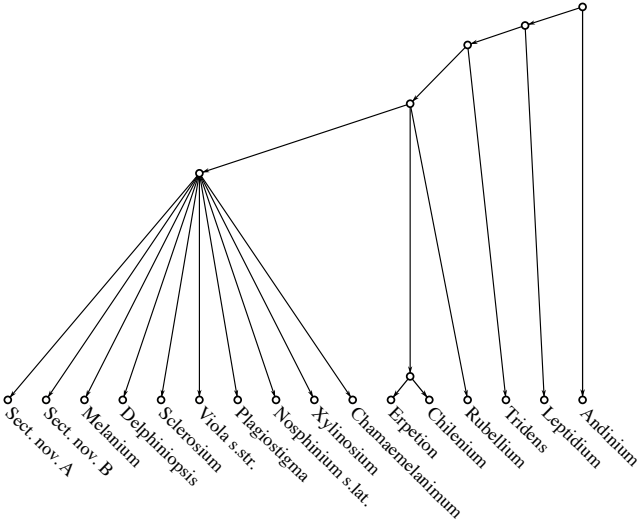

"Trend of evolution" as captured by LSA-tree of N

Strengthen LCA-Relevant DAGs a bit

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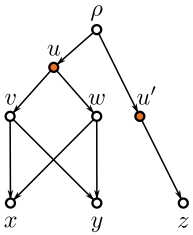

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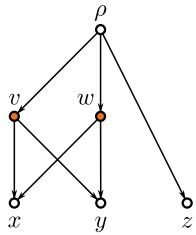

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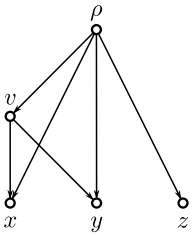

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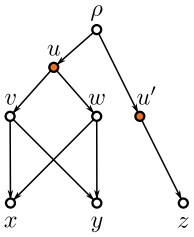

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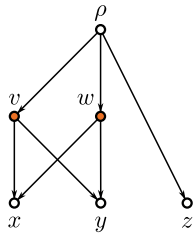

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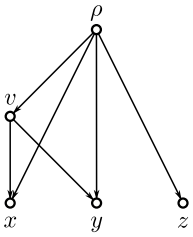

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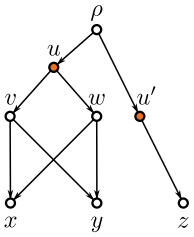

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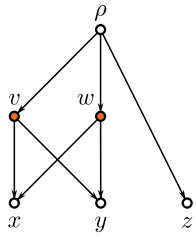

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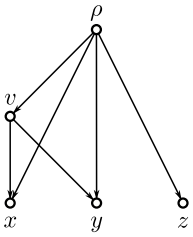

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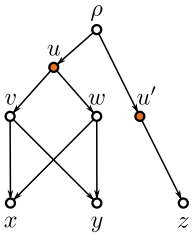

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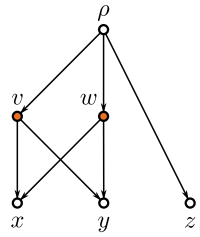

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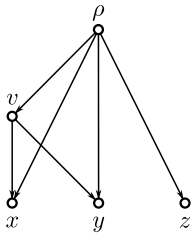

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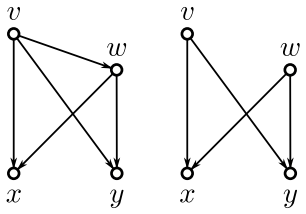

(PCC): there is a vw-path $\iff$ $\mathtt{C}(v)$ and $\mathtt{C}(w)$ are $\subseteq$–comparable.

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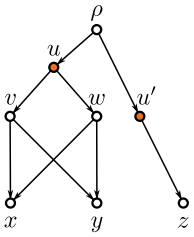

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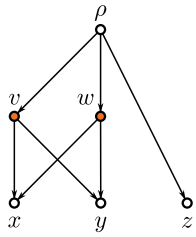

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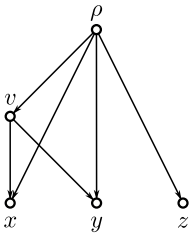

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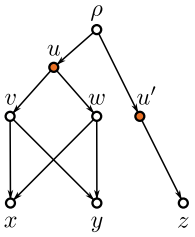

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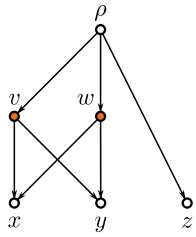

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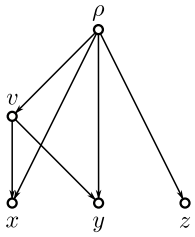

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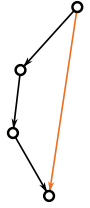

Shortcut: edge (u, v) for which there is some other uv-path

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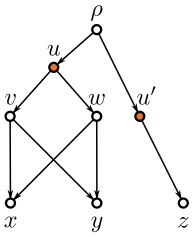

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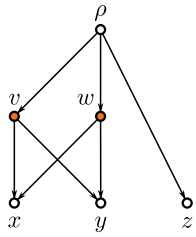

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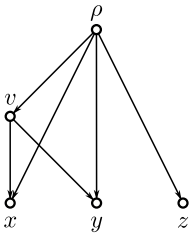

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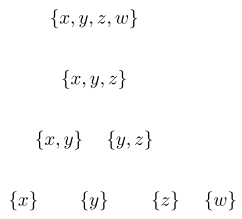

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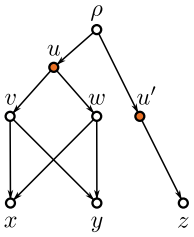

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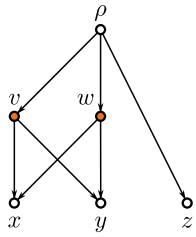

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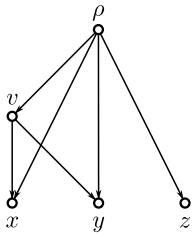

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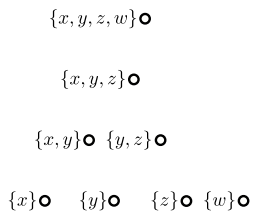

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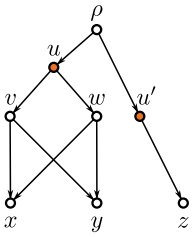

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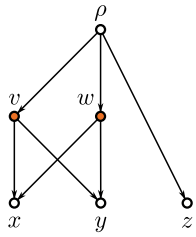

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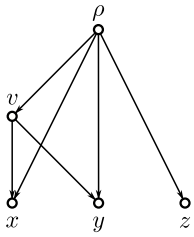

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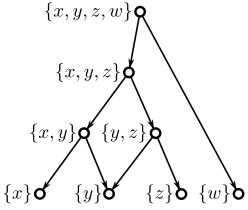

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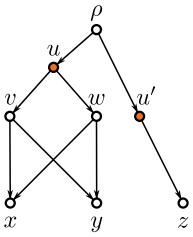

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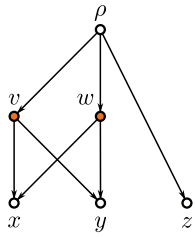

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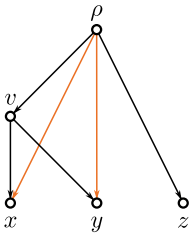

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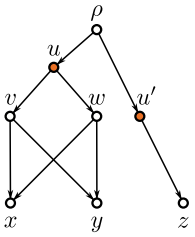

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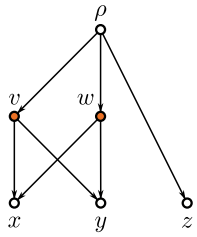

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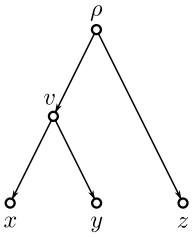

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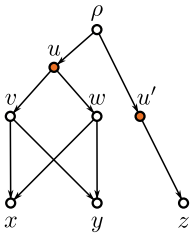
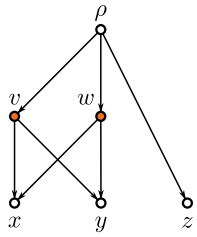
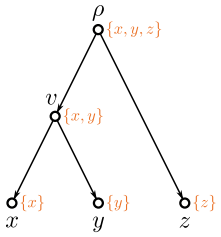


Network N



LCA-Relevant



LCA^u-Relevant

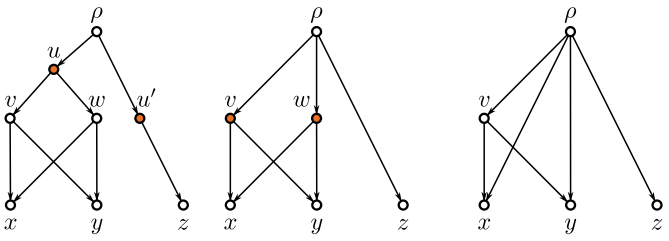
Strengthen LCA-Relevant DAGs a bit

A DAG G is LCA^u-Relevant if for every vertex $v \in V(G)$ there is some $A \subseteq L(G)$ s.t. $\{v\} = \mathrm{LCA}(A)$.

Characterization

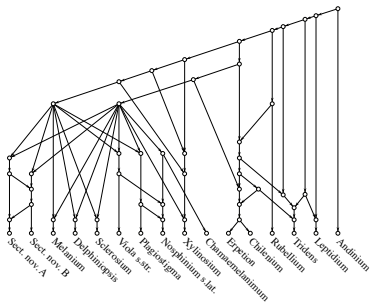
Let G be a DAG. The following are equivalent:

- G is LCA^u-Relevant
- G is LCA-Relevant and satisfy (PCC)
- If you remove all shortcuts from G, what you obtain is isomorphic to the Hasse diagram of $\mathfrak{C}_G$

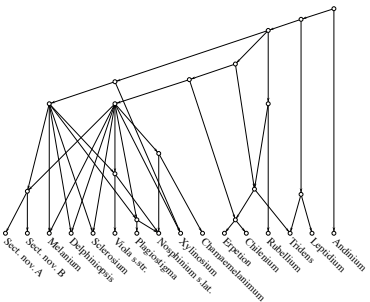


Computing an LCA^u-Relevant version of any DAG G can be done in polynomial-time

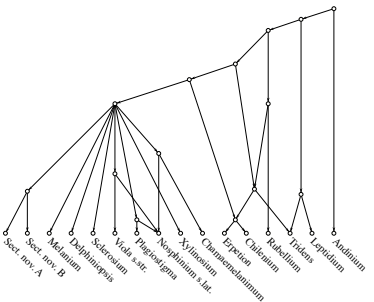
Bigger example (again)



Viola-flower network N



LCA-RELEVANT version



LCA^u-RELEVANT version

Other results and open problems

- Generally worked with a generalization: a DAG is $\mathcal{I}$-LCA-RELEVANT if for every vertex $v \in V(G)$ there is some $A \subseteq L(G)$ s.t. $|A| \in \mathcal{I}$ and $v \in \mathrm{LCA}(A)$.

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Still lots of interesting open questions:

- For $G \ominus W$ being $\mathrm{LCA}-$RELEVANT the set W is uniquely determined and $\mathfrak{C}_{G \ominus W} = \mathfrak{C}_G$. For $G \ominus W$ being LCA^u–RELEVANT the set W is *not* uniquely determined and $\mathfrak{C}_{G \ominus W} \subsetneq \mathfrak{C}_G$ is possible. How to minimize $|W|$? Or minimize $|\mathfrak{C}_G \setminus \mathfrak{C}_{G \ominus W}|$?

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- Is it too much to require vertices to be LCA's of leaves? Recursive definition:
  Every leaf in G is pertinent.
  A vertex is pertinent if it is the LCA of pertinent vertices.
  What is the structure of DAGs in which all vertices are pertinent and how to determine such vertices?

Joint work with

Marc Hellmuth

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Thank you!

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Want to know more? See: Lindeberg & Hellmuth, Simplifying and Characterizing DAGs and Phylogenetic Networks via Least Common Ancestor Constraints, Bulletin of Math. Bio. (2025)