

Locating a Tree in a Reticulation-Visible Network in Cubic Time (Extended Abstract)

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In studies of molecular evolution, phylogenetic trees are rooted trees, whereas phylogenetic networks are rooted acyclic digraphs. Edges are directed away from the root and leaves are uniquely labeled with taxa in phylogenetic networks. An important bioinformatics task is checking the “consistency” of two evolutionary models. This has motivated researchers to study the problem of determining whether a tree is displayed by a network or not, which is called the tree containment problem (TCP) [2, 3]. The cluster containment problem (CCP) is related algorithmic problem that asks whether or not a subset of taxa is a cluster in a tree displayed by a network [2].

Both the TCP and CCP are NP-complete [3], even on a very restricted class of networks [4]. An open question was posed by van Iersel *et al.* asking whether or not the TCP is solvable in polynomial time for binary reticulation-visible networks [1, 2, 4]. A network is reticulation-visible if every reticulation separates the root of the network from some leaves [2], where reticulations are internal nodes of indegree greater than one and outdegree one.

We give an affirmative answer to the open problem of van Iersel, Semple and Steel by presenting a cubic time algorithm for the TCP for arbitrary reticulation-visible networks. The key tool used in our answer is a powerful decomposition theorem. It also allows us to design a linear-time algorithm for the cluster containment problem for networks of this type and to prove that every galled network with n leaves has $2(n - 1)$ reticulation nodes at most. The full version of this work can be found at [arXiv.org \(arXiv:1507.02119v2\)](https://arxiv.org/abs/1507.02119v2).

References

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