

# Constructing a Phylogenetic X-cactus from a Distance Matrix

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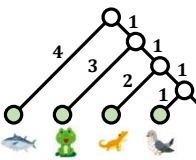
## Background

Trees have been studied due to their usefulness in describing the evolutionary processes of organisms. However, when considering factors such as hybridization between different species, phylogenetic networks become necessary.

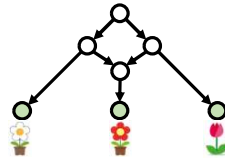
A distance matrix  $D$  on  $X$  for representing dissimilarities

$$D = \begin{pmatrix} 0 & 2 & 4 & 6 & 8 \\ 2 & 0 & 4 & 6 & 8 \\ 4 & 4 & 0 & 6 & 8 \\ 6 & 6 & 6 & 0 & 8 \\ 8 & 8 & 8 & 8 & 0 \end{pmatrix}$$

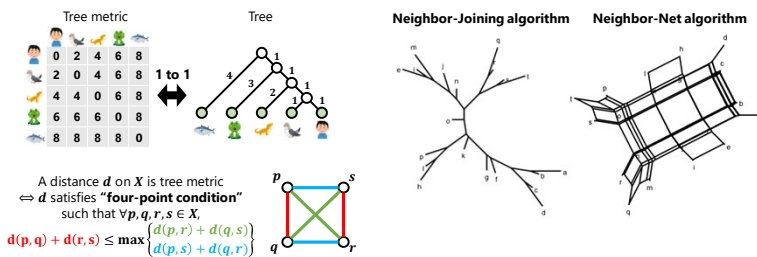
A realization of  $(X, D)$   
( $d_G(x, y) = d(x, y)$ )



A phylogenetic network



1965	1974	1987	2004
Uniqueness of phylogenetic tree [Hakimi & Yau]	Characterization of tree metric [Buneman]	Algorithm of constructing tree [Saitou & Nei]	Algorithm of constructing Network [Bryant & Moulton]



We consider "optimal" realizations which are realizations of least total weight.

Saitou & Nei solved the following problem.

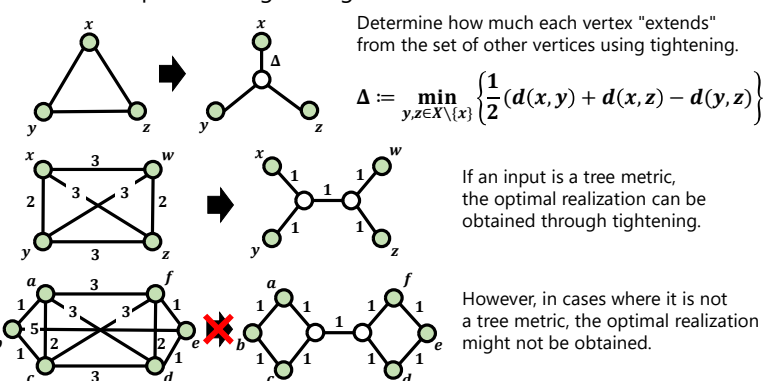
### Problem 1

Propose an algorithm that satisfies the following conditions.

Input: A tree metric  $d$  on  $X$

Output: The optimal realization of  $(X, d)$

Define the operation "tightening".



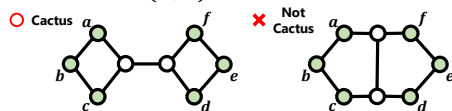
### Problem 2

Propose an algorithm that satisfies the following conditions.

Input: A cactus metric  $d$  on  $X$

Output: The optimal realization of  $(X, d)$

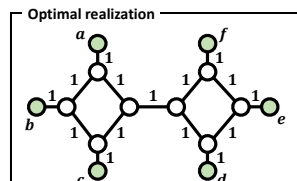
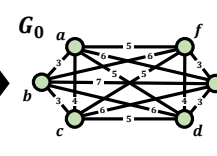
Cactus:  
Each edge belongs to at most one cycle



## The Idea of proposed method

We demonstrate the proposal method with a small example.

Preliminary Step: Input distance matrix

$$D = \begin{pmatrix} a & b & c & d & e & f \\ a & 0 & 3 & 4 & 5 & 6 & 5 \\ b & 3 & 0 & 3 & 6 & 7 & 6 \\ c & 4 & 3 & 0 & 5 & 6 & 5 \\ d & 5 & 6 & 5 & 0 & 3 & 4 \\ e & 6 & 7 & 6 & 3 & 0 & 3 \\ f & 5 & 6 & 5 & 4 & 3 & 0 \end{pmatrix}$$


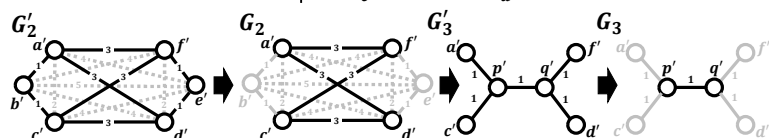
Main Step: Construct  $G^*$

Repeat this "Main Step" until the number of vertices is 2 or fewer.

Step A: Construct  $G_1^*$  from  $G_0$   
Determine how much each vertex "extends" from the set of other vertices using tightening. Investigating adjacency relationships, including newly added vertices, for each vertex where  $d(x, y) = d(x, t) + d(t, y)$  and  $x$  and  $y$  are not adjacent.

Step B: Remove vertices with  $\deg(v) = 0, 1, 2$  and hold the removed elements as determined components of  $G^*$ .

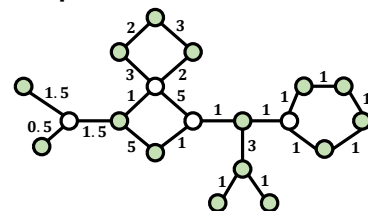
Repeat this operation on  $G_1$ , and create  $G_2, G_3, G_4$ .  $G_3$  has 2 vertices, so the algorithm ends.



## Examples

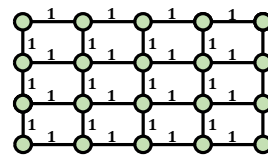
Illustrating successful examples using a Python program. This program runs on a laptop.

### Example 1: A Cactus Metric



We were able to obtain the optimal realization fast using a cactus metric as the input.  
Time: 0.2776 s

### Example 2: A Grid (not cactus)



We were able to obtain the optimal realization fast not only a cactus metric. The Neighbor-Net algorithm failed this example.  
Time: 0.3961 s

Execution Environment

CPU: 11th Gen Intel(R) Core(TM) i7-1195G7 @ 2.90GHz 2.92 GHz

Python version: Python 3.11.4, Memory: 16.0GB, Operating System: Windows 11 22H2

## Future works

Determining the metric spaces in which this method operates correctly. Furthermore, expanding to other metric spaces.

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GitHub  
(Programs)



## References

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- [5] D. Bryant and V. Moulton, "Neighbor-Net: An Agglomerative Method for the Construction of Phylogenetic Networks," Molecular biology and evolution, vol. 21, no. 2, pp. 255–265, 2004.