Algorithms in Comparative Genomics

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https://gi.cebitec.uni-bielefeld.de/teaching/2024summer/cg

Exercise sheet 3, 26.04.2024

Exercise 1 (Small Parsimony under SCJ-Sparsity)

Consider the phylogenetic tree $((\mathbb{A}, \mathbb{B}), (\mathbb{C}, \mathbb{D}))$; with the following genomes at its leaves. Perform the bottom-up phase of the Fitch Algorithm for each adjacency (presence/absence). Only consider adjacencies that occur at any leaf.

\mathbb{A}	=	[1 2 3 4]
$\mathbb B$	=	[1 3 2 4]
\mathbb{C}	=	[1 2 3 4]
\mathbb{D}	=	[2 1 3 4]

- 1. Would initializing the root with the presence of an adjacency in case of ambiguity result in consistent sets of adjacencies?
- 2. How many adjacencies would be reconstructed, if instead the absence of an adjacency is preferred? What is the total cost of the scenario?

Exercise 2 (Small Parsimony under SCJ-Exhaustiveness)

The Fitch-Algorithm as presented in the lecture is not guaranteed to find all optimal solutions.

- 1. Provide an example for the above statement.
- 2. Could your example still be found if the restriction to select **0** for the root node in case of ambiguity is lifted? If not: can you find such an example?
- 3. Does any of the missed solutions in your latter example contain fewer 0s than any of the found solutions? If not: can you find such an example?
- 4. Phrase an algorithm / a modification of the Fitch algorithm that is guaranteed to always find all solutions.

Exercise 3 (Big Parsimony under SCJ-NP-hardness)

As discussed in the lecture, the Big Parsimony Problem under SCJ is NP-hard. Feijão and Meidanis (TCBB 2011) show this by reduction from a Steiner Tree Problem in $\{0, 1\}^N$.

Here, we consider the general Steiner Tree Problem – one of the famous Karp's 21 NP-complete problems. The decision version can be phrased as follows: "Given an undirected graph and a subset of vertices, referred to as *terminals*, is there a subtree of size at most k that includes all terminals?".

Research an NP-hardness proof and understand it.

(5 pts)

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(5 pts)