Fitch's algorithm for SPP under SCJ

Algorithms in Comparative Genomics

For each adjacency α do:

1. (Bottom-up phase) Collect putative states for an adjacency α of each node v, stored in a candidate set $B(\alpha, v)$.

1a. (Leaves) For each leaf l, set

$$B(\alpha, l) := \begin{cases} \{1\} & \text{if } \alpha \in G_l \\ \{0\} & \text{otherwise.} \end{cases}$$

1b. (Internal nodes) Assume an internal node u with children v and w.

$$B(\alpha, u) := \begin{cases} B(\alpha, v) \cap B(\alpha, w) & \text{if } B(\alpha, v) \cap B(\alpha, w) \neq \emptyset, \\ B(\alpha, v) \cup B(\alpha, w) & \text{otherwise.} \end{cases}$$

2. (Top-down refinement) Reconstruct most parsimonious labeling $F(\alpha, v)$:

2a. (Root)

$$F(\alpha, \text{root}) := \begin{cases} s & \text{if } B(\alpha, \text{root}) = \{s\}, \\ 0 & \text{otherwise, i.e., } B(\alpha, \text{root}) = \{0, 1\}. \end{cases}$$

Second case to avoid conflicts. (In the general Fitch version, any state from B can be chosen. But we require consistency.)

2b. (Other nodes) Consider v with parent node p, and let $s = F(\alpha, p)$.

$$F(\alpha, v) := \begin{cases} s & \text{if } s \in B(\alpha, v), \\ 1 - s & \text{otherwise, i.e., set it to the other state.} \end{cases}$$