Fitch's algorithm for SPP under SCJ

Algorithms in Comparative Genomics

For each adjacency Y do:

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

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

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

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

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

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

   2a. (Root)

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

   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 $s = F(Y, p)$.

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