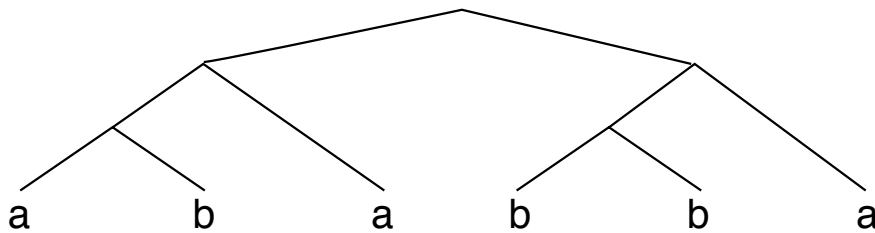


Ancestral Reconstruction: Fitch's Algorithm

Run Fitch's algorithm on the example trees below to obtain assignments of bases to ancestral nodes.

- *Example 1:* two characters, biallelic (typical for SNPs)



- *Example 2:* three characters, triallelic (rare in the same population, more common across species)

