

Fitch Algorithm

- 1 Set the score to be 0.
- 2 Select the next site.
 - 1 Each leaf is given the set corresponding to its base (or possible bases for gaps and ambiguous characters).
 - 2 For each ancestral node whose children have both been processed, let X represent the intersection of the children sets.
 - 3 If X is non-empty, the set for the node is X . Otherwise, the set for the node is the union of the children sets and one is added to the score.
 - 4 Continue to the root.
- 3 Continue until all sites are processed.

Simulation Description

- Simulate DNA evolution on two different trees.
- One tree has all short edges.
- One tree has some short edges and two long edges at opposite ends of the tree.
- Pick a base for data at some node (1=A, 2=C, 3=G, 4=T, 5 or 6 = try again).
- For every edge, roll a die to see if there is a change:
 - ▶ **short edges:** change when a 1 is rolled
 - ▶ **long edges:** change when a 1, 2, or 3 is rolled
- When there is a change, pick a different base at random (1 or 2 = first, 3 or 4 = second, 5 or 6 = third).