Building the Tree

11° We have our sequences, our evolutionary distances, and a metric that corresponds to a phylogenetic tree. How do we actually get our phylogenetic tree? We turn to the *Cherry-Picking Theorem* and the *Neighbor-Joining Algorithm* for the answer. These algorithms are given without too much explanation at this point. Essentially, one begins with a 'template tree' or network, then using the above information, one decides whether or not the nodes in the template tree belong or should be 'pruned'. This process results in a phylogenetic tree T using our metric d_T.

> **Theorem 2 (Computational Cherry-Picking Theorem).** Let d be a tree metric on $[n]$. For every pair $i, j \in [n]$ set
>
> $$Q_d(i,j) = (n-2) \cdot d(i,j) - \sum_{k \neq i} d(i,k) - \sum_{k \neq j} d(j,k).$$
>
> Then the pair $x, y \in [n]$ that minimizes $Q_d(x,y)$ is a cherry in the tree.

The above theorem is a computationally superior form of a more theoretically relevant statement of the Cherry-Picking Theorem. Now that we know how to pick a cherry out of a tree, we use the Neighbor-Joining Algorithm to build our tree.

Algorithm 3 (Neighbor-joining algorithm).
Input: A dissimilarity map d on the set $[n]$.
Output: A phylogenetic tree T whose tree metric d_T is “close” to d.

Step 1: Construct the $n \times n$ matrix Q_d whose (i, j)-entry is given by Theorem 2, and identify the minimum off-diagonal entry $Q_d(x, y)$.

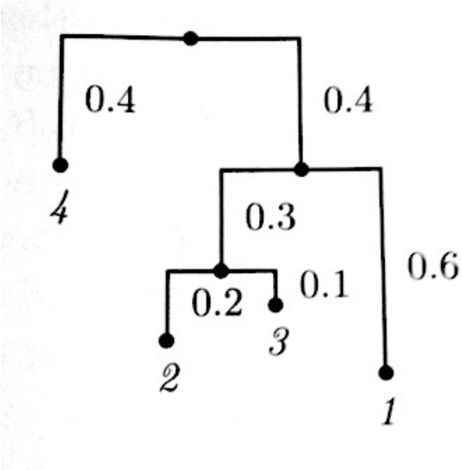
Step 2: Remove x, y from the tree, thereby creating a new leaf z. For each leaf k among the remaining $n - 2$ leaves, set

$$d(z, k) = \frac{1}{2}(d(x, k) + d(y, k) - d(x, y)).$$

This replaces the $n \times n$ matrix Q_d by an $(n - 1) \times (n - 1)$ matrix. Return to Step 1 until there are no more leaves to collapse.

Step 3: Output the tree T. The edge lengths of T are determined recursively: if (x, y) is a cherry connected to node z as in Step 2, then the edge from x to z has length $d(x, k) - d_T(z, k)$ and the edge from y to z has length $d(y, k) - d_T(z, k)$.

Using the Cherry-Picking Theorem and the Neighbor-Joining Algorithm on our metric, we receive the following phylogenetic tree:



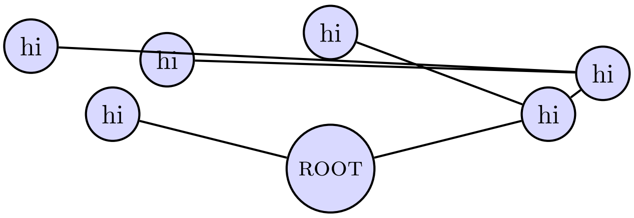


Figure 5: Tree/Form