Explaining Genetic Distances Using Branch Lengths in Phylogenetic Trees

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February 16, 2025

1 Introduction

In molecular evolution and phylogenetics, a **phylogenetic tree** is used to represent the evolutionary relationships among a group of organisms or sequences. Each *branch* in the tree has an associated length, which typically represents the amount of genetic change (such as the number of nucleotide substitutions) that has occurred along that branch. This measure of change is often interpreted as the **genetic distance** between nodes (or taxa) in the tree.

2 Branch Lengths and Genetic Distance

2.1 What Are Branch Lengths?

In a phylogenetic tree:

- **Tips** (or leaves) represent the observed sequences.

- **Internal nodes** represent hypothetical common ancestors.

- **Branch lengths** quantify the amount of genetic change that occurred between two connected nodes. In many cases, these lengths are expressed in units such as the number of substitutions per site.

2.2　Genetic Distance

The **genetic distance** between any two nodes in the tree is computed by summing the branch lengths along the unique path that connects these nodes. Mathematically, if the path between node A and node B passes through branches with lengths $\ell_1, \ell_2, \ldots, \ell_n$, then the genetic distance $d(A, B)$ is given by:

$$d(A, B) = \sum_{i=1}^{n} \ell_i.$$

This distance is a measure of how much genetic change separates the two nodes.

3　Calculating Genetic Distances Between Variant MRCAs

When analyzing variants (such as different viral strains), one common approach is to:

1. **Group sequences by variant.** For example, sequences may be labeled with a prefix indicating their variant, such as `Alpha_1234` or `Mu_5678`.

2. **Determine the Most Recent Common Ancestor (MRCA) for each variant.** The MRCA is the node in the tree from which all sequences of that variant descend.

3. **Compute pairwise distances between the MRCAs of different variants.** Using the formula above, the distance between the MRCA of variant X and the MRCA of variant Y is calculated by summing the branch lengths along the path that connects these two nodes.

3.1　Interpreting the Distance Matrix

Once the pairwise distances between the MRCAs of each variant are computed, the resulting matrix provides a comparative measure of the genetic divergence among variants. Larger distances indicate greater genetic differences, suggesting that the variants diverged earlier in evolutionary time or accumulated more genetic changes.

4 Summary

In summary:

- **Branch lengths** in a phylogenetic tree quantify the amount of genetic change.

- **Genetic distance** between two nodes is the sum of branch lengths along the connecting path.

- By calculating the **MRCA** for each variant and then measuring the distance between these MRCAs, we obtain a matrix that summarizes the genetic divergence among variants.

This approach provides a clear and quantitative way to compare evolutionary relationships among different groups based on their genetic differences.