

AMD Midwest NEWSLETTER

January 2020

IN THIS ISSUE - Are we related? Basics of Phylogenetics

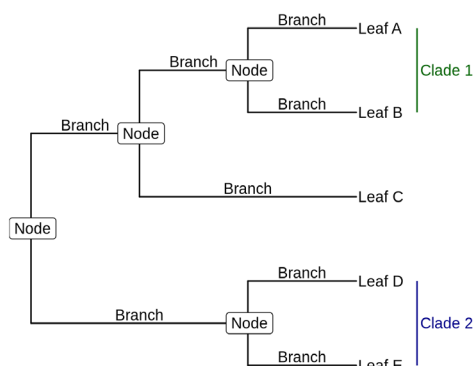
Happy New Year! Aside from a fresh new look, this month's issue is going to focus on the basics of phylogenetic trees.

What's in a name?

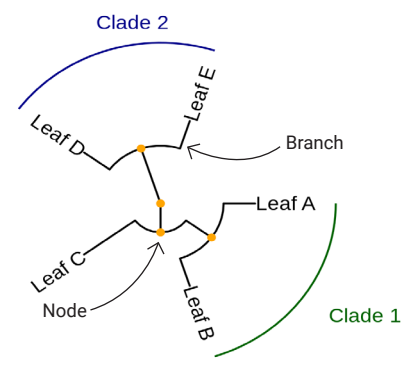
First we'll start by defining the word 'phylogenetic.' The prefix 'phylo' refers to a group of organisms, and 'genetic' refers to genes and a common origin. It follows that 'phylogenetic' refers to examining the common origin (i.e. the relatedness) of a group of organisms using their genetic data. Phylogenetic trees are branching diagrams that allow us to visualize the results of phylogenetic analyses and determine the relatedness of organisms.

Future Events

- AMD Academy
Jan 27-30, 2020
- Inform 2020
Mar 9-12, 2020
- AMD Academy
Apr 20 - 23, 2020
- APHL Annual Meeting
Jun 8 - 11, 2020
- APHL ID Lab Con
Aug 11 - 13, 2020
- AMD-2 Day
Sep 21-22, 2020



Dendrogram Layout

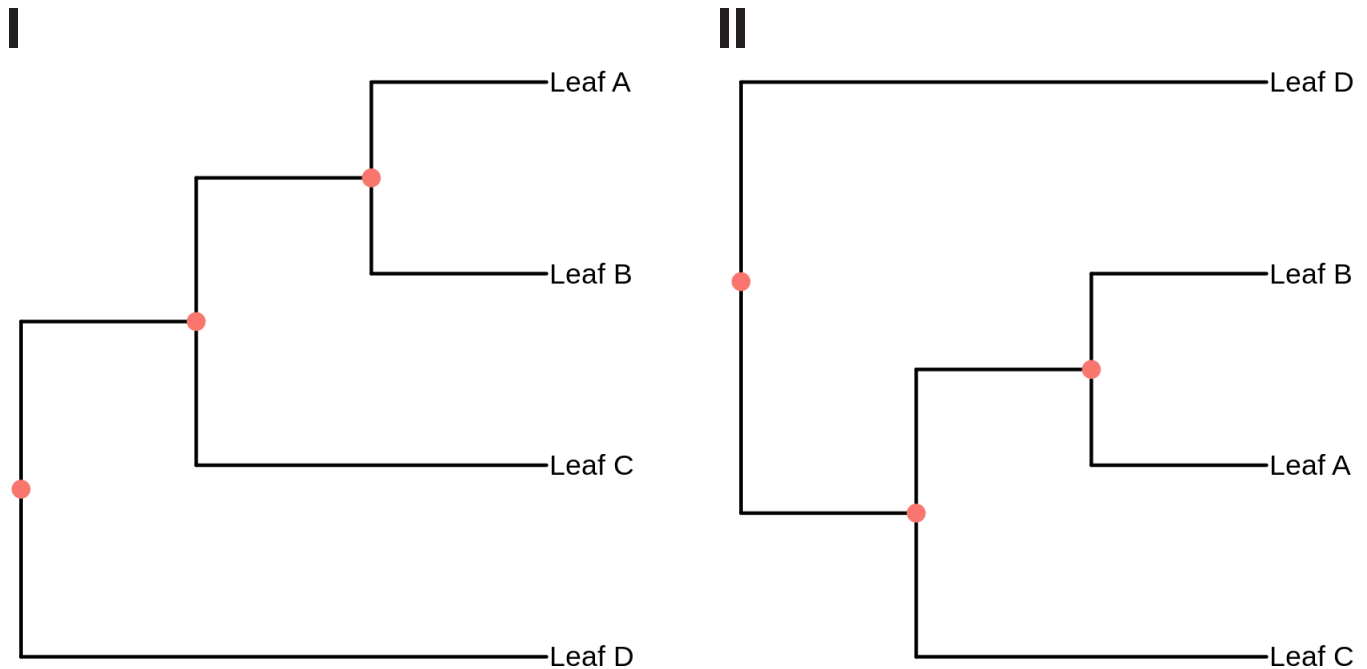


Circular Layout

Branches... and not the ones that we see outside our window

When we look at a phylogenetic tree, there are a few common terms we can use to describe it. The very edge of a phylogenetic tree is where we see the organism's name (whether it's the sample name or the name of a species) which is called the **leaf**. These leaves are connected to each other by **branches**. Two branches connect back to a **node**, which is a common ancestor of the leaf. The node is a hypothetical organism that may not exist in nature. As we go further back on the tree, we start to see more isolates are connected and descend from a common ancestor. Clusters of isolates from a recent ancestor make up a **clade**.

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But the isolates are right next to each other, so why aren't they related?

A common misconception in interpreting phylogenetic trees is that isolates are closely related because they are vertically close to one another on the tree. However, the vertical placement of isolates can be changed by rotating a clade at a particular node. This can take isolates that are vertically close to each other and place them distant from one another.

At first glance, trees I and II look very different from one another. In tree I, it may appear that leaf C is closely related to leaf D and leaf B, while in tree II, it looks as though leaf C is closely related to leaf A. **These are actually the same tree!** Tree II is tree I with the nodes colored in red flipped vertically.

When we read phylogenetic trees, we should look **horizontally** across the tree and identify nodes that are the common ancestor of a clade. In both tree I and tree II, leaf A and B share a recent common ancestor and are more closely related to one another than they are to leaf C. Leaf A, B and C also share a common ancestor and are more closely related to one another than they are to leaf D.

The next issue will focus on how to construct a phylogenetic tree, the statistics behind phylogenetic relatedness and how changes in our analysis may result in different phylogenetic trees.