# Weeks five and six 28/02/2022-07/03/2022

The weeks' objective: Describe a phylogenetic tree, part two

You did a great job last week, bravo!

We can now add more metrics. Knowing that we are in a "particular" setting of the evolutionary tree, the abundant clonotype(s) position might be informative. The question is how we can quantify the position, and maybe the most straightforward answer would be by using the **depth** and **height** of nodes.
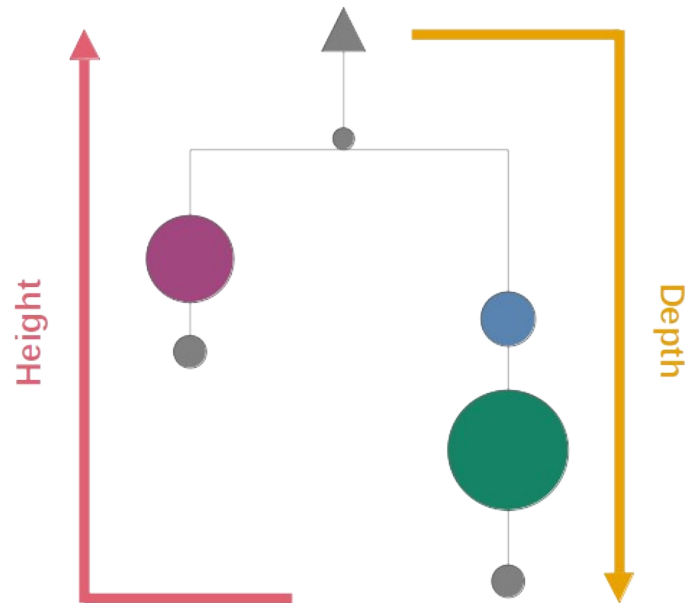
- The **depth** of a node is the number of edges from the node to the tree's root node. A root node will have a depth of 0.
- The **height** of a node is the number of edges on the *longest path* from the node to a leaf. A leaf node will have a height of 0.
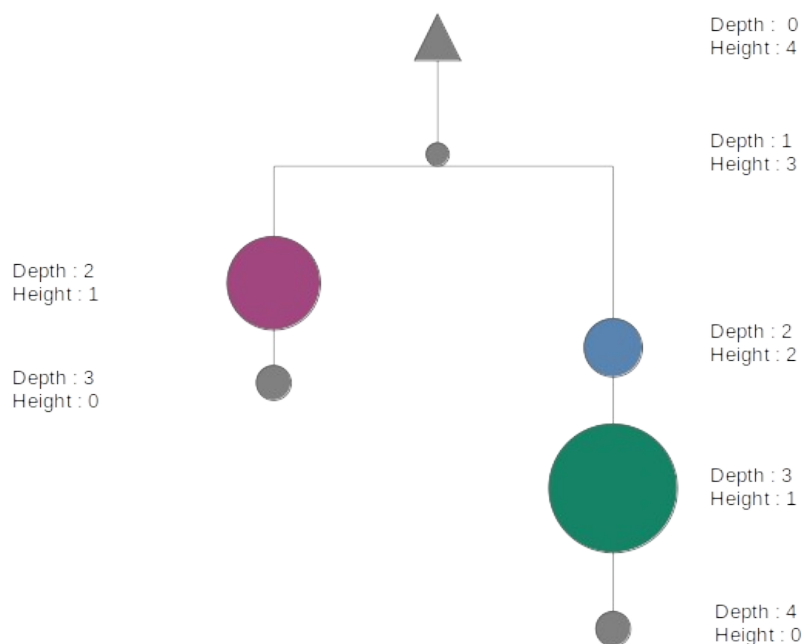
let's calculate :

For a given tree

      For the **three most abundant clonotypes (nodes) :**

            The nodes depth

            The nodes height

So given our example tree, your code will return :

`Clonotype 1` (the most abundant, which is the green one) `D=3, H=1`

`Clonotype 2` (the second most abundant, which is the purple one) `D=2, H=1`

`Clonotype 3` (the third most abundant, which is the blue one) `D=2, H=2`

We will add a **few clones** to our repo on Github as soon as possible. You can then **apply the metrics** you have coded to them. We will further discuss this task during our next meeting on the 8th of mars.

Have a lovely week!

Inspiration for the example :
https://stackoverflow.com/questions/2603692/what-is-the-difference-between-tree-depth-and-height