

Weekly Homework 7

Phylogenetic trees

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In the following essay, I will discuss the concept of phylogenetic trees. The term *phylogenetic* comes from the Greek word *phulon*, which means tribe, specie or race and another greek term *genesis*, which means origin. Therefore, phylogenetic refers to the evolution or genetic development of a certain specie from its beginning. Moving on to the phylogenetic tree, this concept represents a drawing in the shape of a tree in which the closeness of two species comes from the degree of similarities in their genetic encoding. This tree does have vertices and edges, and can be of several types: either rooted or unrooted (if the actual root can be interfered, it will surely have the degree at least 2 – meaning it has at least to species deriving from it, but any rooted tree can become an unrooted one if one decides to omit the starting point), bifurcated or multifurcated (these categories refer to the number of descendants for each node – a bifurcated tree has exactly two descendants for each node, which is not a leaf, while a multifurcated one can have many more descendants for a node), labeled versus unlabeled. In the case of rooted trees, vertices are named either taxonomic units or hypothetical taxonomic units, depending on either they are leaf nodes or internal nodes, and in general the length of one edge represents the timelapse between the node species. An interesting fact is that all life on Earth seems to have the same phylogenetic tree, indicating a certain degree of similarities between all of us, creatures of this planet.

An interesting video that I've found about this topic is the TedxTalk titled 'Building the Tree of Life' and held by Douglas Soltis, a highly respected professor and researcher from The University of Florida. He starts by emphasizing the importance of such structure

where one can see the relationship and the closeness of the genetic code of two species, for several reasons such as: curing disease and developing certain drugs. Given the fact that on Earth there are about 2.3 million species, constructing such tree would request gigantic computational power, but in 2016 he and his team did it. They've managed to build the first exhaustive phylogenetic tree for all life on Earth. Anyway, since this exhaustive tree of life would be so hard to process and understand, they've reduced it to 1000 main categories, including our category, mammals. Moving on, it presents this reduced tree of life in a circle form, color-coded from red to blue, with the meaning that for red encoded species, they have sequenced the whole genome, while for the blue encoded they have no DNA information. Unfortunately, they have DNA information only for about 17% of the currently known species, but there are still a huge number of uncategorized species that are not even yet in that tree of life. Either way, even the existing tree of life contributed majorly to the previously mentioned domains of science. In this video, professor Soltis gives a couple of examples. The first example refers to the Pacific yew, a plant that is the source of a cancer-treating drug, but which unfortunately is very hard to find. Thanks to the tree of life, they've managed to find another plant which is much more common but contributes in the same way to that cancer-treating drug. The second example speaks about crop improvement and how with the tree of life it would be possible to find plants that give similar crops but request less water.

To conclude, phylogenetic trees, also called trees of life, may have an enormous contribution in different fields, but they are still far from being completed for all species. Even though each year around 14000 species are being categorized and described, in this rhythm it would take us 900 more years to fully discover all the species on Earth.