# Homework #7

Lupașcu Marian
Syntactic Modeling of Biological Systems
University of Bucharest

May 3, 2020

Context

The phylogenetic tree is a diagram in the form of a tree (there are brachs / splits) that graphically represents the relationships and evolution of several species in a common ancestor. These graphs are used intensively in the theory of evolution because the branches outline relationships such as: common ancestor (point in the graph) - species that have evolved from the current common ancestor (point in the graph at a higher level in the hierarchy). In the figure below you can see the phytogenetic tree for all large classes of species, obtained with iTOL.[1, 5]
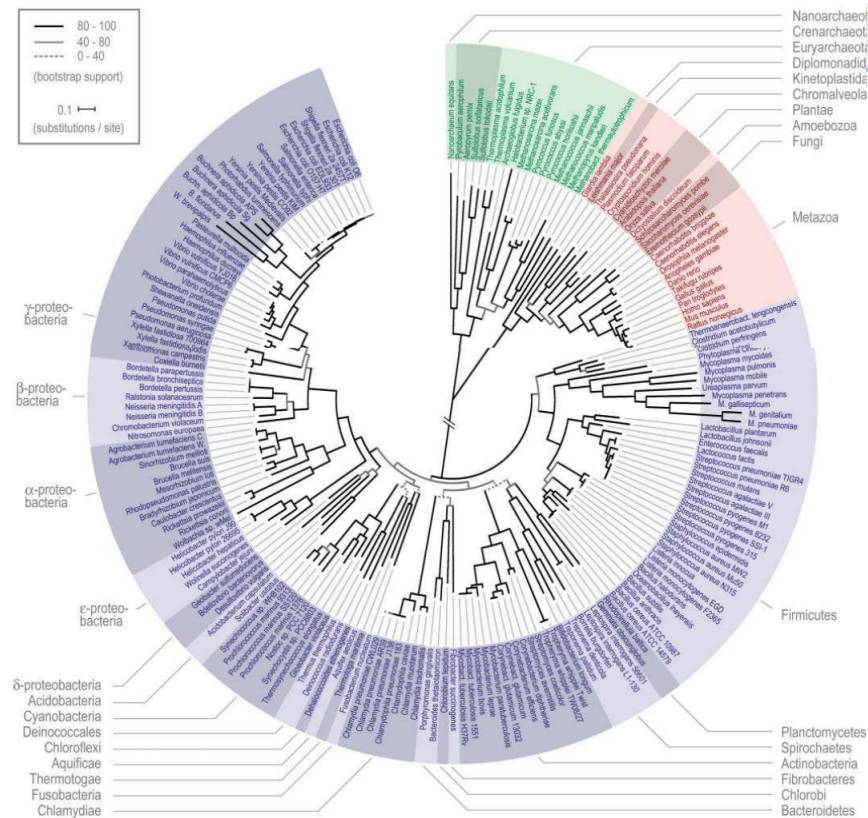
The notion of phylogenetic trees has existed since the time of Charles Darwin, when the relationships between species were outlined based on physical features, internal anatomy or behavior. Currently these relationships are built on the basis of genetic information of existing species or fossils, biochemistry or protein analysis, implies the construction of these graphs also varies with the way of cataloging the species. Currently, all these combined features are used to build these graphics.[1]

Constructions and properties

In a phylogenetic trees, on the terminal nodes are the species of today and on the internal nodes are the species from antiquity that gave birth to two or more other species. Of course, the notion of time can also be introduced in these trees, ie the length of an ancestor segment up to the branch point should be proportional to the time when the ancestor gave birth to a new species. In addition, there is the possibility that in the graph, starting from the root, on a certain evolutionary path, we do not reach a species of the present time, but we have the end in an ancient species, a species that has undergone the process of extinction.[2, 3]

With all these features for a phylogenetic tree, the following natural question arises: which are the most related species in the tree? Well, it can be defined as the shortest path (in terms of species / nodes or time, if the graph has edges proportional to the brach time), which involves determining the lowest common ancestor. For example in Figure 2, it can be seen that the lowest common ancestor between man and platypus (7) is the light green dot from the Triassic era. Another issue that can happen in such a tree is: polymy. That is, in a branch more than two new species are born at the same time (In Figure 2, this can be seen in the pink dot from the Upper Carboniferous era). This does not happen in reality, but in a tree, yes, due to the lack of information.[2]
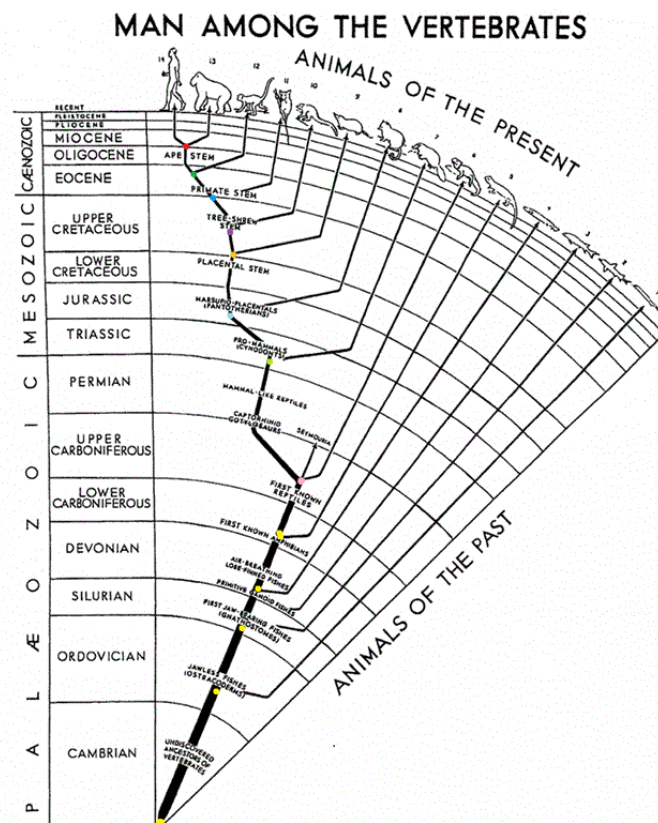

Figure 2 .

These graphs can show in various forms: in the form of a classic tree, cyclic, philogram, coral, dendrogram, etc., but in essence all these forms of the graph are trees. The construction of these trees is a NP-hard problem [3, 4], and currently the construction of phylogenetic trees is done automatically based on the genome using a series of optimizations and heuristics.

Due to noise such as: altered DNA (especially when analyzing fossils), specimens representative of the species, analysis of a particular gene or protein and not a set of features or incorrect setting of the weights of the analyzed features can lead to trees that they are not necessarily evolutionarily correct. But in essence, these trees seem to outline reality, which is why they are an important tool in the analysis of evolution.[1]

References

[1] Francesca D. Ciccarelli, Tobias Doerks, Christian von Mering, Christopher J. Creevey, Berend Snel, Peer Bork Toward Automatic Reconstruction of a Highly Resolved Tree of Life, Bioinformatics, 2006
http://bioinformatics.bio.uu.nl/pdf/Ciccarelli.s06-311.pdf

[2] Constance Areson Clark Evolution for John Doe: Pictures, the Public, and the Scopes Trial Debate, The Journal of American History, 2001

[3] Santamaria, R., Theron, R. Treevolution: visual analysis of phylogenetic trees, Bioinformatics, 2009

[4] Felsenstein J. nferring Phylogenies Sinauer Associates, Sunderland,

[5] Letunic Ivica, Bork Peer, Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation, Bioinformatics, 2007