MODULE 7

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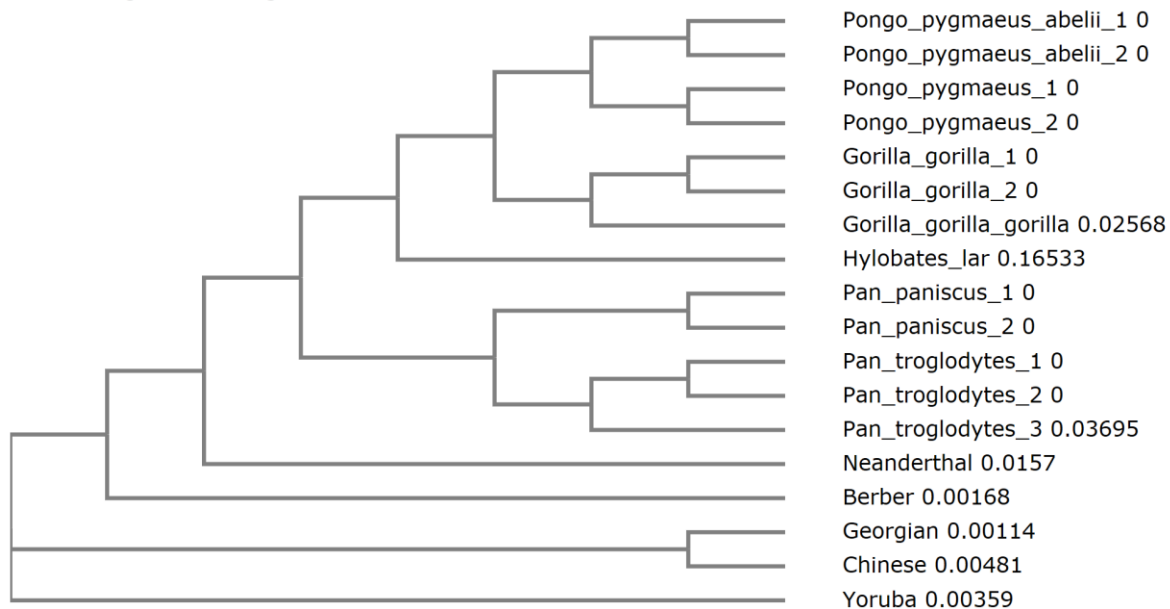
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Exercise 1:

Using mitochondrial DNA data from primates to create two phylogenetic trees: one using the correction JukesCantor and the other without any correction. Discuss the relationship of humans with other primates and the position of the Neanderthal generated trees.

Comments:
The mtDNA data are available in the text book's website (), the case study of the Neanderthal, the Download link Date. The file containing the sequences is human_primates_hvr_2.fasta.

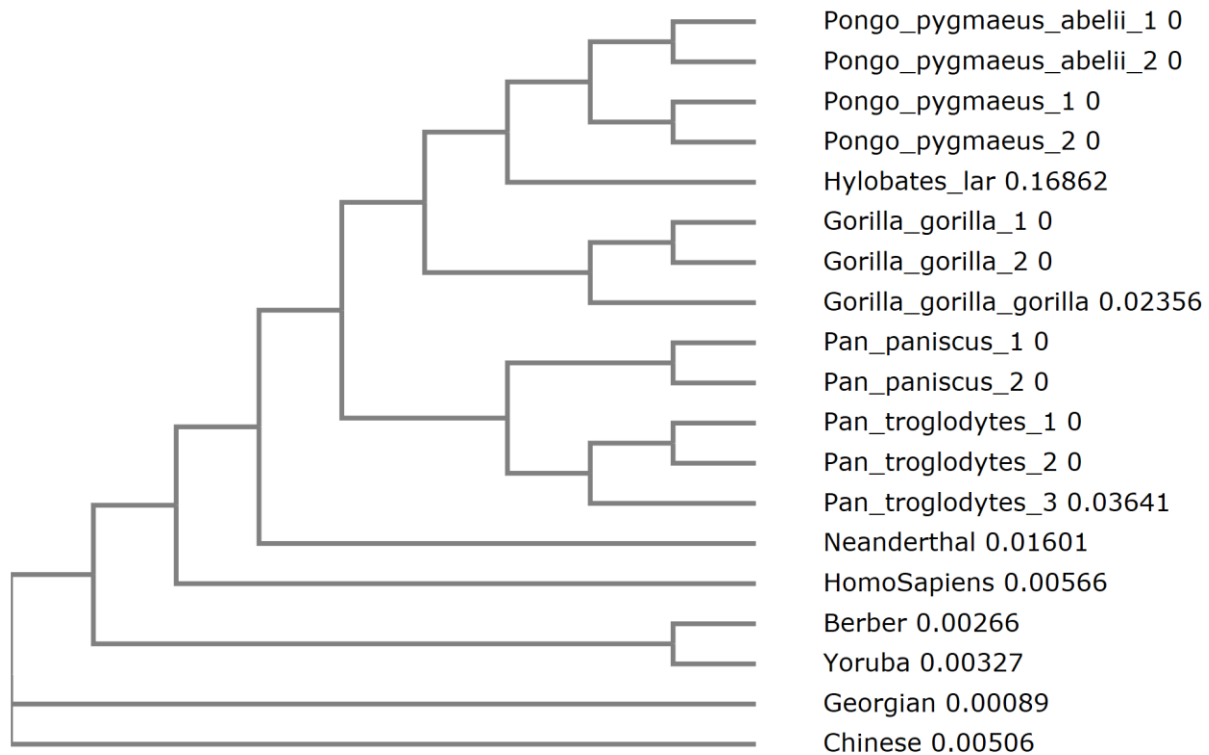*Remove the gaps present in the strings and make the multiple alignment using Clustal OMEGA.*

Answer:


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                                    Pongo_pygmaeus_abelii_1 0
                                    Pongo_pygmaeus_abelii_2 0
                                    Pongo_pygmaeus_1 0
                                    Pongo_pygmaeus_2 0
                                    Gorilla_gorilla_1 0
                                    Gorilla_gorilla_2 0
                                    Gorilla_gorilla_gorilla 0.02568
                                    Hylobates_lar 0.16533
                                    Pan_paniscus_1 0
                                    Pan_paniscus_2 0
                                    Pan_troglodytes_1 0
                                    Pan_troglodytes_2 0
                                    Pan_troglodytes_3 0.03695
                                    Neanderthal 0.0157
                                    Berber 0.00168
                                    Georgian 0.00114
                                    Chinese 0.00481
                                    Yoruba 0.00359
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The Neanderthal is one of the most advanced species among all the human primates. If we number each specie from 1st the most primitive and 18th the most advanced, the Neanderthal is on position 14. Meaning, that there was a long evolution process among its ancestors until the evolution lead to the Neanderthal.

The Homo Sapiens (human) is not in this phylogenetic tree. So even though the exercise tells that the tree above belongs to the human primitive ancestors, it is hard to tell exactly from which branch the Homo Sapiens came from. That is why, I modified the .fasta file obtained from the "computational Genomics" to include the Homo Sapiens mitochondrial DNA.

Pongo_pygmaeus_abelii_1 0
Pongo_pygmaeus_abelii_2 0
Pongo_pygmaeus_1 0
Pongo_pygmaeus_2 0
Hylobates_lar 0.16862
Gorilla_gorilla_1 0
Gorilla_gorilla_2 0
Gorilla_gorilla_gorilla 0.02356
Pan_paniscus_1 0
Pan_paniscus_2 0
Pan_troglodytes_1 0
Pan_troglodytes_2 0
Pan_troglodytes_3 0.03641
Neanderthal 0.01601
HomoSapiens 0.00566
Berber 0.00266
Yoruba 0.00327
Georgian 0.00089
Chinese 0.00506

Adding the Homo Sapiens to the tree, it is possible to conclude that the Neanderthal is a close ancestor of Humans.

Exercise 2:

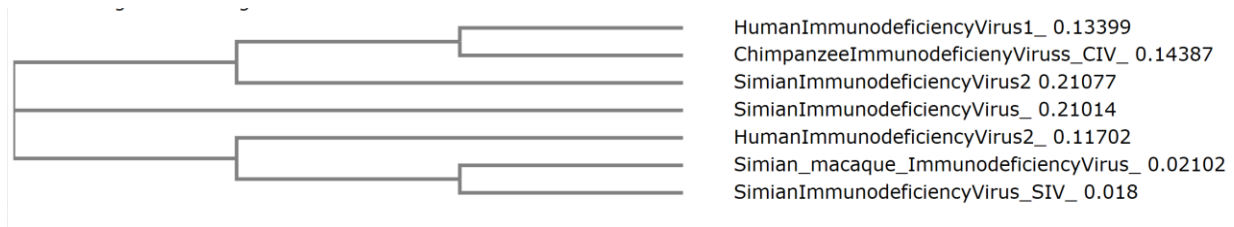Get the following GenBank sequences related to HIV and SIV:

- NC_001802 - HIV1 man
- NC_001722 - HIV2 man
- NC_004455 - SIV mandrill
- NC_001549 - SIV African green monkey
- M19499 - maccaca SIV mulatta
- M32741 - pigtailed macaque SIV
- X52154 - SIV chimpanzee

Build a phylogenetic tree for the variations of HIV and SIV. For the construction of the tree, use the same procedures as the previous year. Can you identify the origins of HIV1 and HIV2? Review the generated tree.

Curiosity: *A well-known tool and used bioinformatics to build phylogenetic trees is Phylip.*
Note 2: *The Clustal OMEGA generates a phylogenetic tree.*

Answer:

HumanImmunodeficiencyVirus1_ 0.13399
ChimpanzeeImmunodeficienyViruss_CIV_ 0.14387
SimianImmunodeficiencyVirus2 0.21077
SimianImmunodeficiencyVirus_ 0.21014
HumanImmunodeficiencyVirus2_ 0.11702
Simian_macaque_ImmunodeficiencyVirus_ 0.02102
SimianImmunodeficiencyVirus_SIV_ 0.018

Based on the phylogenetic tree it is possible to affirm that HIV1 has a close ancestor with the Chimpanzee Immunodeficiency Virus (SIV).While the HIV2 originated from a mutation of the Simian Macaque Immunodeficiency Virus and Simian Immunodeficiency Virus SIV.

Using the Jukes Cantor it is possible to obtain more detailed information about the ancestors, however the Clustal Omega does not provide this correction anymore.