

Assignment 3: Prolog

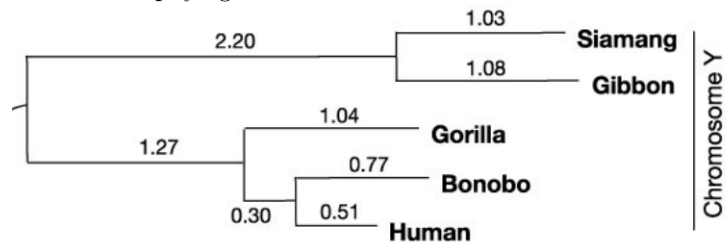
Practical Computing for Bioinformatics

December 9, 2020

For this assignment form pairs, work out the questions, note the names of both members in your answer document, and upload all your answer files as a single compressed archive on Toledo for both participants. When answering the questions, make sure you explain your logic and the steps you took as well as the actual answer. Write your response in such a way that I could follow your steps and come to the same answer. If your answer includes an output file, include it in your archive.

Assignment

Given a rooted phylogenetic tree annotated with branch distances, such as:



Tree extracted from: K. D. Makova, W.-H. Li, "Strong male-driven evolution of DNA sequences in humans and apes", Nature 416, 624-626, April 2002, http://www.nature.com/nature/journal/v416/n6881/fig_tab/416624a_F1.html

Write a prolog script to

- represent the tree in Prolog
- find the most recent common ancestor between two species
- list the ancestor nodes of a given leaf of the tree, up to the root node
- count the number of nodes of a tree