

Assignment 2

Q1) We did the multiple sequence alignment (MSA) using the clustal tool

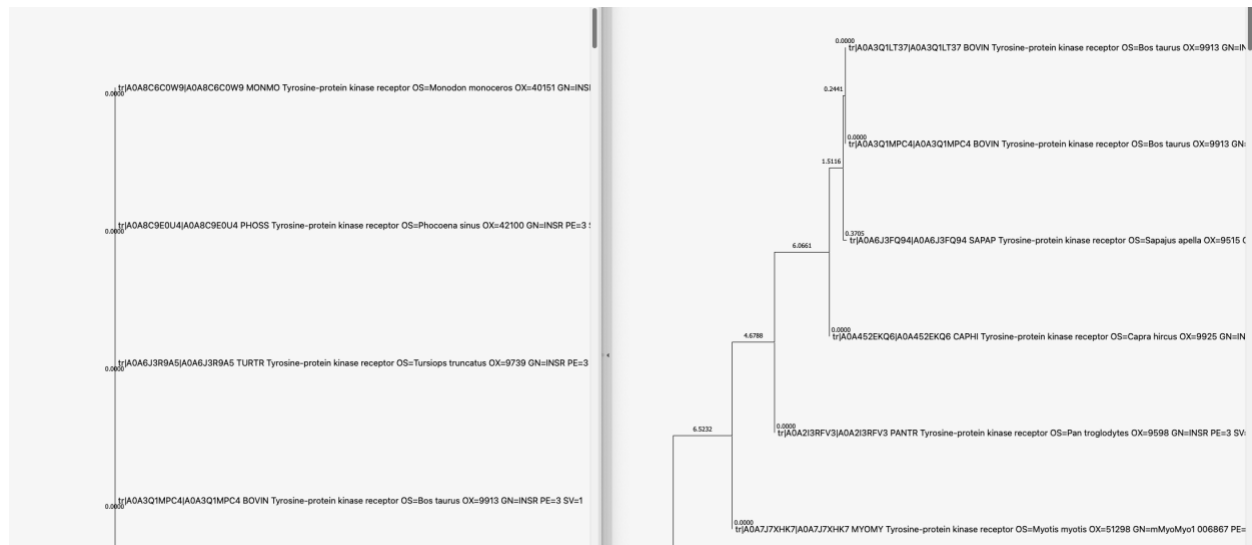
Q2) We did the phylogenies UPGMA and NJ using the MEGA tool

Q3) We will provide pdf of both tree of upgma and NJ

Q4) [cellular organisms](#) > [Eukaryota \(eucaryotes\)](#) > [Opisthokonta](#) > [Metazoa \(metazoans\)](#) > [Eumetazoa](#) > [Bilateria](#) > [Deuterostomia](#) > [Chordata \(chordates\)](#) > [Craniata](#) > [Vertebrata \(vertebrates\)](#) > [Gnathostomata \(jawed vertebrates\)](#) > [Teleostomi](#) > [Euteleostomi \(bony vertebrates\)](#) > [Sarcopterygii](#) > [Dipnotetrapodomorpha](#) > [Tetrapoda \(tetrapods\)](#) > [Amniota \(amniotes\)](#) > [Mammalia \(mammals\)](#) > [Theria](#) > [Eutheria \(placentals\)](#) > [Boreoeutheria](#) > [Laurasiatheria](#) > [Artiodactyla \(whales, hippos, ruminants, pigs, camels etc.\)](#) > [Ruminantia](#) > [Pecora](#) > [Bovidae](#) > [Bovinae](#) > [Bos](#) and this is similar to the one in the NCBI taxonomy database

Q5) Yes, the two trees have the same topology because the internal branching structures and the relationships between the taxa are consistent across both trees, despite any potential differences in branch lengths or the visual arrangement of the tips. Rotations around internal branches do not affect these fundamental topological relationships, indicating that the evolutionary interpretations drawn from both trees would be equivalent in terms of how taxa are grouped and related.

Q6) no



As there

Q7) The differences in the topologies and branch lengths between the UPGMA and Neighbor-Joining trees arise mainly due to their fundamental methodological differences. UPGMA's reliance on the molecular clock hypothesis often simplifies evolutionary relationships, which can be misleading if the actual evolutionary processes are more complex. Neighbor-Joining, by not assuming a constant rate of evolution, is typically better suited for analyzing genetic data that exhibit varying rates of mutation and evolution across different taxa.

Q8) The differences in topology and branch lengths between the UPGMA and Neighbor-Joining trees suggest significant biological implications, revealing distinct evolutionary histories and adaptive responses.

Q9)yes

Q10) all rectangular nodes are orthologous and paralogous there would be many

possibilities if there are a node like this



as show in pic blow

☐ trlF6RLJ3IF6RLJ3_HORSE
☐ trlA0A8C4M0K9IA0A8C4M0K9_EQUAS

Q11) no cause genes didn't transfer between different species

Q12) I include all the necessary files in the rar file