**Assignment** 2Top of FormBottom of Form

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

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

Q3)we will provided pdf of both tree of upgma and NJ

Q4) [**cellular organisms**](https://www.uniprot.org/taxonomy/131567) > **[Eukaryota (eucaryotes)](https://www.uniprot.org/taxonomy/2759" \o "Eukaryota (eucaryotes), taxon ID 2759)** > **[Opisthokonta](https://www.uniprot.org/taxonomy/33154" \o "Opisthokonta, taxon ID 33154)** > **[Metazoa (metazoans)](https://www.uniprot.org/taxonomy/33208" \o "Metazoa (metazoans), taxon ID 33208)** > **[Eumetazoa](https://www.uniprot.org/taxonomy/6072" \o "Eumetazoa, taxon ID 6072)** > **[Bilateria](https://www.uniprot.org/taxonomy/33213" \o "Bilateria, taxon ID 33213)** > **[Deuterostomia](https://www.uniprot.org/taxonomy/33511" \o "Deuterostomia, taxon ID 33511)** > **[Chordata (chordates)](https://www.uniprot.org/taxonomy/7711" \o "Chordata (chordates), taxon ID 7711)** > **[Craniata](https://www.uniprot.org/taxonomy/89593" \o "Craniata, taxon ID 89593)** > **[Vertebrata (vertebrates)](https://www.uniprot.org/taxonomy/7742" \o "Vertebrata (vertebrates), taxon ID 7742)** > **[Gnathostomata (jawed vertebrates)](https://www.uniprot.org/taxonomy/7776" \o "Gnathostomata (jawed vertebrates), taxon ID 7776)** > **[Teleostomi](https://www.uniprot.org/taxonomy/117570" \o "Teleostomi, taxon ID 117570)** > **[Euteleostomi (bony vertebrates)](https://www.uniprot.org/taxonomy/117571" \o "Euteleostomi (bony vertebrates), taxon ID 117571)** > **[Sarcopterygii](https://www.uniprot.org/taxonomy/8287" \o "Sarcopterygii, taxon ID 8287)** > **[Dipnotetrapodomorpha](https://www.uniprot.org/taxonomy/1338369" \o "Dipnotetrapodomorpha, taxon ID 1338369)** > **[Tetrapoda (tetrapods)](https://www.uniprot.org/taxonomy/32523" \o "Tetrapoda (tetrapods), taxon ID 32523)** > **[Amniota (amniotes)](https://www.uniprot.org/taxonomy/32524" \o "Amniota (amniotes), taxon ID 32524)** > **[Mammalia (mammals)](https://www.uniprot.org/taxonomy/40674" \o "Mammalia (mammals), taxon ID 40674)** > **[Theria](https://www.uniprot.org/taxonomy/32525" \o "Theria, taxon ID 32525)** > **[Eutheria (placentals)](https://www.uniprot.org/taxonomy/9347" \o "Eutheria (placentals), taxon ID 9347)** > **[Boreoeutheria](https://www.uniprot.org/taxonomy/1437010" \o "Boreoeutheria, taxon ID 1437010)** > **[Laurasiatheria](https://www.uniprot.org/taxonomy/314145" \o "Laurasiatheria, taxon ID 314145)** > **[Artiodactyla (whales, hippos, ruminants, pigs, camels etc.)](https://www.uniprot.org/taxonomy/91561" \o "Artiodactyla (whales, hippos, ruminants, pigs, camels etc.), taxon ID 91561)** > **[Ruminantia](https://www.uniprot.org/taxonomy/9845" \o "Ruminantia, taxon ID 9845)** > **[Pecora](https://www.uniprot.org/taxonomy/35500" \o "Pecora, taxon ID 35500)** > **[Bovidae](https://www.uniprot.org/taxonomy/9895" \o "Bovidae, taxon ID 9895)** > **[Bovinae](https://www.uniprot.org/taxonomy/27592" \o "Bovinae, taxon ID 27592)** > **[Bos](https://www.uniprot.org/taxonomy/9903" \o "Bos (oxen, cattle), taxon ID 9903)** and this simailiar 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

A screenshot of a computer

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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.Top of Form

Q9)yes

Bottom of Form

Q10) all rectangular nodes are orthologous and paralogous there would be many possibilities if there are a node like this A blue and white diagram

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Description automatically generated



Q11) no cause genes didn’t transferer between different species

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