

BIOL312

Practical 9

Questions

Answer the following questions. Please write the references, if used.

1. Why phylogenetic trees may construct using different regions of the DNA look different?
2. What regions of DNA should you use to compare organisms that are closely related?
3. What kind of genes should you use to compare organisms that are evolutionarily distant from each other?
4. Can you think of reasons why this method of simply comparing the number of differences between the nucleotides may not work if you are comparing organisms that are very different? Remember that we are assuming it takes 20 million years for every nucleotide in a sequence to mutate.
5. Can you think of reasons why, if you are studying more distantly related organisms, it is better to compare amino acid sequences than DNA sequences?

Submission Deadline: 02.06.2020