A brief note about –

1. "Molecular Clock"
2. 16s rRNA as a molecular clock,
3. Rooted & Unrooted phylogenetic tree

1. "Molecular Clock"

Information contained in a macromolecule such as protein or DNA could measure the history of a species. The temporal information contained in a macromolecular sequence is called a **molecular clock**. A molecular clock is based on the acquisition of new random mutations in each round of DNA replication.

Molecular clocks have revolutionized our understanding of the emergence of all living organisms, including human beings.

In practice, the molecular clock works best for a particular gene sequence with the following features:

■ The gene has the same function across all species compared. That is, all versions are orthologous;
they have not evolved to serve different functions. The functional difference may lead to different rates of change.

■ The generation time is the same for all species compared. Shorter generation times (more frequent
reproductive cycles) lead to overestimates of the overall time of divergence because of the increased opportunity for DNA mutation.

■ The average mutation rate remains constant among species and across generations. If different species mutate at different rates, species with more rapid rates of mutation will appear to have diverged over a longer time than is actually the case.

2. 16s rRNA as a molecular clock

Genes that show the most consistent measures of evolutionary time encode components of the transcription and translation apparatus, such as ribosomal RNA and proteins, tRNA, and RNA polymerase. The most widely used molecular clock is the gene encoding the **small-subunit rRNA.** The small-subunit rRNA is also known by its sedimentation coefficient: 16S rRNA (bacteria) or 18S rRNA (eukaryotes). The rRNA sequence is particularly useful because the ribosome structure and function are highly similar across all organisms. Genomic sequences now offer many other genes to measure divergence at different levels of classification.

3. Rooted & Unrooted phylogenetic tree

Comparison of rRNA sequences was used to generate a phylogenetic tree. A phylogenetic tree shows the degrees of relatedness among taxa based on the number of molecular substitutions on each

branch. An unrooted tree does not indicate the position of a common ancestor for all taxa. A rooted tree indicates the position of a common ancestor.

Unrooted phylogenetic tree

Rooted phylogenetic tree