Introductions

Microbiome

Microbiomes are like small people in a crowded city. They live in different places. Inhabitant species normally include bacteria, fungi, archaea, eukaryotes, and viruses. For example, they can help us to digest better in the digestive system and provide resistance to protect us from getting sick in the immune system. They also exist in the plant root system, which helps plants take nutrients and tolerate tension. These species also live in environments as part of natural cycles. Their composition can be influenced by diet, environment, and medication. In such a dynamic nature, they are always evolving, and humans still need to learn more about their influence on health and the environment.

Challenge of microbiome data

Examining microbiome data is not straightforward. Lots of species and genes de­mand our attention, so directing our focus on significant ones is imperative. The data demonstrate­s the proportional presence of each type, not their precise quantities. Therefore, unique statistical techniques are required for proper comprehension. A large number of zero values are normally found in data. This means that no microbes are present. It may be because of the way we collected the data. This will assist ensure that our findings are correct. There is no universally accepted method for dealing with this type of data. Different strategies produce different outputs. This demonstrates that we must all use the same methodologies in microbiome research.

16S rRNA sequence

16S rRNA, found in bacteria and archaea, represents a conserved gene that is valuable for microbiome research. The gene was sequenced by scientists to detect and categorize microorganisms, especially those which had never been cultivated. Whereas 16S rRNA sequencing offers great taxonomic specificity at the level of species and taxa within a given sample, its effectiveness diminishes with decreasing taxonomic granularity owing to sequence homology. Additionally, biases introduced by PCR amplification at every step may compromise accurate diversity as well as compositional assessments. In spite of these limitations, however, 16S rRNA sequencing still remains an affordable method suitable for large-scale studies on microbiomes.

Operational Taxonomic Units OTUs

Operational Taxonomic Units (OTUs) are groups of closely related 16S rRNA gene sequences. These sequences resemble fingerprints for several bacteria. Scientists utilize 16S rRNA sequencing to investigate bacteria. This approach generates a large amount of data, with each sequence representing a single bacterium. Grouping comparable sequences into OTUs facilitates the management of a large number of species. It simplifies data analysis for academics. Scientists assume that identical 16S rRNA sequences indicate that the microbes are related. However, the definitions of OTUs can change. A modest difference in similarity level can result in distinct groupings of sequences. This can have a nonlinear effect on the outcomes.

Phylogenetic Tree

A phylogene­tic tree is a chart that re­veals how different spe­cies are connecte­d through evolution. These links trace­ back to a single ancestor, showing how current spe­cies came to be. To build this chart, we­ usually use genetic se­quence data. Each branch on the chart re­presents a unique line­ of hereditary. The root of the­ tree stands for the first species, the one from which all others have descended. For creating these trees, there are some different methods used to create the phylogenetic tree. The­se include those based on distance and simple methods known as parsimony. The­y can also use likelihood methods. This looks at how similar diffe­rent genes are­. But also, how they might be differe­nt.