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Quantifying Microbial Diversity

Abstract :

The microbiome is the ecological community of commensal, symbiotic and pathogenic microorganisms found in and on all multicellular organisms from plants to animals. It includes bacteria, archaea, protists, fungi and viruses.

The microbiome has been found to be crucial for immunologic, hormonal and metabolic homeostasis of its host, e.g. type 1 diabetes, Crohn's disease, Parkinson's, obesity, depression, ... The microbiome is nowadays interrogated via high-throughput-sequencing platforms producing terabytes of raw data on various levels, e.g. whole metagenomic shotgun sequencing, metatranscriptomic sequencing or the much cheaper 16S rRNA amplicon sequencing for the bacterial part which allows to process hundreds to several thousand individual samples in one experiment. I will cover the necessary pre-processing steps to convert these big data into two dimensional feature-tables and introduce the most common interactive visualization tools, most popular diversity metrics and statistical testing of those.