



METAGENOMICS

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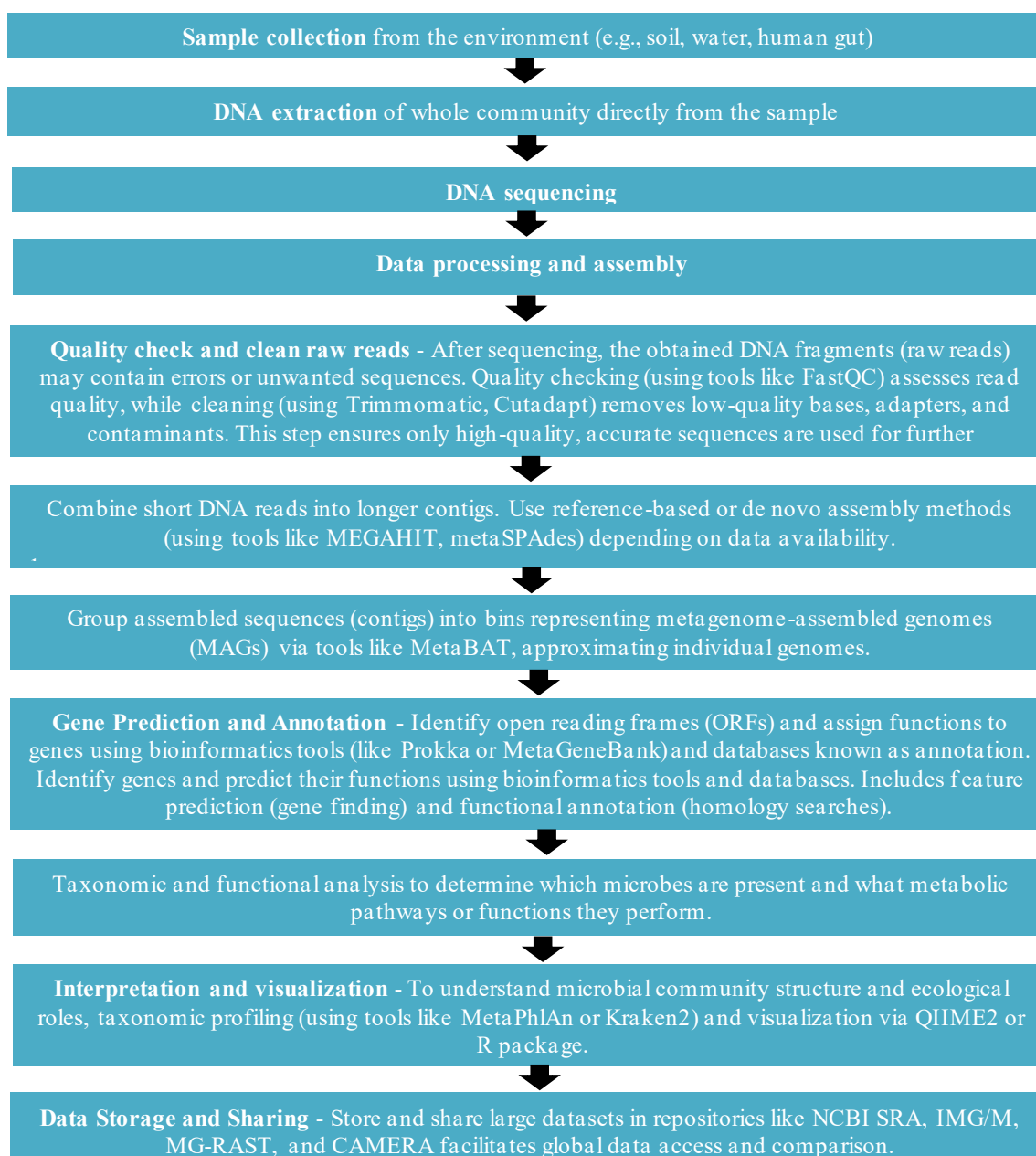
INTRODUCTION

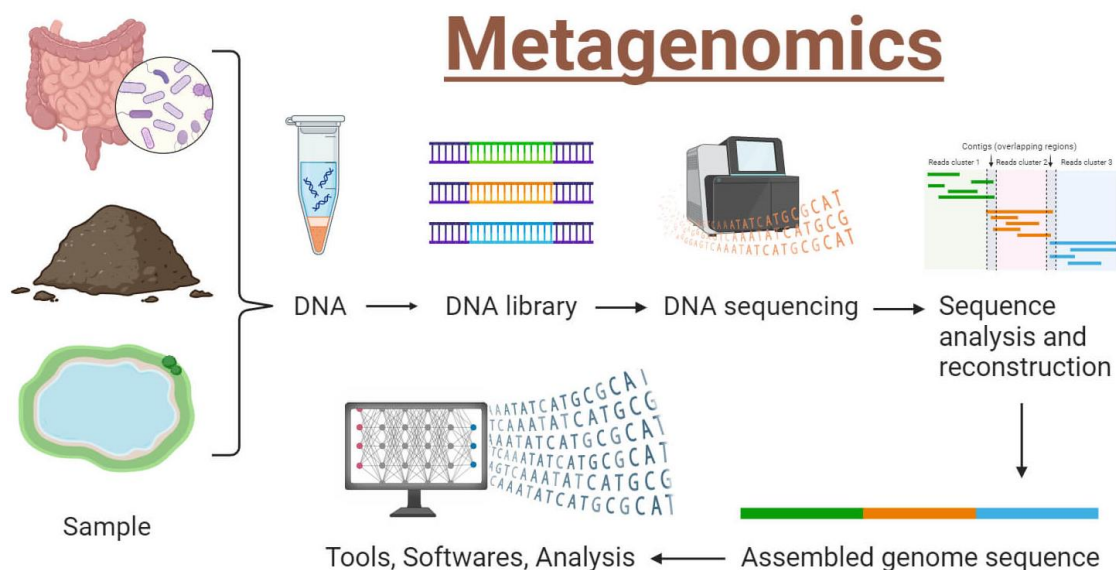
Metagenomics is the study of genetic material (DNA or RNA) directly obtained from environmental samples — such as soil, water, gut, or ocean — without the need to culture the organisms in the laboratory. It can be defined as “the genomic analysis of microbial communities in their natural environments through direct extraction and sequencing of their genetic material.” The concept of metagenomics emerged in 1990s when scientists realized that most microbes (~99%) cannot be cultured in the laboratory using traditional methods. In 1998, Jo Handelsman and colleagues first use the term “metagenomics”. In 2004, The Sargasso Sea metagenome project by Craig Venter marked a milestone — sequencing millions of environmental DNA fragments from ocean samples. Global Ocean Sampling Expedition (GOS)- Led by J. Craig Venter in 2004 to explore ocean microbial diversity. It used shotgun metagenomic sequencing on samples collected globally by the Sorcerer II vessel. Human Microbiome Project (HMP)- Launched by National Institute of Health (NIH) in 2007 to study microbial communities in the human body (gut, skin, mouth, etc.) to understand the role of microbiomes in health and disease. Integrated Microbial Genomes and Microbiomes (IMG/M) System- a database and analysis platform for microbial genomes and metagenomes that provides tools for comparative genomic analysis and functional annotation of microbial communities. Metagenomics allows scientists to study all microorganisms — including those that are non-culturable and to understand their diversity, functions, and interactions, thus helps discover new genes, enzymes, drugs, biofuel, metabolic pathways, etc.

Principle of Metagenomics:

The principle of metagenomics lies in approach of studying the genome of microbial communities in bulk. It may be of two types depending on fragment of DNA that are used for sequencing. Firstly, Targeted metagenomics, also known as amplicon-based sequencing, involves sequencing specific genetic markers or conserved regions within microbial communities, such as 16S rRNA for bacteria and 18S rRNA or Internal Transcribed Spacer (ITS) regions for fungi. These regions have variable sequences that are useful for the identification of different organisms present in

various environmental samples. This method generally does not provide strain-level resolution. Secondly, Shotgun metagenomics or Whole Genome Shotgun (WGS) metagenomics- involves random sequencing of all genetic material in a sample. Unlike targeted sequencing methods that focus on specific genetic markers, shotgun metagenomics sequences all the DNA present in a sample. This provides detailed information on both the taxonomic and functional composition of the microbial community. It also allows species-level identification. The following steps are involved in metagenomic analysis.





Advantages of Metagenomics

- Enables study of non-culturable microorganisms
- Provides both taxonomic and functional insights of microbial communities
- Identifies new genes, enzymes, and biomolecules
- Helps understand human microbiome and its link to diseases
- Improves understanding of ecosystems and explains how microbes affect soil, water, human health and global nutrient cycles
- Leads to discovery of new antibiotics, biofuels and diagnostic tools
- Supports microbiome research for studying the human gut, oral, and skin microbiomes.

Applications of Metagenomics

- Environmental Microbiology- study of soil, ocean and extreme environments to understand microbial ecology and biogeochemical cycles

- Human Health- analysis of human microbiome to study its role in digestion, immunity, and diseases like obesity or diabetes
- Biotechnology- discovery of new enzymes, antibiotics, and biocatalysts from environmental microbes
- Agriculture- understanding soil and plant associated microbes for crop improvement and pest control.
- Bioremediation- identification of microbes capable of degrading pollutants and cleaning up contaminated sites
- Industrial Applications- use of microbial genes for biofuel production, waste treatment, etc.

Note: With the development of next-generation sequencing (NGS) technologies (e.g., Illumina, PacBio), metagenomics became faster, cheaper, and more accurate.