

Preface

When E.O. Wilson wrote his seminal article “The little things that run the world (The importance and conservation of invertebrates)” in the journal *Conservation Biology* in 1987, the whole world was awakening to a new world of tremendous diversity, abundance and biomass of the insects, their functions and ecosystem services. At that moment, no one would have realized that microscopic organisms were really ruling the world, including the world of invertebrates. Today, we can clearly say that the microscopic organisms, i.e., bacteria, archaea, fungi, and viruses, are the planet’s actual dominant life forms. As a result of natural selection, microorganisms have evolved over billions of years to occupy extremely diverse niches on the earth, from deep sea to deep inside our gut. They have played a significant role in the formation of soils, seas, oils, gases, minerals and metals that, all together, form the earth’s surface. They are required for the proper physiological and ecological functions of animals and plants.

The microbial world was largely underestimated before the birth of metagenomics. Metagenomics is an approach that analyzes DNA directly extracted from environmental samples. This provides access to the genetic information of entire life forms present in the particular niche. Using the next-generation sequencing technology to read the sequences of these DNAs and then checking these sequences against fast-growing databases of DNA sequences of the known organisms, we are now slowly obtaining an estimate of our underestimation.

Metagenomics has shown that the simplest living forms existing on our planet are in fact the most sophisticated and well-organized organisms. It has been used today to inventory the diversity of microorganisms, discover new gene families and study the dynamism of microbe-host interactions. In industries, the method has been used to synthesize commercially important microbial products. The simple but precise isolation protocol, high-throughput technologies, and bioinformatics tools are taking us to a novel microbiome.

I have carefully invited chapters from the global experts in the field of metagenomics through a rigorous peer-review process. This volume begins with an update on the current state of our knowledge on the theory and conceptual background and a brief history of the evolution of metagenomics as a discipline (Chapter 1). Chapter 2 describes the essential methods

and protocols used (sample collection to DNA isolation, construction and screening of the libraries and data analysis) in metagenomic study. A comprehensive overview of strategies, computational tools and pipelines for analyzing metagenome data, including big data analytics, is provided in Chapters 3 to 6. Chapter 7 introduces the bioinformatic tools used for interrogating population characteristics of viral quasispecies populations and environmental viral populations. Chapter 8 captures the significant advances made in macroecology by the leading statistical ecologists, including Chao, Ellison, Gotelli, Jost and others, which are not yet widely adopted in the studies of microbiome diversity. In Chapters 9–13, detailed accounts of diverse microbiomes of specialized ecological niches are given, i.e., the human oral and gut microbiome, rumen microbiome, desert Crassulacean acid metabolism (CAM) plant microbiome, and marine invertebrate microbiome. The next three chapters (Chapters 14, 15, and 16) are dedicated to introducing the methods and techniques used for the exploitation of unculturable bacterial resources from environmental samples, with greater emphasis on thermoenzymes. In the last chapter, Matallana-Surget et al. encapsulate the history and future trends of metaproteomics as well as its advantages and limitations, through a case study in aquatic ecosystems.

Altogether, the 17 chapters comprehensively cover diverse aspects of metagenomics with greater emphasis on data analysis and application potential. I strongly believe that this robust rendering in the metagenomics genre will be equally informative for current researchers in the field and aspirants who want to get into this applied area of research.

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