Book Review

Metagenomics: Theory, Methods, and Applications

Edited by Diana Marco
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Metagenomics is a young overarching discipline that seeks to understand population dynamics and interactions among vast microbial worlds that have not been revealed by traditional culture methods in the microbiology laboratory. Metagenomics is emerging as an essential scientific discipline: there are far-reaching implications in understanding ecosystem responses to changes in the natural environment, their adaptation to artificial niches resulting from human activities and their role as a source of human disease. And there are substantial opportunities for beneficial applications of metagenomics knowledge — for example, in energy production, medicinals and bioremediation.

Advances in instrumentation and computational and molecular tools enable high-throughput gathering and analyses of environmental samples at several levels: sequence information for microbial DNA, RNA and protein, and analysis of metabolic intermediates. As a new field of study, metagenomics integrates large-scale data about molecules to describe the biodiversity and relationships of an enormous microbial 'underground' in their natural environment. The impact of such ambitious inquiry, however, cannot be understated. It begins by interrogating the microbial world, but metagenomics has the potential to provide a molecular view of interrelationships among all living organisms.

Metagenomics: Theory, Methods, and Applications reviews the field at several levels. Chapter 1 is an overview of how culture-independent metagenomic analysis of environmental DNA sequences of small subunit ribosomal RNA genes increased knowledge about the diversity of all microbial groups. Multiple strand amplification of microbial DNA using Phi29 DNA polymerase, shotgun sequencing and pyrosequencing enabled high-throughput sequencing of microbial DNA. The development of metagenomic bioinformatics tools enabled genome assembly and classification of large-scale sequencing data. These metagenomic approaches have so far expanded bacterial classification into 30 new divisions. Archaea are now represented by 50 distinct phylogenetic groups in both extreme and non-extreme environments. Fungi are now estimated at over one million species, distributed among 49 distinct phylotypes. New eukaryotic microbes in anoxic environments are being identified as well. In addition, metagenomic identification and analyses of environmental viruses is revealing their role in shaping microbial ecosystems. The challenge that follows large-scale classification and genome sequencing of new organisms is to define the composition, structure and temporal connectivity of microbial ecosystems. The combination of several 'omics' approaches and bioinformatics should help model microbial communities in the future.

Chapter 2 complements Chapter 1, and is an in-depth review of meta'omics approaches that measure active genes in microbial populations at the levels of RNA (metatranscriptomics) and protein (metaproteomics) sequences, and their metabolite (metabolomics) intermediates. Metatranscriptomics is powered by high-throughput pyrosequencing of reverse-transcribed mRNA and rRNA. It generates, respectively, gene expression profiles and taxonomic data of microbial communities in the same sample. Mass spectrometric peptide fingerprint analysis and electrospray ionisation peptide-sequencing technologies enable identification and metaproteomic analyses of protein expression profiles. In combination with genomic and gene transcription data of a given microbial ecosystem, metaproteomics provides functional and structural data, and helps to identify metabolic pathways. Finally, metabolomics improves our understanding of ecosystem adaptation to environmental cues. From the application standpoint, however, metabolic pathways may be harnessed for bioremediation or the production of biomolecules for human and industrial use.

Chapter 3 deals with horizontal gene transfer (HGT) among different bacterial species, and the well recognised role of HGT in bacterial evolution. HGT could influence the interpretation of metagenomic data in a given bacterial community. The authors incorporated computational tools and were able to quantitate HGT sequences in different bacterial ecosystems in both the physical environment and the gut of mice and humans.

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An interesting finding is that the adherence substrate of bacterial flora influences the rate of HGT. These results have potential for the understanding of host–pathogen interactions, particularly pertaining to bacterial biofilm formation in human disease (for example, in cystic fibrosis, and pathogenic adaptation of the intestinal flora in the development of prominent diseases such as diabetes and food-borne allergies).

Chapters 4 and 5 present detailed sampling and computational methods for acquisition and analysis of metagenomic data. Chapters 6–9 are comprehensive examples of metagenomic applications in plant–microbe interactions, bioremediation, identification and generation of bioproducts for medicinal and industrial uses. In particular, the archaeal metagenome is a promising source of basic knowledge about microbial communities in extreme environments and a source of novel genes that could be deployed for biotechnological and medical applications. Importantly, Chapter 10 describes how the human microbial flora is now subject to metagenomic interrogation. Undoubtedly, characterisation of the human microbiome could feed into new basic research into understanding the increased incidence of major human illnesses such as asthma, diabetes, heart disease and allergies that are only partly explained by genetic predisposition.

Lastly, Chapter 11 is a highly readable philosophical journey on how metagenomics shapes long-held arguments about evolutionary processes and the interactions of living organisms at multiple levels. This chapter defends metagenomics as a scientific discipline and its promise in advancing hypothesis-driven research at molecular and organismal levels. Overall, *Metagenomics: Theory, Methods, and Applications* is a well-written and balanced presentation of an emerging area of research. In terms of nomenclature, it is suggested that the word 'metagenomics' is capitalised as 'Metagenomics' when it is used as an overall subject of inquiry covering several 'omics' approaches, but not capitalised when it specifically refers to the anlaysis of DNA sequences. Each chapter clearly lays out metagenomics as an evolving discipline, its promise and its limitations. This book will easily find an audience in undergraduate and graduate classrooms, and as a tool of independent research.

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