

Metagenomics

Current Innovations and Future Trends



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Metagenomics is one of the fastest advancing fields in biology. By permitting access to the genomes of entire communities of bacteria, viruses and fungi otherwise inaccessible, metagenomics is extending our comprehension of the diversity, ecology, evolution and functioning of the microbial world, as well as contributing to the emergence of new applications in many different areas. The continual and dynamical development of faster sequencing techniques, together with the advancement of methods to cope with the exponentially increasing amount of data generated, are expanding our capacity for the analysis of microbial communities from an unlimited variety of habitats and environments. The synergism with the new emerging 'omics' approaches is showing the path to functional metagenomics and to adopting integrative, wider viewpoints like systems biology.

This book covers the most innovative and recent advances in theoretical, methodological and applied areas of metagenomics. Topics covered include metagenomics integration with complementary technologies, bacterial genealogy, viral metagenomics, the regulation of prokaryotic communities, functional metagenomics, systems biology, next-generation sequencing, stable isotope probing, DNA sequencing of uncultured microbes, cyberinfrastructure resource, identification of novel viruses, metagenomics of fungal communities, the human microbiome, microbial bioremediation, metagenomic enzyme discovery, quorum-sensing, plant-pathogen interactions, and metagenomics of belowground microbial communities.

The book is aimed at researchers and environmental managers involved in metagenomics, students starting research in this field and teachers interested in the new developments.

Chapter 1. Metagenomics and beyond: current approaches and integration with complementary technologies. *Tracy L. Meiring, Rolene Bauer, Ilana Scheepers, Colin Ohlhoff, Marla I. Tuffin and Donald A. Cowan*

Chapter 2. Bacterial genealogy: not dead. *Robert L. Dorit and Margaret A. Riley*

Chapter 3. Viral metagenomics and the regulation of prokaryotic communities. *Fernando Santos and Josefa Antón*

Chapter 4. Functional metagenomics and systems biology: understanding the human organismal complexity in disease and health. *Liping Zhao and Jian Shen*

Chapter 5. Next-generation sequencing approaches to metagenomics. *John Walshaw, Graham J. Etherington and Dan MacLean*

Chapter 6. Stable isotope probing: uses in metagenomics. *Ondrej Uhlík, Lucie Musilová, Katerina Demnerová, Tomas Macek and Martina Macková*

Chapter 7. DNA sequencing of uncultured microbes from single cells. *Roger S. Lasken, Mary-Jane Lombardo, Mark Novotny, Joyclyn Yee-Greenbaum and Rashel V. Grindberg*

Chapter 8. A Community cyberinfrastructure resource for metagenomics research: CAMERA 2.0. *Jing Chen, Shulei Sun, Weizhong Li and John C. Wooley*

Chapter 9. Metagenomics for the identification of novel viruses. *Vincent Montoya, Eunice C. Chen, Charles Y. Chiu and Patrick Tang*

Chapter 10. Metagenomics applied to arbuscular mycorrhizal fungal communities. *Valeria Bianciotto, Erica Lumini, Alberto Orgiazzi, Roberto Borriello and Paola Bonfante*

Chapter 11. The human microbiome: exploring and manipulating our microbial selves. *Corinne F. Maurice and Peter J. Turnbaugh*

Chapter 12. Metagenomics and integrative omics technologies in microbial bioremediation: current trends and potential applications. *Varun Shah, Kunal Jain, Chirayu Desai and Datta Madamwar*

Chapter 13. *Escherichia coli* host engineering for efficient metagenomic enzyme discovery. *Reia Hosokawa-Okamoto and Kentaro Miyazaki*

Chapter 14. Recent contributions of metagenomics to studies on quorum-sensing and plant-pathogen interactions. *Denis Faure, Mélanie Tannières, Samuel Mondy and Yves Dessaux*

Chapter 15. Metagenomics analysis of belowground microbial communities using microarrays. *Joy D. Van Nostrand, Zhili He and Jizhong Zhou*

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