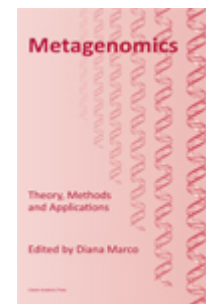


# Metagenomics

## Theory, Methods and Applications



Edited by: **Diana Marco**

*Universidad Nacional de Cordoba, Argentina*

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Metagenomics is a rapidly growing field of research that has had a dramatic effect on the way we view and study the microbial world. By permitting the direct investigation of bacteria, viruses and fungi irrespective of their culturability and taxonomic identities, metagenomics has changed microbiological theory and methods and has also challenged the classical concept of species. This new field of biology has proven to be rich and comprehensive and is making important contributions in many areas including ecology, biodiversity, bioremediation, bioprospection of natural products, and in medicine.

This book addresses in a coherent manner the diverse and multiple aspects of metagenomics and the multiplicity of its potential applications. Renowned authors from around the world have contributed chapters covering the new theoretical insights, the more recent applications, and the dynamically developing methods of data acquisition and analysis. Topics include: Conceptual frameworks, tools and methods, integration of complementary approaches, horizontal gene transfer, analysis of complex microbial communities, public data resources, plant-microbe interactions, bioremediation, industrial bioproducts, archaeal metagenomics, bioprospecting novel genes, the human microbiome, and philosophical themes in metagenomics.

The book is essential reading for all researchers currently performing metagenomics studies and is highly recommended for all students and scientists wishing to increase their understanding of this field.

**Chapter 1.** Metagenomics and Ecosystems Biology: Conceptual Frameworks, Tools, and Methods. *Jianping Xu*

**Chapter 2.** Beyond Metagenomics: Integration of Complementary Approaches for the Study of Microbial Communities. *Andrés Cubillos-Ruiz, Howard Junca, Sandra Baena, Ivonne Venegas and María Mercedes Zambrano*

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**Chapter 4.** Analysis of Complex Microbial Communities Through Metagenomic Survey. *María-Eugenia Guazzaroni, Peter N. Golyshin and Manuel Ferrer*

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