

# Metagenomics

Current Advances and Emerging Concepts

<https://doi.org/10.21775/9781910190593>

Edited by

Diana Marco

Faculty of Biological Sciences  
Córdoba National University; and CONICET  
Córdoba  
Argentina



Copyright © 2017

Caister Academic Press  
Norfolk, UK

[www.caister.com](http://www.caister.com)

British Library Cataloguing-in-Publication Data  
A catalogue record for this book is available from the British Library

ISBN: 978-1-910190-59-3 (paperback)

ISBN: 978-1-910190-60-9 (ebook)

Description or mention of instrumentation, software, or other products in this book does not imply endorsement by the author or publisher. The author and publisher do not assume responsibility for the validity of any products or procedures mentioned or described in this book or for the consequences of their use.

All rights reserved. No part of this publication may be reproduced, stored in a retrieval system, or transmitted, in any form or by any means, electronic, mechanical, photocopying, recording or otherwise, without the prior permission of the publisher. No claim to original U.S. Government works.

Cover design adapted from images provided by Diana Marco.

### **Ebooks**

Ebooks supplied to individuals are single-user only and must not be reproduced, copied, stored in a retrieval system, or distributed by any means, electronic, mechanical, photocopying, email, internet or otherwise.

Ebooks supplied to academic libraries, corporations, government organizations, public libraries, and school libraries are subject to the terms and conditions specified by the supplier.

# Contents

	<b>Preface</b>	<b>v</b>
<b>1</b>	<b>Integration of Ecology and Environmental Metagenomics Conceptual and Methodological Frameworks</b>	<b>1</b>
	Diana Marco	
<b>2</b>	<b>Guidelines to Statistical Analysis of Microbial Composition Data Inferred from Metagenomic Sequencing</b>	<b>17</b>
	Vera Odintsova, Alexander Tyakht and Dmitry Alexeev	
<b>3</b>	<b>Methods for the Metagenomic Data Visualization and Analysis</b>	<b>37</b>
	Konstantin Sudarikov, Alexander Tyakht and Dmitry Alexeev	
<b>4</b>	<b>Comparing Viral Metagenomic Extraction Methods</b>	<b>59</b>
	Jeanette Klenner, Claudia Kohl, Piotr W. Dabrowski and Andreas Nitsche	
<b>5</b>	<b>Spatiotemporal Variations in the Abundance and Structure of Denitrifier Communities in Sediments Differing in Nitrate Content</b>	<b>71</b>
	David Correa-Galeote, Germán Tortosa, Silvia Moreno, David Bru, Laurent Philippot and Eulogio J. Bedmar	
<b>6</b>	<b>Using Metagenomics to Connect Microbial Community Biodiversity and Functions</b>	<b>103</b>
	Lucas W. Mendes, Lucas Palma Perez Braga, Acacio A. Navarrete, Dennis Goss de Souza, Genivaldo G. Z. Silva and Siu M. Tsai	
<b>7</b>	<b>Application of Omics Approaches to Studying Methylotrrophs and Methylotrroph Communities</b>	<b>119</b>
	Ludmila Chistoserdova	
	<b>Index</b>	<b>143</b>

# Current Books of Interest

Illustrated Dictionary of Parasitology in the Post-Genomic Era	2017
Next-generation Sequencing and Bioinformatics for Plant Science	2017
The CRISPR/Cas System: Emerging Technology and Application	2017
Brewing Microbiology: Current Research, Omics and Microbial Ecology	2017
<i>Bacillus</i> : Cellular and Molecular Biology (Third Edition)	2017
Cyanobacteria: Omics and Manipulation	2017
Foot-and-Mouth Disease Virus: Current Research and Emerging Trends	2017
Brain-eating Amoebae: Biology and Pathogenesis of <i>Naegleria fowleri</i>	2016
<i>Staphylococcus</i> : Genetics and Physiology	2016
Chloroplasts: Current Research and Future Trends	2016
Microbial Biodegradation: From Omics to Function and Application	2016
Influenza: Current Research	2016
MALDI-TOF Mass Spectrometry in Microbiology	2016
<i>Aspergillus</i> and <i>Penicillium</i> in the Post-genomic Era	2016
The Bacteriocins: Current Knowledge and Future Prospects	2016
Omics in Plant Disease Resistance	2016
Acidophiles: Life in Extremely Acidic Environments	2016
Climate Change and Microbial Ecology: Current Research and Future Trends	2016
Biofilms in Bioremediation: Current Research and Emerging Technologies	2016
Microalgae: Current Research and Applications	2016
Gas Plasma Sterilization in Microbiology: Theory, Applications, Pitfalls and New Perspectives	2016
Virus Evolution: Current Research and Future Directions	2016
Arboviruses: Molecular Biology, Evolution and Control	2016
<i>Shigella</i> : Molecular and Cellular Biology	2016
Aquatic Biofilms: Ecology, Water Quality and Wastewater Treatment	2016
Alphaviruses: Current Biology	2016
Thermophilic Microorganisms	2015
Flow Cytometry in Microbiology: Technology and Applications	2015
Probiotics and Prebiotics: Current Research and Future Trends	2015
Epigenetics: Current Research and Emerging Trends	2015

# Preface

Metagenomics continues to be one of the most dynamic scientific fields, due in part to the development of new and cheaper sequencing techniques. What constitutes a great step ahead, the new facility for obtaining data from microbiomes, however, leads to a cascade of new methodological troubles. As a contribution to this problem, this book is mainly oriented to the new conceptual and methodological tools arising in metagenomics and other meta-omics to deal with these newly appearing problems.

The diversity of habitats explored with metagenomics and other meta-omics has increased exponentially, from field to microcosm experiments through organism-specific microbiomes. However, although being placed at the very beginning of any metagenomics (or meta-omics) pipeline, the issue of how to get reliable data from an adequate sampling either from field, microcosm or other types of habitats is still largely disregarded. This may be in part due to an early divorce between ecological and metagenomics theoretical and methodological frameworks in spite of the large common grounds shared by the two disciplines. Fortunately, this is beginning to change, and a fruitful confluence between ecology and metagenomics (and other meta-omics) is on work (see Chapter 1). At present, another big challenge lies on the steps of organizing, classifying, analysing and interpreting the vast number of data generated by metagenomics and meta-omics. Due to researchers' efforts, new statistical and bioinformatic techniques are continuously appearing (see Chapters 2, 3 and 6). Exploring new microbiomes means that the diversity of samples taken is also increasing, thus creating new challenges for sample processing techniques, for example to check for effectiveness of extraction methods of nucleic acids in virus clinical samples (see Chapter 4). The next two chapters illustrate how a better understanding of microbial community ecology can be reached through metagenomics, focusing both on structure and function. In Chapter 5, a three-year study showed that the abundance and diversity of denitrifier communities in sediments were influenced by hydric seasonality and nitrate concentration along a stream in Southern Spain. Chapter 6 explores some advances in bioinformatics tools to connect the microbial community biodiversity to their potential metabolism, and shows how this information can be useful for a better understanding of the microbial role in tropical soils. Finally, Chapter 7 shows how some recent advances in application of omics technologies like metaproteomics and DNA-SIP improve the study of the methylotrophs guild, that performs an important function in natural environments.

The book is especially aimed, among other users, to researchers and students interested in starting projects in this field, to researchers already performing studies in metagenomics,

teachers interested in the latest developments of the field, and persons involved in biotechnological applications like bioremediation.

I would like to thank all the authors for their invaluable contributions. I am very grateful to Hugh Griffin for his unconditional support, and to Caister Academic Press for trusting me again with the editing of a volume on such a dynamic and changing field.

Diana Marco  
Córdoba, Argentina