

# 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.

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