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# Preface

From its beginning with the pioneering work of Woese and Fox in 1977 on ribosomal RNA to its formal recognition as a new comprehensive microbiological approach with the work of Jo Handelsman and colleagues in 1998, metagenomics has become one of the most active scientific fields in the last years. Scientific publications containing the terms *Metagenome* or *Metagenomics* have grown exponentially since 2000, with works covering an ever-increasing range of habitats explored and potential applications. This growth is a direct consequence of the advantages posed by the new ability of accessing microbial genetic information bypassing cultivation, proportioned by metagenomics.

By its intrinsic nature, Metagenomics is a complex field positioned at the intersection of many disciplines, such as molecular biology, microbiology, ecology, chemistry, bioinformatics, and medicine among others, with new ones rapidly becoming involved. The theoretical and methodological richness arising from this complex and dynamic structure also constitutes the greatest challenge for Metagenomics. Integrating the theoretical basis from different disciplines and dealing with changes of paradigm from the traditional organism-centred approach to a new, organism- and species-free context require an epistemological re-foundation. Extracting the genetic material from an ever-increasing range of metagenomic samples involves developing new and suitable methodologies. Obtaining the metagenomic data requires more and more sophisticated and cheaper sequencing methods, and even

sequencing-free strategies are being developed. As if this does not sound complicated enough, one of the biggest challenges is to organise, classify, analyse and interpret the vast amount of data generated by metagenomic studies. Fortunately, these challenges have not prevented researchers from coming into useful applications in many fields, from medicine to obtaining bioproducts.

Taking all this complexity into account, this book intends to provide a comprehensive view of the main facets involved in metagenomics thinking and practice. The first three chapters deal with the general conceptual background and tools employed in metagenomics, its relationship with other related emergent meta-disciplines, and genetic horizontal transfer, an important microbial trait that contributes to the shaping of the ecological and evolutionary prokaryotic scenario. Chapters 4 and 5 are devoted to the methodological challenges of metagenomics, from sampling to the development of integrated and global resources for data management. Chapters 6 to 10 present appealing applications of Metagenomics, giving insights for forthcoming uses. Finally, although not least, a thorough discussion of the main epistemological aspects involved in metagenomics is provided in Chapter 11.

I would like to thank all the authors for their invaluable contributions. I also would like to thank Caister Academic Press for the opportunity of editing a book in one of the most exciting scientific fields nowadays.

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