

## Preface

Metagenomics is a key technology to explore the DNAs from not-yet-cultivated microbes in their natural habitats. Theoretically, the microbial DNA isolated from an environmental sample represents the collective DNA of all the indigenous microorganisms and is named the metagenome. Metagenomes can be quite diverse, and, depending on the microbial community analyzed, several hundred up to several thousand different species and genomes can be present in a single metagenome. Typically, soil metagenomes are rather complex with several thousand species present, while microbial communities growing under extreme conditions (i.e., hot springs) are usually rather limited in their complexity and biodiversity. The primary goal of metagenomics is to explore this almost unlimited biodiversity. The last 10 years have already paved the way for the culture-independent assessment and exploitation of complex microbial populations for basic and applied research. Metagenomics has been defined as function-based or sequence-based cultivation-independent analysis of the collective microbial genomes present in an environment. The developed metagenomic technologies are used to complement or replace culture-based approaches and bypass some of their inherent and well-known limitations.

Besides identification of new biomolecules, metagenomics has proven to be a powerful tool for exploring the ecology, metabolic profiling, and comparison of complex microbial communities. Profiling the functions encoded by a microbial community rather than the types of organisms producing them provides a means to distinguish environmental samples on the basis of the functions selected for by the local environment and reveals insights into features of that environment. Another application of metagenomics is the genomic characterization of uncultivated microorganisms and complex communities. In addition, large-scale sequencing approaches of metagenomic DNA have been applied to reconstruct genome fragments and near-complete genomes from uncultivated species and natural consortia.

The main application area of metagenomics is the mining of metagenomes for genes encoding novel biocatalysts and drug molecules for biindustries. Due to the complexity of most metagenomes, new sensitive and efficient high-throughput screening techniques that allow for fast and reliable identification of genes encoding suitable biocatalysts from complex metagenomes have been invented. Screens of metagenomic libraries have been based either on nucleotide sequence (sequence-driven approach) or on metabolic activity (function-driven approach).

This current book gives an overview and introduction to basic methods commonly used in laboratories that have a strong background in microbial metagenomics. All chapters are written by experts in the field, and our goal is that this book serves those who are interested in establishing metagenomics in their laboratories as a manual. Within the book, we have tried to address all working steps involved in this field: Starting from the DNA isolation from soils and marine samples to the construction and screening of the libraries, and finally we offer some advice with respect to the bioinformatic tools available to screen large sequences. An overview on strategies involved in the isolation of DNAs from environmental samples is given in the first four chapters together with the main strategies that

are currently used for the construction of metagenome libraries. Chapters 5–8 describe protocols linked to the expression of metagenome libraries in different host strains. Those include simple protocols for the construction of a library in broad host range vectors but also rather sophisticated protocols to handle *Sulfolobus* as a host strain. Furthermore, the book contains a significant number of chapters that describe a wide variety of screening technologies used for the identification of different enzymes or other biomolecules using function- and sequenced-based technologies. Altogether, the 15 chapters describe a diverse range of screening protocols for metagenome libraries. In our view, this is a very complete description of available screening protocols for all major biocatalysts and allows an easy setup of these screens in any microbiology lab.

**Wolfgang R. Streit**  
**Rolf Daniel**