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Nota di contenuto	1. Integration of ecology and environmental metagenomics conceptual and methodological frameworks -- 2. Guidelines to statistical analysis of microbial composition data inferred from metagenomic sequencing -- 3. Methods for the metagenomic data visualization and analysis -- 4. Comparing viral metagenomic extraction methods -- 5. Spatiotemporal variations in the abundance and structure of denitrifier communities in sediments differing in nitrate content -- 6. Using metagenomics to connect microbial community biodiversity and functions -- 7. Application of omics approaches to studying methylotrophs and methylotroph communities.
Sommario/riassunto	Metagenomics continues to be one of the most dynamic scientific fields due largely to the development of new and cheaper sequencing technologies. The diversity of habitats explored with metagenomics and other meta-omics techniques has increased exponentially in recent years. The resulting cascade of data has led to a new range of methodological problems and solutions. In this collection of reviews, expert authors describe the cutting-edge and emerging conceptual and methodological tools being employed to deal with current issues in metagenomics. Topics covered include the integration of ecology and metagenomics; the organization, classification, analysis and interpretation of the vast amount of data; the new statistical and bioinformatic techniques; sample extraction and processing techniques; and various applications of metagenomics in specific areas.

The volume is essential reading for researchers and students commencing projects in this field, for researchers active in metagenomics areas, and for educators interested in the latest developments. The volume is also of value to anyone involved in biotechnology, bioremediation, biodegradation and environmental microbiology.
