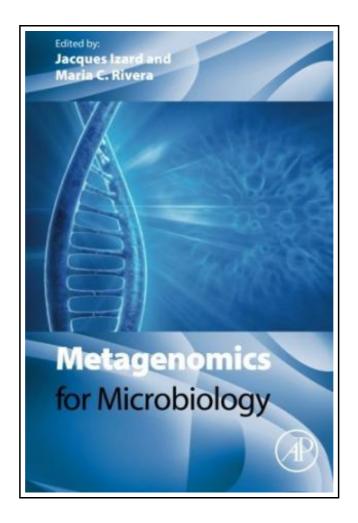
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Oxford Elsevier LTD Okt 2014, 2014. Taschenbuch. Book Condition: Neu. 228x151x12 mm. Neuware - We are now realizing both as a scientific community and a society that we are not living alone in our body. For each of our human cells, we are hosting in harmony 10 microbes. With the next-generation genomic sequencing revolution increasingly permitting researchers to decipher the coding information of the microbes living with us, we now have a unique capacity to compare multiple sites within individuals and at higher resolution and greater throughput than hitherto possible. The recent articulation of this paradigm points to unique possibilities for investigation of our dynamic relationship with these cellular communities, and excitingly the probing of their therapeutic potential in disease prevention or treatment of the future. Concisely discussing the practical uses of high throughput analysis to move our understanding of biological principles, this book provides a solid base for the design of metagenomic studies, with the objective of aiding successful phylometagenomic, whole shotgun metagenomic, and transcriptomic studies across the multiplying audiences within molecular biology, microbiology, genomic expression, infectious disease, and cancer research. Expertly describes present-day methodologies with best-practice prescription, from sample to data analysis, for current metagenomic studies Includes clear-headed pointers and quick starts to direct research efforts and increase study efficacy, eschewing ponderous prose and heavy-going methologies Interdisciplinary and translational approach ranges across sample preparation, data production, data clean up, data analysis, statistics and experimental biology with accompanying descriptions for varied research populations and complementary viewpoints 144 pp. Englisch.



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