Encyclopedia of Metagenomics: Environmental Metagenomics

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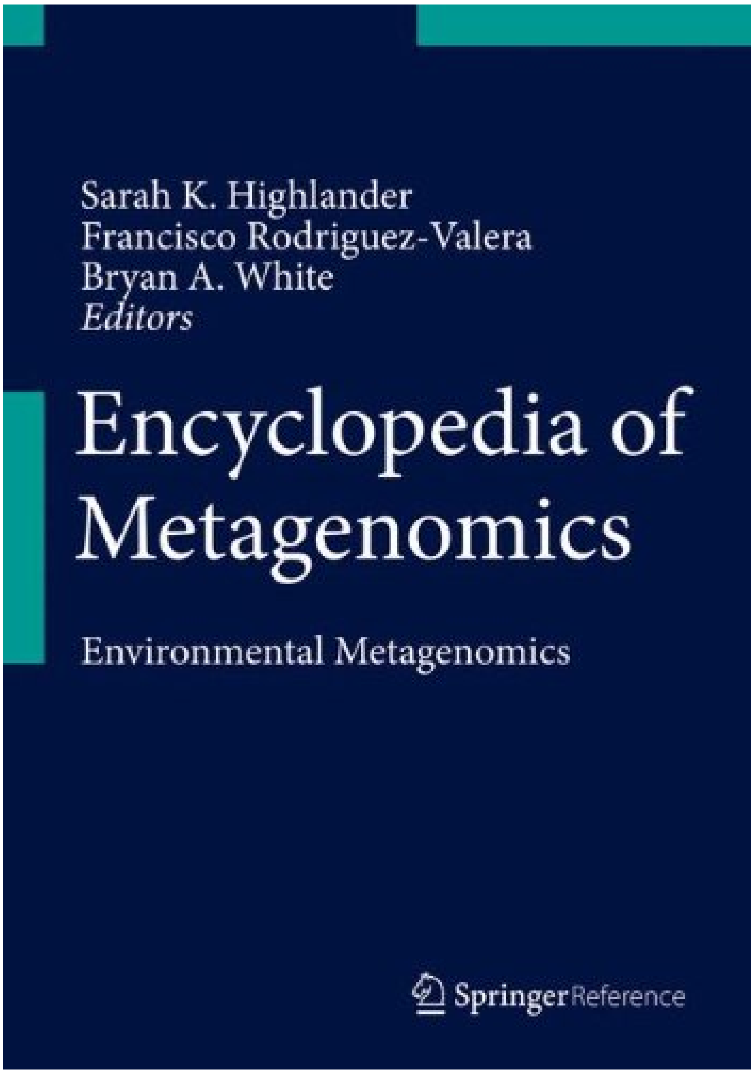

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Encyclopedia of Metagenomics

Environmental Metagenomics

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From Springer : Encyclopedia of Metagenomics: Environmental Metagenomics before purchasing it in order to gage whether or not it would be worth my time, and all praised Encyclopedia of Metagenomics: Environmental Metagenomics:

Metagenomics has taken off as one of the major cutting-edge fields of research. The field has broad implications for human health and disease, animal production and environmental health. Metagenomics has opened up a wealth of data, tools, technologies and applications that allow us to access the majority of organisms that we still cannot access in pure culture (an estimated 99% of microbial life). Numerous research groups are developing tools, approaches and applications to deal with this new field, as larger data sets from environments including the human body, the oceans and soils are being generated. See for example the human microbiome initiative (HMP) which has become a world-wide effort and the Global Ocean Sampling (GOS) surveys. The number of publications as measured through PubMed that are focused on metagenomics continues to increase. The field of metagenomics continues to evolve with large common datasets available to the scientific community. A concerted effort is needed to collate all this information in a centralized place. By having all the information in an Encyclopedia form, we have an opportunity to receive seminal contributions from the leaders in the field and at the same time provide this information to a significant number of junior and senior scientists, via colleges, libraries, and just through online access. This format also allows scientists in the developing world to have continued access to this growing field. It is anticipated that the Encyclopedia will also be used by many other groups including, clinicians, undergraduate and graduate level students, as well as ethical and legal groups associated with or interested in the issues surrounding metagenome science.

About the AuthorSarah K. Highlander is Associate Professor in the Department of Molecular Virology and Microbiology and The Human Genome Sequencing Center at Baylor College of Medicine in Houston, Texas. She received her Bachelor of Science from the University of Michigan and M.S. and Ph.D. degrees in Medical Microbiology from the Sackler School of Graduate Biomedical Sciences at New York University. She performed her postdoctoral research at the University of Texas Health Science Center in Houston. Her current research interests are in microbial genomics, metagenomics related to gastrointestinal disease and bacteriotherapy. Her laboratory has been involved since 2007 in the NIH Human Microbiome Project (HMP) where a primary focus of her lab has been the cultivation of strains, followed by sequencing and annotation of reference genomes to contribute to a catalog of strains that serves as a database against which human metagenomic data are compared. Her group also played a key role in processing and characterizing samples collected from the HMP healthy cohort and she developed mock metagenomic communities to aid in benchmarking protocols for HMP DNA extraction, sequencing and sequence evaluation. Francisco Rodriguez-Valera is professor of Microbiology in the University Miguel Hernandez in San Juan de Alicante Spain. He has been working on microbial diversity for over 30 years and was among the pioneers that started using metagenomics in Microbiology with iconic studies such as the deep Mediterranean Sea or the River. He has described multitude of new microbes, including the new Ca. Actinomarinidae, the smallest free living marine prokaryote, that turned out to be a member of the Actinobacteria, classically considered mycelial soil inhabitants. He has also advanced the Constant-Diversity model to explain genomic diversity in prokaryotes and described recently more than 1000 different genomes of marine viruses using metagenomic approaches. Bryan White is currently a Professor of Animal Sciences in the Institute for Genomic Biology and Director, Mayo Clinic/University of Illinois Strategic Alliance for Technology-Based Healthcare at the University of Illinois. He received his Bachelor of Science at Virginia Wesleyan College and his Ph.D. in Microbiology from the Medical College of Virginia and was a NIH Postdoctoral Fellow in the Department of Oral Biology at the University of Michigan. His major research interests are in using microbial genomics, metagenomics and microbial ecology to understand host-microbe interactions in vertebrates. These interests are in production species such as cattle, swine and poultry and in models of disease for humans. With respect to productions species, he has studied models that address nutrient utilization, primarily the rumen fiber-adherent microbiome as a model for improving forage utilization. He has also investigated the roles of beneficial and pathogenic organisms and antibiotic use in domestic production animals, as well as approaches that will enable the detection of diseases in livestock and provide critical genetic contexts for understanding food safety. He uses human and non-human primate models of disease to link microbiomes to important clinical outcomes in gastrointestinal and womens reproductive tract diseases.