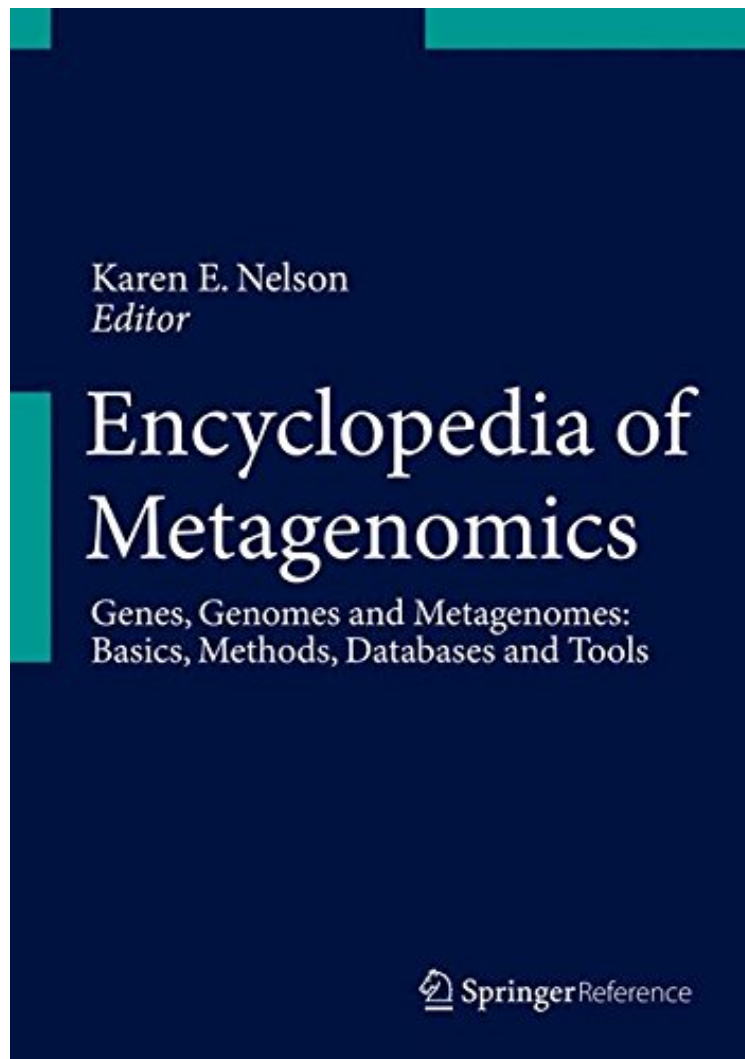


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Modeling, and gene analysis starting with extraction of DNA. The book progresses to purification of genes, enzymes, and products of DNA samples including clones. The book has diverse coverage of mathematical differential analysis, algorithms, and statistical modeling. Software and math software for use in genomics, proteonomics, bioinformatics, and cloning is presented in one segment of the book. Statistics is a major portion of the coverage. A brief statement and table of contents would be helpful as well as an index. The authorship of this good encyclopedia/text is international from bioinformatics specialists. It is hard to follow and I think this could and should be transformed into a textbook format. This should be used as an encyclopedia for experienced investigators. Springer has several other books on encyclopedic formats including Bioinformatics, Statistics, Mathematical, and Computational sciences. Students and scientists may be lost and find it difficult in laboratory translational work.

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 gather 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. 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 Author Dr. Nelson is the President of the J. Craig Venter Institute (JCVI). Dr. Nelson has extensive experience in microbial ecology, microbial genomics, microbial physiology and metagenomics. Since joining the JCVI legacy institutes, Dr. Nelson has led several genomic and metagenomic efforts and led the first human metagenomics study that was published in 2006. Additional ongoing studies in her group include metagenomic approaches to study the ecology of the gastrointestinal tract of humans and animals, studies on the relationship between the microbiome and various human and animal disease conditions, reference genome sequencing and analysis primarily for the human body and other omics studies. Dr. Nelson received her undergraduate degree from the University of the West Indies and her Ph.D. from Cornell University. She has authored or co-authored over 100 peer reviewed publications and edited three books and is currently Editor-in-Chief of the journal Microbial Ecology. She also serves on the Editorial Boards of BMC Genomics, Giga Science and the Central European Journal of Biology. She is also a standing member of the NRC Committee on Biodefense, a member of the National Academy of Sciences Board of Life Sciences and a Fellow of the American Academy of Microbiology.