What do microbes and internet commerce have in common? Both exhibit long-tail distributions in which very high-frequency populations precede low-frequency populations that gradually "tail off" asymptotically. Internet events at the far end of the tail have a very low probability of occurrence but they never completely disappear. For microbes and other biological forms, the long tail corresponds to a "rare biosphere" composed of many low abundance taxa. The International Census of Marine Microbes first described a "rare biosphere" that accounts for an estimated 500,000 kinds of microbes contained within less than one part out of 10¹⁸ parts of the world's oceans. New algorithms capable of discriminating between closely related taxa show that the sheer size of the microbial "rare biosphere" may be much greater than previously reported. The recently introduced techniques of oligotyping and minimum entropy decomposition permit the description of microbial diversity at finer scales for closely related but subtly distinct 16S rRNA gene amplicon sequences that represent distinct genomes in a microbial community. These analytical paradigms take advantage of Shannon entropy calculations to identify information rich nucleotide positions that differentiate between closely related taxa within the same genus. When applied to studies of microbial communities in aquatic, marine and animal microbiomes, we detect increased diversity and identify ecologically important differences between closely related taxa. These analyses of next generation DNA sequencing data sets reveal the rare biosphere has temporal and spatial dimensions that impact our perceptions of microbial ecology and how anthropogenic activities influence human health and well-being. Some members of the rare biosphere might always represent low-abundance populations. Others might normally persist in very low numbers but have the capacity to become more abundant in response to environmental change. Yet other members of the rare biosphere might disperse over long distances from their yet to be discovered endemic sites. The extraordinary length of the long tail is consistent with a model where large numbers of very rare and highly divergent taxa stably coexist because they do not compete for niche space. The long tail of internet commerce exhibits analogous unlimited capacity for nearly infinite information storage.



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Dr. Mitchell Sogin is a MBL Distinguished Scientist and Professor in the Department of Molecular Biology, Cell Biology and Biochemistry at Brown University. His work focuses on microbial evolution and diversity. Dr. Sogin has played key roles in landmark, large-scale collaborations including the first International Census of Marine Microbes and surveys of microbial populations in the human body. He was recently named co-chair of the Deep Carbon Observatory's Deep Life Directorate, an international program to explore the microbes that live beneath the subseafloor and continental surfaces. With his colleagues, Sogin has made major methodological contributions to the study of the microbial world, and has offered fundamental insights on its structure and evolution. Dr. Sogin received his B.S. in Chemistry and Microbiology and his Ph.D. in Microbiology and Molecular Biology from the University of Illinois. In 1976, he joined the faculty of National Jewish Hospital and became an Associate Professor in the Microbiology Department at the University of Colorado Health Sciences Center. He came to the MBL in 1989 as Senior Scientist, and eight years later founded the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, where he served as Director until 2013. Dr. Sogin is a fellow of the American Association for the Advancement of Science, the American Academy of Arts and Sciences, and the American Academy of Microbiology, and was a Miller Professor at the University of California, Berkeley. He is also the recipient of the Stoll Stunkard Award and Roger Porter Award from the American Society for Microbiology.