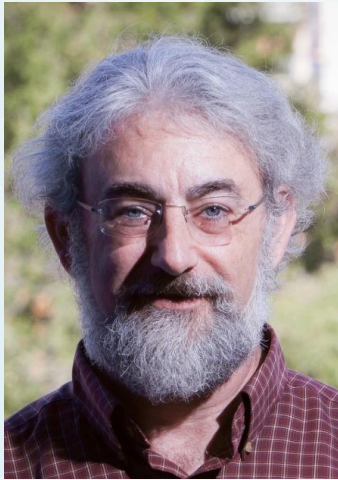


# iFAST: The International Forum on Advanced Environmental Sciences and Technology

*A series of distinguished seminars by eminent scientists*

8 p.m. CDT; 9 p.m. EDT; March 24, 1 a.m. GMT; 9 a.m. Beijing

Wednesday, March 23, 2022



**Jed Alan Fuhrman**

UNIVERSITY OF  
SOUTHERN CALIFORNIA

<http://dornsife.usc.edu/labs/fuhrmanlab>,  
[scholar.google.com/citations?user=VjvupJUA](https://scholar.google.com/citations?user=VjvupJUA&hl=en)  
AAJ&hl=en

J. A. Fuhrman is the McCulloch-Crosby Chair of Marine Biology in the Department of Biological Sciences at the University of Southern California. Fuhrman received his bachelor's degree in biology from Massachusetts Institute of Technology in 1977 and doctoral degree in 1981 from Scripps Institution of Oceanography, University of California San Diego, working with Dr. Farooq Azam. He joined the faculty at Stony Brook in 1981 and moved to the University of Southern California in 1988. His discoveries have covered multiple aspects of marine microbial ecology, including the magnitude of the microbial loop, the ubiquity of viral infection of marine microbes, the existence and abundance of widespread "non-extremophile" archaea, and repeating seasonal patterns of microbial composition. He is a recipient of the G. Evelyn Hutchinson Medal from the Association for the Sciences of Limnology and Oceanography, and a Fellow of the American Academy of Arts and Sciences, the American Academy of Microbiology, the Association for the Sciences of Limnology and Oceanography, and American Association for the Advancement of Science.

## Ecological patterns of marine bacteria, archaea, protists and viruses over large temporal and spatial scales

Professor Fuhrman will discuss results of several years of studies to investigate fundamental questions about the dynamics, distributions and interactions among marine microorganisms of all types – Bacteria, Archaea, protists and viruses. Much of the work will center on results from the 20-year San Pedro Ocean Time Series, and recent application of whole-community molecular genetic analyses. Topics will include discussion of methodological advances, such as quantitative validation of "universal rRNA primers" with 3-domain mock communities and metagenomes, and improvement of the estimation of taxon-specific maximum growth rates based on codon usage bias (including from 'omics data). Results from field studies include interannual stability and repeating seasonal patterns in community composition of prokaryotes and viruses (much more so than protists), surprising rapid succession of phytoplankton during a spring bloom, and Red Queen dynamics in viruses in which the same "species" persist at comparable abundances for years while consisting of a succession of exact sequence variants, each lasting only months.



INSTITUTE FOR ENVIRONMENTAL GENOMICS  
The UNIVERSITY of OKLAHOMA



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Zoom webinar ID: 934 8142 2012 (<https://zoom.us/j/93481422012>)

More details and previous iFAST seminar videos are available on <https://www.ou.edu/ieg/seminars>.

Organizing Committee Chair: Jizhong Zhou (University of Oklahoma, USA; <https://www.ou.edu/ieg>)  
Xueduan Liu (Central South University, China)

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