iFAST: The International Forum on Advanced Environmental Sciences and Technology

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8 p.m. CDT; <u>9 p.m. EDT</u>; 1 a.m. GMT (June 24); 9 a.m. Beijing (June 24) Wednesday, June 23, 2021



Phil Hugenholtz
University of Queensland
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From a Ph.D. in 1994 at the University of Queensland, Phil Hugenholtz has developed a career in microbiology and genomics in the United States and in Australia. His last position in the United States was as staff scientist (2004-2010) at the U.S. Department of Energy Joint Genome Institute. In late 2010, he returned home to establish the Australian Centre for Ecogenomics at the University of Queensland, now comprising over 50 research and support staff. The centre conducts culture-independent sequence-based research across a wide range of environmental, engineered and clinical ecosystems underpinned by a genome-based evolutionary framework.

Microbial taxonomy run amok?

Microbial taxonomy is in a state of flux as new genome-based methods for classifying microorganisms supplant older phenotypic and gene-based classifications. Moreover, genome sequences from uncultured microbial species are now readily obtainable, with thousands of metagenome-assembled genomes putting pressure on a classification system not well-suited to the volume of new data. In this talk, I will discuss our attempts at producing a standardized microbial taxonomy that incorporates both cultured and uncultured taxa, called the Genome Taxonomy Database, or GTDB for short, and the lessons learned to date.









Register for the Zoom conference at 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)