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CIVIL AND ENVIRONMENTAL ENGINEERING DISTINGUISHED DEPARTMENT SEMINAR



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Date: Thursday, November 19th, 2026
Time: 10:00am - 11:00pm EST
Zoom Link: Here

Atmospheric Metagenomics: Charting the Air Microbiome and its Impact on Human and Planetary Health

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Abstract: The atmosphere represents one of Earth's largest yet least understood planetary ecosystems. Every day, humans inhale thousands of litres of air containing a diverse mixture of bacteria, fungi, and other biological particles. Despite its significance for microbial dispersal, ecosystem connectivity, and human health, the atmospheric microbiome has remained largely unexplored, primarily because of the technical challenges associated with analysing extremely low concentrations of airborne biomass. Over the past decade, our research group has developed ultra-low-biomass sampling, shotgun metagenomic sequencing, and computational approaches that enable species-level characterization of airborne microbial communities. These technologies have allowed us to investigate the temporal dynamics, vertical stratification, and global distribution of atmospheric microorganisms. Building on more than 10,000 environmental samples, we established the Global Air Microbiome Encyclopedia (GAME), incorporating a standardized global survey of more than 1,170 air samples from 104 locations across 33 countries. Our analyses identified over 20,000 bacterial and 1,500 fungal species, revealing striking differences in their global biogeography. While airborne bacteria frequently exhibit geographically restricted distributions associated with local terrestrial sources, fungi are much more widely dispersed, suggesting that atmospheric transport contributes substantially to their global connectivity. Our findings further demonstrate that airborne microbial communities undergo pronounced diurnal oscillations driven by atmospheric convection and boundary-layer dynamics. By integrating high-resolution metagenomics with environmental metadata and AI-assisted species annotation, we can now investigate microbial dispersal, ecological adaptation, and population-level genomic variation on a global scale. Beyond microbial ecology, atmospheric metagenomics opens new opportunities for environmental surveillance and public health. Studies of residential environments, healthcare facilities, and urban infrastructure reveal connections between environmental microbial exposure and the human respiratory microbiome, with implications for asthma, allergies, and chronic respiratory diseases.

Bio: Prof. Stephan C. Schuster (Dr. rer. nat., Dr. habil.) holds degrees in Chemistry (U. Konstanz) and Biochemistry (LMU Munich) and conducted research at the Max-Planck Institute for Biochemistry. After postdoctoral work at CalTech, he transitioned to Molecular Biology and Genomics. He led research groups at two Max-Planck-Institutes before becoming a Professor of Molecular Microbial Ecology at Penn State University (USA) in 2005. In 2011, he joined Nanyang Technological University (NTU), Singapore, as a Professor of Environmental Genomics. Prof. Schuster is a founding member of SCELSE (Singapore Centre for Environmental Life Sciences Engineering), where he serves as a research director and deputy director. In 2018, he was appointed the "President's Chair in Genomics" at NTU, overseeing next-gen sequencing and bioinformatics for environmental genome projects, while leading the GenomeAsia100k consortium as Scientific Director.