



The University of Hong Kong
School of Biological Sciences

Guest Seminar

Functional genomics as a window into the drivers of community structure and dynamics in temperate and tropical forests

Date: March 11, 2025

Time: 4:30-5:30 pm

Venue: 3N-01



About the speaker:

Dr. Nate Swenson is the Martin J. Gillen Director of the University of Notre Dame Environmental Research Center and a professor in the Department of Biological Sciences. Swenson completed his PhD at the University of Arizona and was an NSF postdoctoral fellow at Harvard University. His research studies woody plant ecology and evolution in a dynamic world. Swenson has published >180 research articles and 3 books on these topics. He has been cited >35,000 times and is a Fellow of the American Association for the Advancement of Science and of the John Simon Guggenheim Memorial Foundation.



Abstract:

Tree community structure and dynamics are, ultimately, the emergent properties of differential individual-level performance. This differential performance is governed by interaction between the environment and organismal functional. Over the past two decades there has been an incredible increase in the use of functional traits to predict plant population and community structure and dynamics. However, the results of these studies have often been underwhelming with indications that richer and more dynamic assays of function are necessary. That is, functional traits are rough and static approximations of some organismal functions and, generally, do not consider functions of interest and the dynamic response of organisms to changing environmental contexts. In this presentation, I will begin by discussing this fundamental problem in trait-based tree ecology. Next, I will argue that functional genomics provides a potential pathway for improving our understanding of tree populations and communities and I will buoy this argument by providing examples from our work in temperate and tropical tree communities. Finally, I will end the presentation with a novel integration of functional genomic and hyperspectral data as a pathway for mapping functional genomic diversity on broad spatial extents.