

Department of Biological Sciences Faculty of Science

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## Modeling community assembly processes for useful and reproducible microbiome transplantations

## By Geoffrey Zahn

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Fungi have a powerful influence on plants' traits, and there has been a recent surge of efforts to harness them to aid in agriculture and plant conservation through mycobiome transplantation. But research on these interactions has largely focused on one fungus at a time; a perspective that is never encountered in nature. Mycobiome transplantations are increasingly seen as a viable intervention for steering ecosystem recovery and succession, as well as influencing the fitness of host organisms. But they have shown mixed results in practice, and it is unclear why some transplants succeed and others fail. If we want to move beyond the "hope and pray" method of transplanting fungal communities, we need process-based understanding and predictive modeling for how entire donor fungal communities interact with hosts, the environment, and resident microbial communities. Here, I present the CommunityAssemblR R package to facilitate large-scale simulations of microbiome transplantation under defined biotic interactions within existing ecological theory. These simulated data sets are being used for supervised training of DeepInsight convolutional neural net (CNN) models that can detect key ecological processes such as niche overlap, antagonism, and facilitation.



## About the Speaker

Geoff Zahn received his PhD in Biology at the University of Arkansas, and postdoctoral training at the University of Hawaii at Manoa. His research is in host-microbe community structure and interactions. He is particularly interested in microbiome community formation processes and in translational work to engineer and transplant microbial communities to achieve environmental and conservation goals.