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Department of Medicine  
Channing Division of Network Medicine

## Channing Microbiome Seminar

January 26 (Friday), 2024, 9AM (ET)

MCP 4<sup>th</sup>-floor conference room & Zoom:

<https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09>

Meeting ID: 810 7095 9105; Passcode: 984617



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## Predicting microbiome function from genomic and taxonomic composition

Microbial communities exhibit complex abundance dynamics driven by a myriad of interactions between constituents. Despite the apparent complexity of their dynamics, communities consistently perform critical functions across the biosphere including protecting hosts from pathogens and driving global biogeochemical cycles. How do functional aspects of communities emerge from interactions between constituents? How does the structure of a collective – the genotypes present, their phenotypes and interactions – determine emergent community function? How does Nature construct such robustly functional communities? In this talk I will present our recent work on this ‘structure-function problem’ in communities. First, using denitrification, a key part of the nitrogen cycle, as a model process we showed that the dynamic flux of metabolites through a community can be predicted simply from knowledge of the genes each strain possesses. Thus, the details of which species are present is not necessary to predict function, and instead genotypes and resulting phenotypes fully determine metabolite flows. Second, we ask whether species composition alone is sufficient to predict emergent community function. We develop a new concept of community-function landscapes-analogues to fitness landscapes-that capture how changes in community composition alter collective function. Using datasets that represent a broad set of community functions we show that statistically inferred landscapes quantitatively predict community functions from knowledge of species presence or absence. Landscapes allow prediction without explicit knowledge of abundance dynamics or interactions between species. Together, our results open the door to the rational design of consortia without detailed knowledge of abundance dynamics or interactions and for the mechanistic dissection of complex communities.

*Seppe Kuehn is working to uncover the ecological and evolutionary principles that have allowed these complex microbial communities to assemble, function, and persist. To solve this problem, he combines insights from microbial ecology with conceptual, mathematical, and experimental approaches from physics. His research has been published in Cell Systems, Proceedings of the National Academy of Sciences, The ISME Journal, Physical Review Letters, and eLife. Dr. Kuehn, who is also a core member of the University's Center for the Physics of Evolving Systems, holds a BS magna cum laude in physics from Beloit College and a PhD in chemical physics from Cornell University. While at Cornell, he was honored with the Howard Neal Wachter Memorial Prize for excellence in physical chemistry and the Tunis Wentink Prize for outstanding PhD thesis. Most recently, he was an assistant professor in physics at the University of Illinois at Urbana-Champaign.*