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Channing Microbiome Seminar

March 5th, 2021, 12pm (ET)

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Predicting microbiome compositions using deep learning

Microbes can form complex communities that perform critical functions in maintaining the integrity of their environment or their hosts' wellbeing. Rationally managing these microbial communities requires improving our ability to predict how different species assemblages affect the final species composition of the community. However, making such a prediction remains challenging because of our limited knowledge of the diverse physical, biochemical, and ecological processes governing microbial dynamics. To overcome this challenge, we present a deep learning framework that automatically learns the map between species assemblages and community compositions from training data only, without knowing any of the above processes. First, we systematically validate our framework using synthetic data generated by classical population dynamics models. Then, we apply our framework to data from in vitro and in vivo microbial communities, including ocean and soil microbiota, *Drosophila melanogaster* gut microbiota, and human gut and oral microbiota. We find that our framework learns to perform accurate out-of-sample predictions of complex community compositions from a small number of training samples. Our results demonstrate how deep learning can enable us to understand better and potentially manage complex microbial communities.

Hosted by Yang-Yu Liu