NAU NORTHERN ARIZONA UNIVERSITY

Department of Mathematics and Statistics Colloquium
Tuesday   November 27
AMB 164   4:00 pm

Inferring Microbial Co-occurrence Network from 16s rRNA-seq Data

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Abstract

In natural habitats, microorganisms live together within complicated networks through various types of interactions, which could be either positive (e.g. mutualism) or negative (e.g. competition). Such interactions can be depicted as a network model, in which each vertex represents a species, the edge linking two vertices represents the relationship between these two species, the edge weight represents the strength of the relationship. With 16s rRNA-seq, we may quantify the abundance of microbial species in multiple samples, which then were used to infer co-occurrence networks. In this talk, I will review some popular microbial co-occurrence network inference methods, address the strength and weakness of each of them, and the successful application of these methods in my recent projects.

With the co-occurrence networks being set up under different conditions, defining the network similarity measure is naturally raised. I will introduce the community level and network level approaches, and the possible directions in this field.

Refreshments at 3:45