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

The high-throughput sequencing provides rich data in understanding the complex microbial communities. With 16s rRNA-seq, we may quantify the abundance of microbial species in a sample. To understand the whole-community-scale patterns organized by the interactions between the microbial species, the network modeling approach in the systems biology level is in need. The microbial co-occurrence network analysis approach has been used in many studies to unravel the complex microbial system, and served as useful visualizations of microbiome data.

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 represent the strength of the relationship, and the weight of a vertex represents the abundance of species or the node properties. With the help of high-throughput sequencing across many samples, pairwise relations between different species can be obtained from some statistical tests, which then were used to infer cooccurrence 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 applications of these methods in my recent projects.

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

Refreshments at 3:45