Title:
A General Framework for Association Analysis of Microbial Communities on a Taxonomic Tree

Speaker:
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Time & Place:
Wednesday, September 27, 2017
4:00p
Room 133 SMI
Cookies & Coffee @ 3:30, Rm 1210MSC

Abstract:
Biological and empirical evidence have suggested that microbiome plays an important role in human health and disease. Recent advances in high-throughput sequencing technologies have made it possible to obtain data on the composition of microbial communities and to study the effects of dysbiosis on the human host. We have developed a general framework to (a) perform robust association test at any taxonomic level for the microbiome data exhibiting arbitrary inter-taxon correlation; (b) identify the covariate-associated lineages on a taxonomic tree; (c) assess the overall association of the whole microbial community. Unlike the existing association analysis of microbial communities, our framework does not make any distributional assumptions on the taxa abundances, allows for adjustment of the confounding variables, accommodates excessive zero observations, and incorporates the information of the taxonomic tree. We performed extensive simulation studies to evaluate the new methods under a wide-range of scenarios and demonstrated their advantages over existing methods. The usefulness of the proposed framework are further demonstrated with real datasets from two microbiome studies.