

BIOSTATISTICS SEMINAR

THE 2020 J.E GRIZZLE DISTINGUISHED ALUMNI AWARDEE



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Robust testing for differential abundance in microbiome data

Studies on the human microbiome have revealed that differences in microbial communities are associated with many human disorders such as inflammatory bowel disease, type II diabetes, and even Alzheimer's disease and some cancers. The microbiome is a particularly attractive target for establishing new biomarkers for disease diagnosis and prognosis, and for developing low-cost, low-risk interventions. Microbiome data have two unique features. First, they are compositional, i.e., the total number of sequencing reads per sample is an experimental artifact and only the relative abundance of taxa (e.g., genera or species) can be measured. Second, they are subject to a wide variety of experimental biases (e.g., DNA extraction and PCR amplification) that plague most analyses that directly analyze relative abundance data. These features call for analyses that are based on log-ratio transformation of the raw count data. Existing methods often failed to handle the extensive (50-90%) zero counts adequately as well as accommodating other complexities in microbiome data, including high-dimensionality, over-dispersion, small sample size, and various types of covariates of interest and confounding factors. In this talk, we present a new logistic-regression-based method that takes into account all of these features of microbiome data for robust testing of differential abundance (i.e., detecting taxa whose absolute abundance is associated with the covariate of interest). Our simulation studies indicate that our method is the only one that universally controls the FDR while at the same time maintaining high power. We illustrate our method by the analysis of a throat microbiome dataset.

Thursday April 29, 2021

2:00pm – 3:00pm

Zoom meeting: Please also find a link in the email invite, with the password.
<https://uncsph.zoom.us/j/95116832073?pwd=TnV4QUtGLzMwaFRBTlRsd2xmTjVMQT09>



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