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Channing Microbiome Seminar

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MMZIP: A scalable multivariate variable selection approach for zero-inflated count data

Abstract: I will present a new multivariate method for the analysis of microbiome sequencing data: the marginalized multivariate zero-inflated Poisson (MMZIP) model. Within a Bayesian variable selection framework, this can be thought of as a feature-selection model in which "features" are covariate-taxon associations. Key attributes of the proposed MMZIP include, i) joint differential abundance analysis of zero-inflated count data, ii) enhanced scalability, iii) an automated procedure for selecting relevant associations, iv) straightforward population-averaged (marginalized) interpretation of analysis results, and v) flexible model specification that facilitates an efficient and stable estimation of high-dimensional parameters.

Comprehensive numerical studies demonstrate the superior performance of the MMZIP over existing univariate/multivariate zero-inflated models.

Bio: *Dr. Lee is an Assistant Professor of Integrative Genomic Epidemiology at Harvard Chan School of Public Health. His research focuses on the development of multivariate statistical methods for a wide range of biomedical data. For microbiome applications, one research goal is to develop point pattern analysis approaches for understanding the spatial organization of microbes by using spectral imaging data. Another research goal is to develop comprehensive multivariate variable selection methods for microbiome sequencing count data. The overarching goal of his work is to provide more robust and valid quantitative analysis tools to scientists in microbiology and bioinformatics.*

Hosted by Yang-Yu Liu