



Department of Statistics Seminar

Tuesday, May 2, 2017

3:45 – 4:45 p.m., Room 420, Olmsted Hall

Reception in Olmsted 1331 at 3:15 p.m.

Statistical Analysis of Microbiome Data When Samples Have Unequal Sequence Counts



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Abstract:

Microorganisms play key roles in ecosystems and human civilization. They are involved in soil formation, nutrient cycling, and detoxifying contaminated environments. They contain a wealth of useful compounds and enzymes for biotechnology. In addition, microbes can both cause and prevent infectious diseases. To examine the roles these organisms play in all of the aforementioned situations, researchers currently identify the microorganisms using Illumina-based sequence analysis of rRNA genes. rRNA genes are used because they are found in all living organisms and they contain both conserved and variable regions. One problem with Illumina-based sequence analyses is that they produce samples comprised of unequal sequence counts, which are not based on any biological parameter the researcher is investigating, but which are instead caused by uncontrollable factors in the sequencing process. Unequal sequence counts among samples causes problems for downstream statistical analyses. This seminar will present several approaches currently being used to address this problem. We hope that this presentation will facilitate discussion of the advantages and disadvantages of the different approaches, and possibly lead to new approaches to address this problem.

Biography:

Professor James Borneman has been a faculty member at UCR in the Department of Plant Pathology and Microbiology since 1997. His research focuses on two general topics: (i) the role of microorganisms in suppressing plant pathogens and (ii) the role of intestinal microorganisms that promote health or disease in obesity and diabetes, inflammatory bowel disease, cancer, wound healing and chemotherapy-induced pain and cognitive deficits.