



UNC
GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

BIostatistics Seminar

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Improving microbiome data by modeling the noise process

The study of microbiomes - complex microbial communities that inhabit various environmental niches including the human body - has been energized by high-throughput analysis methods. The most ubiquitous is amplicon sequencing, in which a taxonomically informative genetic element is PCR amplified from a complex community and then sequenced. Amplicon sequencing is cheap and avoids the difficult (and often impossible) bacterial culture step. It is also imperfect, and the biases and errors that arise during the process are increasingly recognized as a critical impediment to accurate and reproducible microbiome research. I'll discuss recent progress we have made towards better inference of true microbial communities from amplicon data based on models of the PCR and high-throughput sequencing error processes. I'll also touch on the danger of applying statistical methods to data which do not meet the assumptions of the method.

Thursday, January 12, 2017

3:30 pm - 4:30 pm

Blue Cross Blue Shield Auditorium

0001 Michael Hooker Research Center