BIOSTATISTICS SEMINAR

Robert Gentleman, PhD

V.P. of Computational Biology, Leading Computational Biology and Informatics, at 23andMe

Using genetic data to identify potential causal disease genes

"I will discuss some of the problems that arise when using genome wide association data to identify potentially causal genes. I will focus on the statistical issues that arise when identifying variants that associate with changes in gene expression (so-called eQTLs). Especially aspects of identifying unknown batch effects and identifying multiple signals per gene."

Dr. Gentleman's career has spanned more than 30 years. During his tenure as Professor at Harvard University, Dr. Gentleman founded the Bioconductor Project, an open source, open development software project to provide tools for the analysis and comprehension of high-throughput genomic data.

Tuesday January 10, 2019   **3:30 pm - 4:30 pm**
Blue Cross and Blue Shield of North Carolina Foundation Auditorium

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