BIOSTATISTICS SEMINAR

Di Wu, PhD,
Assistant Professor, UNC Biostatistics & School of Dentistry

Transcriptional gene set tests and microbial omics data analysis

Both scRNAseq and the microbial DNAseq/RNAseq data are zero inflated over dispersed counts data. That brings the challenges for model fitting which will be addressed in the talk. Gene set tests, in that gene sets are defined a priori (e.g., as regulatory pathways), are valuable for increasing statistical power, organizing and interpreting results, and for relating gene expression patterns across different experiments. For bulk RNAseq data, the rotation gene set test, ROAST, as a self-content test, overcomes the limitation of small sample size and inter-gene correlation. ROMER and CAMERA gene set tests, as the competitive tests, test different statistical hypotheses. For the recent single cell RNAseq (scRNAseq) data, to accommodate their zero inflated over dispersed counts, we develop multiple strategies to test genes by sets, for differential expression, correlation-based pathway, and differential variability. Another recent research direction in my group is integration of microbial omics data, comprising multiple layers of genomic measurements from bacteria and host in the same cohort. That can typically include microbial DNAseq (to answer which bugs are there), RANseq (to answer what these bugs are doing) and metabolome data.

Matthew Biggs, PhD,
Adjunct Assistant Professor, UNC Biostatistics

Exploration in rugged landscapes: genomics-guided discovery

Biological discovery often begins with high-throughput screening. Biological sequence data provides a basis for planning a screening strategy. At AgBiome, in a search for plant-protective bacteria, we screen thousands of bacterial isolates for fungicidal activity. As part of these screening pipelines, we implemented genomics-based sampling of our bacterial search space and ad hoc exploration of local optima. We found that by leveraging genomic information as part of our workflow we were able to discover more fungicidal bacteria, of higher quality, than previous uniform sampling-based approaches.

Thursday October 24, 2019   **3:30 pm - 4:30 pm**
Blue Cross and Blue Shield of North Carolina Foundation Auditorium

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