JOHNS HOPKINS BLOOMBERG SCHOOL of PUBLIC HEALTH

Department of Biostatistics

BIOSTATISTICS SEMINAR,

Modeling and Testing in High-throughput Cancer Drug Screenings

FACULTY CANDIDATE
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Abstract

High-throughput drug screens enable biologists to test hundreds of candidate drugs against thousands of cancer cell lines. The sensitivity of a cell line to a drug is driven by the molecular features of the tumor (e.g. gene mutations and expression). In this talk, I will consider two scientific goals at the forefront of cancer biology: (i) predicting drug response from molecular features, and (ii) discovering gene-drug associations that represent candidates for future drug development. I will present an end-to-end model of cancer drug response that combines hierarchical Bayesian modeling with deep neural networks to learn a flexible function from molecular features to drug response. The model achieves the first goal of state-of-the-art predictive performance, but the black box nature of deep learning makes the model difficult to interpret, presenting a barrier to the second goal of uncovering gene-drug associations. I will use this challenge as motivation for the development of a new method, the holdout randomization test (HRT), for conditional independence testing with black box predictive models. Applying the HRT to the deep probabilistic model of cancer drug response yields more biologically-plausible gene-drug associations than the current analysis technique in biology. I will use these projects to illustrate how statisticians can work closely with biologists to create a virtuous cycle where cutting-edge experiments lead to new statistical models and methods, which in turn drive all of science forward.

Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics
Thursday, January 16, 2020,12:15-1:15pm, Room 3008 (Refreshments 12:00pm)

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