BIOSTATISTICS SEMINAR

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Discovering how complex traits are regulated using unsupervised learning

A central goal of single cell genomics is to understand how cells interact and influence each other, and how tissues grow and respond to specific interventions. In my talk, I will give three examples of how we can use machine learning approaches to begin to quantify relationships between cells. First, using pathology images and paired bulk RNA-seq data, I show how canonical correlation analysis models can be used to find image morphology that covaries with gene expression, and we use these results to identify image QTLs. Second, I describe a method for dimension reduction that allows us to augment disassociated single cell RNA-seq data with spatial information and, conversely, expand often sparse spatial transcriptomic data to all 20,000 genes in the human genome. Third, I show how Hawkes processes can be used to quantify spatial signaling between groups of heterogeneous cells across time and space, and illustrate the results through changes to spatial signaling in response to drugs inhibiting signaling and with respect to distance from a wound. Using these single cell data and models, we begin to quantify how specific cellular neighbors influence each other, and to predict how tissues might respond to interventions.

Thursday October 29, 2020 **3:00 pm - 4:30 pm**

Zoom meeting: Please also find a link in the email invite, with the password.
https://uncsph.zoom.us/j/92138801086?pwd=Y011NUNQcS9lZERjalVhbVZSZ3AwQT09

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