

## Graduate Statistics Seminar

### *Integrative network analysis of TCGA data for ovarian cancer*

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**Abstract:** Traditional cancer studies have been mainly focusing on single gene or single type of data including mRNA expression, DNA methylation, copy number variation, and etc. However, such analyses lack power to reveal the molecular mechanisms from the view of system biology. In this talk, I will present an integrative framework to identify important genetic and epigenetic features and to quantify the causal relations among these features. I will first talk about what is a Bayesian Network and what the TCGA data looks like. Then I will introduce the proposed feature selector and Bayesian Network model. Simulated and real data sets will be used for illustration.

Tuesday, April 22 at 3:30 PM in SEO 636