



2018 Pre-Ostrom Colloquium



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Pathway- and Network-based Integrative Bayesian Modeling of Multiplatform Genomics Data

The identification of gene pathways and networks involved in cancer development and progression and characterization of their activity in terms of multiplatform genomics can provide information leading to discovery of new targeted medications. We propose a two-step model that integrates multiple genomic platforms, as well as gene pathway membership information, to efficiently and simultaneously (a) identify the genes significantly related to a clinical outcome, (b) identify the genomic platform(s) regulating each important gene, and (c) rank the pathways by importance to clinical outcome. We propose hierarchical Bayesian pathway- and network-based frameworks, which allows us not only to identify the important pathways and the important genes within pathways, but also to gain insight as to the platform(s) driving the effects mechanistically. The approaches will be illustrated using several case examples integrating high-throughput pan-omic (e.g. genomic, epigenomic, transcriptomic, proteomic) across multiple tumor types.

Tuesday, April 10th, 2018

4:10 pm in Neill 5W

Reception at 3:30 pm in Neill 216

Hosted by Washington State University Department of Mathematics & Statistics

The Annual Theodore G. Ostrom brings internationally renowned mathematics scholars to campus each spring. The lectures honor Emeritus Ostrom, who retired from WSU in 1981 after 21 years on faculty.

Ostrom Lecture Wednesday, April 11th, 2018 at 7:00 pm, Wegner G50