



The Department of Biological Sciences and the Biomedical  
Informatics Student Club

*Proudly present the seminar*

## Evaluation of genomic prediction models of patient outcomes across studies

**Guest Speaker: Prof. Levi Waldron**

*Assistant Professor, Hunter College*

**When: Thursday, Dec 4th, 2014**

**Time: 1:00 pm- 2:00 pm**

**Place: N523**

Public databases such as the Gene Expression Omnibus now provide an almost overwhelming free resource for developing and validating models of association between tumor gene expression and patient outcome in cancer. More than a million gene expression profiles are available, covering most disease types and study designs. These resources are challenging to utilize due to their unstructured nature and the potential for unknown sources of heterogeneity between studies. In this talk I will discuss building smaller curated databases for answering focused research questions, and how experimental and cohort heterogeneity between independent studies can be identified and leveraged as an advantage for finding robust, generalizable prediction models and biomarkers. I will briefly discuss more recent areas of research interest in biomedical informatics, including visualization of publicly available health surveillance datasets.

**Bio:** Levi Waldron completed his PhD at the University of Toronto and did post-doctoral training in Toronto and at the Harvard School of Public Health and Dana-Farber Cancer Institute. He is now an assistant professor of biostatistics at the CUNY School of Public Health at Hunter College, and a member of the Bioconductor technical advisory board. He is actively involved in developing core Bioconductor data structures for integrative analysis of multi-assay genomic experiments such as The Cancer Genome Atlas, and has ongoing research interests in methodology for using potentially heterogeneous collections of independent, publicly available gene expression datasets for discovery and validation of prediction models and biomarkers.

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