

JOINT SEMINAR WITH THE CENTER FOR INTEGRATIVE PROTEOMICS RESEARCH



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***Exogenous functional information-assisted
statistical analysis of omics data***

March 30, 2016

3:20 – 4:20pm

Light refreshments will be served

110 Frelinghuysen Road, Hill Center, Room 552

Abstract: An important challenge in statistical analysis of omics data concerns integrating experimental data with exogenous functional information. The functional information is accumulated by bioinformatics projects like GO and KEGG and is usually used in two complementary ways. One mode is about data reduction, for example, construction of summary statistics on functional categories. The other mode is about boosting signal-to-noise ratio, for example, a weak gene-level signal differentiating two cellular states is easier to detect if it is consistent over a set of genes having some shared function. In this talk, I will present some recent developments on functional information integration in areas of risk prediction, meta-analysis, integrative clustering and precision medicine. The methodologies are illustrated on a TCGA ovarian cancer study and their statistical properties are further explored.

Bio: Dr. Sijian Wang has a Ph.D. in Biostatistics from The University of Michigan and a B.S. in Mathematics from Tsinghua University, China. He is currently an associate professor in the Department of Statistics and Department of Biostatistics & Medical Informatics at the University of Wisconsin, Madison. His research interests include high-dimensional data analysis, proteomics, cancer genomics, bioinformatics, survival analysis, longitudinal data analysis and statistical modeling in health sciences.

