TITLE:
Network-based Analysis to Identify Common Disease Genes

SPEAKER:
Professor Hongyu Zhao
Ira V. Hiscock Professor of Public Health (Biostatistics)
and Professor of Genetics and of Statistics
Yale School of Public Health

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Wednesday, April 23, 2014
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(Cookies & Coffee @ 3:30 in Rm 1210 MSC)

ABSTRACT:
Although Genome Wide Association Studies (GWAS) have identified many chromosomal regions associated with disease risk, these loci only explain a small portion of heritability. It is challenging to identify the remaining disease loci because their association signals are likely weak and difficult to identify among millions of candidates. One potentially useful direction to increase statistical power to prioritize GWAS signals is to incorporate network information, such as annotated pathways and gene expression networks. In this presentation, we will describe statistical approaches to integrating network information for such analysis. The usefulness of these methods will be demonstrated through their applications to a number of GWAS data sets.