



Temple University

ANNOUNCES A
COLLOQUIUM

Dr. Xiaohua Zhang

*Biometrics Research
Merck Research Laboratories*

will speak on

Data Analysis in Genome-Scale RNAi Research

Time: 3:00 – 4:00 PM

Date: Friday, December 5, 2008

Place: Tuttleman Learning Center 203AB

Abstract

RNA interference (RNAi) has revolutionized functional genomics and has been seen as the third class of drugs, after small molecules and proteins. The importance of RNAi was further recognized when the Nobel Prize in Medicine and Physiology was awarded to Drs. Fire and Mello in 2006 for their research in this field. Merck has one of the largest labs for conducting genome-wide RNAi research. A central challenge in genome-wide RNAi research is to glean biological significance from mounds of data, which relies on the development of effective analytic methods for selecting effective small interfering RNAs (siRNAs). Recently, we have developed new methods for genome-wide screens of effective siRNAs through assessing and testing the size of siRNA effects. Central to these methods is their capability in quantifying siRNA effects, which allows scientists to select siRNAs with desired size of effects. In the seminar, I will introduce RNAi biotechnologies briefly, illustrate the issues in commonly used analytic methods based on p-values, present new development of analytic methods and demonstrate how to use them in genome-scale RNAi research.

**Guest Parking Available in Visitors' Parking Area 3
(Park Avenue between Cecil B. Moore Avenue & Oxford Street)**