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Seminar

Speaker: **Zhaohui Qin**
Associate Professor
Department of Biostatistics and Bioinformatics
School of Public Health
Emory University

Title: **Towards the Understanding of the Three-Dimensional Genome Organization**
Statistical Challenges and Opportunities for Analyzing Hi-C data

Time: **3:20 – 4:20pm, Wednesday, October 24, 2012**

Place: **552 Hill Center**

Abstract

Understanding how chromosomes fold provides insights into transcription regulation hence functional state of the cell. Recently, chromosomal conformation capture (3C)-related technologies have been developed to provide a genome-wide view of chromatin organization. Despite great technologies, multiple layers of noise and uncertainties stem from the sophisticated experiments, coupled with various sequencing-related artifacts, making the analysis of such data extremely challenging. Here using Hi-C as an example, we review the critical issues of analyzing this latest type of genomics data, including normalization, modeling and inference. We describe a novel Bayesian probabilistic approach, denoted “Bayesian 3D constructor for Hi-C data” (BACH), to infer chromosome three-dimensional (3D) structures from Hi-C data. We also discuss the observations we made when applying BACH to real Hi-C datasets. This is a collaboration with Ming Hu, Ke Deng and Jun Liu.

**** Refreshments will be served at @2:50pm in Room 502 Hill Center ****

