



JOHNS HOPKINS  
BLOOMBERG  
SCHOOL of PUBLIC HEALTH

*Department of Biostatistics*

# BIOSTATISTICS SEMINAR

## FALSE DISCOVERY RATES AND COPY NUMBER VARIATION

Professor Bradley Efron, Department of Statistics  
Stanford University  
and  
Nancy Zhang  
Department of Statistics, Stanford University

### *Abstract*

Copy number variations, the gains and losses of chromosome segments, are an important source of genetic variability among healthy individuals. Microarray technology enables us to simultaneously measure, with moderate accuracy, copy number variation at hundreds of thousands of chromosome locations and for hundreds of subjects. This leads to massive data sets and complicated inference problems concerning which locations for which subjects are genuinely variable. In this talk we consider a relatively simple false discovery rate approach to CNV analysis. More careful parametric change-point methods can then be focused on promising regions of the genome.

**The Johns Hopkins Bloomberg School of Public Health  
Department of Biostatistics, Wednesday, October 20, 2010  
Room W2030 School of Public Health, 4:00-5:00pm (Refreshments: 3:30)**

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