



JOHNS HOPKINS
BLOOMBERG
SCHOOL of PUBLIC HEALTH

Department of Biostatistics

BIOSTATISTICS SEMINAR

The Structure of Epigenetic Changes in Cancer as Revealed by Whole-genome Shotgun Bisulfite Sequencing

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Abstract

DNA methylation is a widely studied epigenetic mark known to be implicated in tissue differentiation and disease, specifically cancer. We have performed the first genomewide analysis of changes in DNA methylation in cancer, using whole-genome shotgun bisulfite sequencing of 3 paired tumor-normal samples. We describe our statistical analysis of this new type of data, which involves smoothing a binomial process. Our analysis led to a number of new insights into cancer epigenetics, including a description of the structure of local, small-scale changes in cancer. We also show hypo-methylation of large scale genomic domains encompassing more than half the genome.

**The Johns Hopkins Bloomberg School of Public Health
Department of Biostatistics, Monday, February 6, 2012
Room W2030 School of Public Health, 4:00-5:00pm (Refreshments: 3:30)**

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