

## Colloquium on Epigenetics and Their Analysis

Given the minimum contribution from genetic predisposition, epigenetic changes are drawing tremendous attention. Findings from high throughput data such as genome-wide methylation data will have strong potential to provide a better understanding of the epigenetic control on



disease, and critically impact the prevention and treatment of the disease. However, given the size of the data, analyzing high throughput data to obtain informative conclusions is challenging. Efficient but also effective methods are critical for this type of data.

The Department of Epidemiology and Biostatistics and the Research Consortium on Children and Families will jointly sponsor a colloquium by two experts on public health studies via high throughput data, Wilfried Karmaus and Michael Wu from **1 to 3 PM on March 21 in Discovery I (915 Green Street) room 140.**

Wilfried Karmaus, a professor of Epidemiology at the University of South Carolina, has worked on gene-environment interactions and has an R01 on epigenetic inheritance in a birth cohort. He will demonstrate that environment and genetic polymorphism in concert influence the DNA methylation, and that the combination of all three result in a much better explanation of the occurrence of diseases.



Michael Wu, an assistant professor of biostatistics at UNC, is a rising expert in statistical genomics who is known for his development and application of powerful computational and statistical tools for analyzing large scale genomic studies. He will discuss new tools and strategies for the analysis of epigenetic data within the context of understanding how a mother's behavior and environmental exposures during pregnancy can influence the child's health.