Epigenome-wide association studies of whole blood using DNA methylation microarray data
DNA methylation changes associated with mammographic density

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Studying differences in DNA methylation according to disease status or risk status can provide important information about the molecular changes underlying disease risk, while also serving as potential biomarkers. For example, DNA methylation in easily accessible tissues such as blood can be used to predict smoking status and the development of cancer. Because DNA methylation is influenced by the environment, epigenomic changes may provide a history of past exposures. Commercially available DNA methylation microarrays, such as Illumina’s HumanMethylationEpic BeadChip, provide a cost-effective and efficient method for characterizing DNA methylation across the epigenome. This seminar will describe a recent epigenome-wide association study which identified DNA methylation markers of mammographic density, an important risk factor for breast cancer. This will provide an overview of the typical data analysis pipeline for such studies. The structure and goals of UCI’s Markers for Environmental Exposures study will also be described.