



Mediation analysis in epigenetic studies

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In many epigenetic studies, we would like to explore whether the methylomic profiles form indirect paths between intervention/exposure and health outcomes. Mediation analysis can be used to test the null hypothesis of no causal mediation through the mediating variable (i.e., methylomic markers). However, complexity arises due to the high dimension of the mediator variables, e.g., 486K CpG sites in Illumina 450K arrays (Illumina, Inc., San Diego, CA). We will discuss methods to address the multiple comparison issues in mediation analysis. Model selection methods for high-dimensional data will be used to analyze such data. We apply our methods to the Normative Aging Study.

Keywords: methylation markers, high dimensional data, casual inference, model selection.