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An evaluation of statistical methods for DNA methylation microarray data analysis

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DNA methylation offers a process for elucidating how epigenetic information affects gene expression. β values and M values are commonly used to quantify DNA methylation. Statistical methods applicable to DNA methylation data analysis span a number of approaches such as Wilcoxon rank sum test, t-test, Kolmogorov-Smirnov test, permutation test, empirical Bayes method, and bump hunting method. Selection of an optimal statistical method, however, can be challenging when different methods generate inconsistent results for the same data set. We compared six statistical approaches relevant to DNA methylation microarray analysis in terms of false discovery rate control, statistical power, and stability through simulation studies and a real data example. Our results provide guidance for optimal statistical methods selection under different scenarios. For DNA methylation data analysis purposes, similar results are obtained using either β or M values in terms of false discovery rate control, power, and stability. The empirical Bayes method is recommended for DNA methylation studies with small sample size. All methods are acceptable for medium or large sample sizes. The bump hunting method has much lower stability than the other methods when the true proportion of differentially methylated loci is large, a caveat to be considered when choosing the bump hunting method.

Biography

Dongmei Li completed her PhD in Biostatistics from Department of Statistics at The Ohio State University. She is currently an interim Associate Professor in the Department of Clinical & Translational Research at the University of Rochester School of Medicine and Dentistry. She has published more than 25 methodology and collaborative papers in reputed journals and been served as Co-Investigator or Statistician on multiple federal funded grants and contracts.

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