

Analyzing High-Dimensional Gene Expression and DNA Methylation Data with R is the first practical book that shows a "pipeline" of analytical methods with concrete examples starting from raw gene expression and DNA methylation data at the genome scale. Methods on quality control, data pre-processing, data mining, and further assessments are presented in the book, and R programs based on simulated data and real data are included. Codes with example data are all reproducible.

Features

- Provides a sequence of analytical tools for genome-scale gene expression data and DNA methylation data, starting from quality control and pre-processing of raw genome-scale data.
- Organized by a parallel presentation with explanation on statistical methods and corresponding R packages/functions in quality control, pre-processing, and data analyses (e.g., clustering and networks).
- Includes source codes with simulated and real data to reproduce the results. Readers are expected to gain the ability to independently analyze genome-scale expression and methylation data and detect potential biomarkers.

This book is ideal for students majoring in statistics, biostatistics, and bioinformatics and researchers with an interest in high dimensional genetic and epigenetic studies.

Hongmei Zhang is a Professor in Biostatistics at the University of Memphis. She has been working with gene expression and DNA methylation data for a long time, and her methodological research interest is to develop statistical methods and techniques applied to these types of data to learn underlying patterns and connections and identify markers for health conditions or exposures. She has been teaching courses in this field for a number of years.



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