

Part I Single-Cell Analysis

Computational and Statistical Methods for Single-Cell RNA

Sequencing Data	3
Zuoheng Wang and Xiting Yan	

Pre-processing, Dimension Reduction, and Clustering for

Single-Cell RNA-seq Data	37
Jialu Hu, Yiran Wang, Xiang Zhou, and Mengjie Chen	

Integrative Analyses of Single-Cell Multi-Omics Data: A Review from a Statistical Perspective

	53
Zhixiang Lin	

Approaches to Marker Gene Identification from Single-Cell

RNA-Sequencing Data	71
Ronnie Y. Li, Wenjing Ma, and Zhaohui S. Qin	

Model-Based Clustering of Single-Cell Omics Data

	85
Xinjun Wang, Haoran Hu, and Wei Chen	

Deep Learning Methods for Single-Cell Omics Data

	109
Jingshu Wang and Tianyu Chen	

Part II Network Analysis

Probabilistic Graphical Models for Gene Regulatory Networks

	135
Zhenwei Zhou, Xiaoyu Zhang, Peitao Wu, and Ching-Ti Liu	

Additive Conditional Independence for Large and Complex

Biological Structures	153
Kuang-Yao Lee, Bing Li, and Hongyu Zhao	

Integration of Boolean and Bayesian Networks

	173
Meng-Yuan Tsai and Henry Horng-Shing Lu	

**Computational Methods for Identifying MicroRNA-Gene
Regulatory Modules 187**
Yin Liu

Causal Inference in Biostatistics..... 209
Shasha Han and Xiao-Hua Zhou

Bayesian Balance Mediation Analysis in Microbiome Studies 237
Lu Huang and Hongzhe Li

Part III Systems Biology

Identifying Genetic Loci Associated with Complex Trait Variability 257
Jiacheng Miao and Qiongshi Lu

Cell Type-Specific Analysis for High-throughput Data 271
Ziyi Li and Hao Wu

**Recent Development of Computational Methods in the Field
of Epitranscriptomics 285**
Zijie Zhang, Shun Liu, Chuan He, and Mengjie Chen

Estimation of Tumor Immune Signatures from Transcriptomics Data 311
Xiaoqing Yu

Cross-Linking Mass Spectrometry Data Analysis 339
Chen Zhou and Weichuan Yu

**Cis-regulatory Element Frequency Modules and their Phase
Transition across Hominidae 371**
Lei M Li, Mengtian Li, and Liang Li

Improved Method for Rooting and Tip-Dating a Viral Phylogeny 397
Xuhua Xia