

Contents

1 Statistical Analyses of Next Generation Sequencing Data: An Overview	1
Riten Mitra, Ryan Gill, Susmita Datta, and Somnath Datta	
2 Using RNA-seq Data to Detect Differentially Expressed Genes	25
Douglas J. Lorenz, Ryan S. Gill, Ritendranath Mitra, and Susmita Datta	
3 Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR	51
Yunshun Chen, Aaron T.L. Lun, and Gordon K. Smyth	
4 Analysis of Next Generation Sequencing Data Using Integrated Nested Laplace Approximation (INLA)	75
Andrea Riebler, Mark D. Robinson, and Mark A. van de Wiel	
5 Design of RNA Sequencing Experiments	93
Dan Nettleton	
6 Measurement, Summary, and Methodological Variation in RNA-sequencing	115
Alyssa C. Frazee, Leonardo Collado Torres, Andrew E. Jaffe, Ben Langmead, and Jeffrey T. Leek	
7 DE-FPCA: Testing Gene Differential Expression and Exon Usage Through Functional Principal Component Analysis.....	129
Hao Xiong, James Bentley Brown, Nathan Boley, Peter J. Bickel, and Haiyan Huang	
8 Mapping of Expression Quantitative Trait Loci Using RNA-seq Data	145
Wei Sun and Yijuan Hu	

9	The Role of Spike-In Standards in the Normalization of RNA-seq	169
	Davide Rissi, John Ngai, Terence P. Speed, and Sandrine Dudoit	
10	Cluster Analysis of RNA-Sequencing Data	191
	Peng Liu and Yaqing Si	
11	Classification of RNA-seq Data	219
	Kean Ming Tan, Ashley Petersen, and Daniela Witten	
12	Isoform Expression Analysis Based on RNA-seq Data	247
	Hongzhe Li	
13	RNA Isoform Discovery Through Goodness of Fit Diagnostics	261
	Julia Salzman	
14	MOSAiCS-HMM: A Model-Based Approach for Detecting Regions of Histone Modifications from ChIP-Seq Data	277
	Dongjun Chung, Qi Zhang, and Sündüz Keleş	
15	Hierarchical Bayesian Models for ChIP-seq Data	297
	Riten Mitra and Peter Müller	
16	Genotype Calling and Haplotype Phasing from Next Generation Sequencing Data	315
	Degui Zhi and Kui Zhang	
17	Analysis of Metagenomic Data	335
	Ruofei Du and Zhide Fang	
18	Detecting Copy Number Changes and Structural Rearrangements Using DNA Sequencing	355
	Venkatraman E. Seshan	
19	Statistical Methods for the Analysis of Next Generation Sequencing Data from Paired Tumor-Normal Samples	379
	Mengjie Chen, Lin Hou, and Hongyu Zhao	
20	Statistical Considerations in the Analysis of Rare Variants	405
	Debashis Ghosh and Santhosh Girirajan	
Index		423