

Contents

<i>List of Contributors</i>	page vii
<i>Preface</i>	xi
1. An Introduction to Next-Generation Biological Platforms <i>Virginia Mohlere, Wenting Wang, and Ganiraju Manyam</i>	1
2. An Introduction to The Cancer Genome Atlas <i>Bradley M. Broom and Rehan Akbani</i>	31
3. DNA Variant Calling in Targeted Sequencing Data <i>Wenyi Wang, Yu Fan, and Terence P. Speed</i>	54
4. Statistical Analysis of Mapped Reads from mRNA-Seq Data <i>Ernest Turro and Alex Lewin</i>	77
5. Model-Based Methods for Transcript Expression-Level Quantification in RNA-Seq <i>Zhaonan Sun, Han Wu, Zhaohui Qin, and Yu Zhu</i>	105
6. Bayesian Model-Based Approaches for Solexa Sequencing Data <i>Riten Mitra, Peter Mueller, and Yuan Ji</i>	126
7. Statistical Aspects of ChIP-Seq Analysis <i>Jonathan Cairns, Andy G. Lynch, and Simon Tavaré</i>	138
8. Bayesian Modeling of ChIP-Seq Data from Transcription Factor to Nucleosome Positioning <i>Raphael Gottardo and Sangsoon Woo</i>	170
9. Multivariate Linear Models for GWAS <i>Chiara Sabatti</i>	188
10. Bayesian Model Averaging for Genetic Association Studies <i>Christine Peterson, Michael Swartz, Sanjay Shete, and Marina Vannucci</i>	208
11. Whole-Genome Multi-SNP-Phenotype Association Analysis <i>Yongtao Guan and Kai Wang</i>	224

12.	Methods for the Analysis of Copy Number Data in Cancer Research <i>Bradley M. Broom, Kim-Anh Do, Melissa Bondy, Patricia Thompson, and Kevin Coombes</i>	244
13.	Bayesian Models for Integrative Genomics <i>Francesco C. Stingo and Marina Vannucci</i>	272
14.	Bayesian Graphical Models for Integrating Multiplatform Genomics Data <i>Wenting Wang, Veerabhadran Baladandayuthapani, Chris C. Holmes, and Kim-Anh Do</i>	292
15.	Genetical Genomics Data: Some Statistical Problems and Solutions <i>Hongzhe Li</i>	312
16.	A Bayesian Framework for Integrating Copy Number and Gene Expression Data <i>Yuan Ji, Filippo Trentini, and Peter Mueller</i>	331
17.	Application of Bayesian Sparse Factor Analysis Models in Bioinformatics <i>Haisu Ma and Hongyu Zhao</i>	350
18.	Predicting Cancer Subtypes Using Survival-Supervised Latent Dirichlet Allocation Models <i>Keegan Korthauer, John Dawson, and Christina Kendziorski</i>	366
19.	Regularization Techniques for Highly Correlated Gene Expression Data with Unknown Group Structure <i>Brent A. Johnson</i>	382
20.	Optimized Cross-Study Analysis of Microarray-Based Predictors <i>Xiaogang Zhong, Luigi Marchionni, Leslie Cope, Edwin S. Iversen, Elizabeth S. Garrett-Mayer, Edward Gabrielson, and Giovanni Parmigiani</i>	398
21.	Functional Enrichment Testing: A Survey of Statistical Methods <i>Laila M. Poisson and Debashis Ghosh</i>	423
22.	Discover Trend and Progression Underlying High-Dimensional Data <i>Peng Qiu</i>	445
23.	Bayesian Phylogenetics Adapts to Comprehensive Infectious Disease Sequence Data <i>Jennifer A. Tom, Janet S. Sinsheimer, and Marc A. Suchard</i>	460
	<i>Index</i>	477

Color plates follow page 104.