

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 Risso, 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 |

Statistical Analysis of Next Generation Sequencing Data

Datta, S.; Nettleton, D. (Eds.)

2014, XIV, 432 p. 87 illus., 68 illus. in color., Hardcover

ISBN: 978-3-319-07211-1