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Nota di contenuto	Some Themes in High-Dimensional Statistics: A. Frigessi et al -- Laplace Approximation in High-Dimensional Bayesian Regression: R. Barber, M. Drton et al -- Preselection in Lasso-Type Analysis for Ultra-High Dimensional Genomic Exploration: L.C. Bergersen, I. Glad et al -- Spectral Clustering and Block Models: a Review and a new Algorithm: S. Bhattacharyya et al -- Bayesian Hierarchical Mixture Models: L. Bottolo et al -- iBATCGH; Integrative Bayesian Analysis of Transcriptomic and CGH Data: Cassese, M. Vannucci et al -- Models of Random Sparse Eigenmatrices and Bayesian Analysis of Multivariate Structure: A.J. Cron, M. West -- Combining Single and Paired End RNA-seq Data for Differential Expression Analysis: F. Feng, T. Speed et al -- An

Imputation Method for Estimation the Learning Curve in Classification Problems: E. Laber et al -- Bayesian Feature Allocation Models for Tumor Heterogeneity: J. Lee, P. Mueller et al -- Bayesian Penalty Mixing: The Case of a Non-Separable Penalty: V. Rockova et al -- Confidence Intervals for Maximin Effects in Inhomogeneous Large Scale Data: D. Rothenhausler et al -- Chisquare Confidence Sets in High-Dimensional Regression: S. van de Geer et al. .

Sommario/riassunto

This book features research contributions from The Abel Symposium on Statistical Analysis for High Dimensional Data, held in Nyvågar, Lofoten, Norway, in May 2014. The focus of the symposium was on statistical and machine learning methodologies specifically developed for inference in “big data” situations, with particular reference to genomic applications. The contributors, who are among the most prominent researchers on the theory of statistics for high dimensional inference, present new theories and methods, as well as challenging applications and computational solutions. Specific themes include, among others, variable selection and screening, penalised regression, sparsity, thresholding, low dimensional structures, computational challenges, non-convex situations, learning graphical models, sparse covariance and precision matrices, semi- and non-parametric formulations, multiple testing, classification, factor models, clustering, and preselection. Highlighting cutting-edge research and casting light on future research directions, the contributions will benefit graduate students and researchers in computational biology, statistics and the machine learning community.
