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Nota di contenuto	Cover; Title Page; Copyright; Contents; List of Contributors; Chapter 1 Using the DiffCorr Package to Analyze and Visualize Differential Correlations in Biological Networks; 1.1 Introduction; 1.1.1 An Introduction to Omics and Systems Biology; 1.1.2 Correlation Networks in Omics and Systems Biology; 1.1.3 Network Modules and Differential Network Approaches; 1.1.4 Aims of this Chapter; 1.2 What is DiffCorr?; 1.2.1 Background; 1.2.2 Methods; 1.2.3 Main Functions in DiffCorr; 1.2.4 Installing the DiffCorr Package 1.3 Constructing Co-Expression (Correlation) Networks from Omics Data - Transcriptome Data set 1.3.1 Downloading the Transcriptome Data set; 1.3.2 Data Filtering; 1.3.3 Calculation of the Correlation and Visualization of Correlation Networks; 1.3.4 Graph Clustering; 1.3.5 Gene Ontology Enrichment Analysis; 1.4 Differential Correlation Analysis by DiffCorr Package; 1.4.1 Calculation of Differential Co-Expression between Organs in Arabidopsis; 1.4.2 Exploring the Metabolome Data of Flavonoid-Deficient Arabidopsis; 1.4.3 Avoiding Pitfalls in (Differential) Correlation Analysis; 1.5 Conclusion

Acknowledgments Conflicts of Interest; References; Chapter 2 Analytical Models and Methods for Anomaly Detection in Dynamic, Attributed Graphs; 2.1 Introduction; 2.2 Chapter Definitions and Notation; 2.3 Anomaly Detection in Graph Data; 2.3.1 Neighborhood-Based Techniques; 2.3.2 Frequent Subgraph Techniques; 2.3.3 Anomalies in Random Graphs; 2.4 Random Graph Models; 2.4.1 Models with Attributes; 2.4.2 Dynamic Graph Models; 2.5 Spectral Subgraph Detection in Dynamic, Attributed Graphs; 2.5.1 Problem Model; 2.5.2 Filter Optimization; 2.5.3 Residuals Analysis in Attributed Graphs 2.6 Implementation in R 2.7 Demonstration in Random Synthetic Backgrounds; 2.8 Data Analysis Example; 2.9 Summary; Acknowledgments; References; Chapter 3 Bayesian Computational Algorithms for Social Network Analysis; 3.1 Introduction; 3.2 Social Networks as Random Graphs; 3.3 Statistical Modeling Approaches to Social Network Analysis; 3.3.1 Exponential Random Graph Models (ERGMs); 3.3.2 Latent Space Models (LSMs); 3.4 Bayesian Inference for Social Network Models; 3.4.1 R-Based Software Tools; 3.5 Data; 3.5.1 Bayesian Inference for Exponential Random Graph Models 3.5.2 Bayesian Inference for Latent Space Models 3.5.3 Predictive Goodness-of-Fit (GoF) Diagnostics; 3.6 Conclusions; References; Chapter 4 Threshold Degradation in R Using iDEMO; 4.1 Introduction; 4.2 Statistical Overview: Degradation Models; 4.2.1 Wiener Degradation-Based Process; 4.2.1.1 Lifetime Information; 4.2.1.2 Log-Likelihood Function; 4.2.2 Gamma Degradation-Based Process; 4.2.2.1 Lifetime Information; 4.2.2.2 Log-Likelihood Function; 4.2.3 Inverse Gaussian Degradation-Based Process; 4.2.3.1 Lifetime Distribution; 4.2.3.2 Log-Likelihood Function; 4.2.4 Model Selection Criteria 4.2.5 Choice of t
