1. Record Nr. UNINA9910790052003321

Autore	Hill Emma, Dr.
Titolo	So you want to be a medical mum? [[electronic resource]] : a guide for female medics who have ever thought that maybe, somehow, one day, they might want to have a baby / / Emma Hill
Pubbl/distr/stampa	Oxford ; ; New York, : Oxford University Press, 2008
ISBN	0-19-176845-6 1-283-58197-3 9786613894427 0-19-155336-0 0-19-157980-7
Descrizione fisica	1 online resource (246 p.)
Collana	Medical careers guide
Disciplina	610.7306/9
Soggetti	Pregnant women - Great Britain Women physicians - Great Britain Work and family - Great Britain Working mothers - Great Britain
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Dedication; Thanks; Preface; Glossary and abbreviations; Contents; Introduction; 1 Before you take the plunge; 2 Trying to get pregnant; 3 Life as a pregnant hospital doctor; 4 Life as a pregnant general practitioner; 5 Academic medicine; 6 Pregnancy as an undergraduate; 7 Know your rights: employment law; 8 Maternity leave; 9 Before the baby arrives; 10 Doctors giving birth; 11 Early days ... Yes, it was a baby (not flatus or fluid); 12 Planning your return to work; 13 Breastfeeding and working; 14 Childcare; 15 Being back at work; 16 Working fathers; 17 'Planning' further pregnancies 18 Now we are six ... Watching your children grow19 Money matters; 20 Do you still wish you'd been a lawyer?; Frequently asked questions; Appendix 1: Useful contacts; Index; A; B; C; D; E; F; G; H; I; J; L; M; N; O; P; R; S; T; U; V; W
Sommario/riassunto	In 2006 over 60% of medical graduates in the UK were female, and the number of women going to medical school as 'mature students' is

	steadily increasing. Some of these women will, at some point, choose to have a baby, but the question always asked is how to fit it in with a medical career? Along with the problem of finding time to actually have a baby, and coping as a pregnant doctor, there is the problem of finding information when it is most needed. This book addresses thisproblem, bringing a wealth of information together in one easy-to-use resource. Written by a mother, who has faced the j

2.

Record Nr.	UNISA996503551803316
Titolo	Handbook of statistical bioinformatics / / Henry Horng-Shing Lu [and three others]
Pubbl/distr/stampa	Berlin : , : Springer, , [2022] ©2022
ISBN	3-662-65902-6
Edizione	[2nd ed.]
Descrizione fisica	1 online resource (406 pages)
Collana	Springer Handbooks of Computational Statistics
Disciplina	570.285
Soggetti	Bioinformatics - Statistical methods Bioinformatics Bioinformàtica Biologia computacional Informàtica mèdica Estadística matemàtica Llibres electrònics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Intro -- Preface -- Contents -- Part I Single-Cell Analysis -- Computational and Statistical Methods for Single-Cell RNA Sequencing Data -- 1 Introduction -- 2 Data Preprocessing -- 2.1 Reads Mapping -- 2.2 Cell Barcodes Demultiplexing -- 2.3 UMI Collapsing -- 2.4 Cell Barcodes Selection -- 2.5 Summary -- 3 Data Normalization and Visualization -- 3.1 Background -- 3.2 Global Scaling Normalization for UMI Data -- 3.3 Probabilistic Model-Based Normalization for UMI

Data -- 3.4 Dimension Reduction and Cell Clustering -- 4 Dropout Imputation -- 4.1 Background -- 4.2 Cell-Cell Similarity-Based Imputation -- 4.3 Gene-Gene Similarity-Based Imputation -- 4.4 Gene-Gene and Cell-Cell Similarity-Based Imputation -- 4.5 Deep Neural Network-Based Imputation -- 4.6 G2S3 -- 4.7 Methods Evaluation and Comparison -- 5 Differential Expression Analysis -- 5.1 Background -- 5.2 DE Methods Ignoring Subject Effects -- 5.3 DE Methods Considering Subject Effects -- 5.4 iDESC -- 5.5 DE Methods Evaluation and Comparison -- 5.5.1 Type I Error Comparison -- 5.5.2 Statistical Power Comparison -- 6 Concluding Remarks -- References -- Pre-processing, Dimension Reduction, and Clustering for Single-Cell RNA-seq Data -- 1 Introduction -- 2 Pre-processing of scRNA-seq Data -- 2.1 Removal of Batch Effects -- 2.2 Quality Control and Feature Selection -- 3 Dimension Reduction and Clustering -- 3.1 Dimension Reduction -- 3.2 Clustering -- 4 Conclusion -- References -- Integrative Analyses of Single-Cell Multi-Omics Data: A Review from a Statistical Perspective -- 1 Multi-Omics Data Profiled on Different Cells -- 2 Multi-Omics Data Profiled on the Same Single Cells -- 3 Challenges and Future Perspectives -- References -- Approaches to Marker Gene Identification from Single-Cell RNA-Sequencing Data -- 1 Introduction.
2 Marker Gene Selection Relies on Identifying Differentially Expressed Genes -- 3 Methods for Marker Gene Selection -- 3.1 Highest Expressed, Highest Variable -- 4 Supervised Methods -- 4.1 COMET -- 4.2 scGeneFit -- 5 Unsupervised Methods -- 5.1 Seurat -- 5.2 SC3 -- 5.3 SCMarker -- 5.4 scTIM -- 5.5 RankCorr -- 6 Discussion -- References -- Model-Based Clustering of Single-Cell Omics Data -- 1 Introduction -- 2 Single-Cell Transcriptomic Data Clustering -- 2.1 Single-Cell Transcriptomic Data Structure -- 2.2 DIMM-SC -- 2.3 Real Data Example -- 3 Population-Scale Single-Cell Transcriptomic Data Clustering -- 3.1 Population-Scale Single-Cell Transcriptomic Data Structure -- 3.2 BAMM-SC -- 3.3 Real Data Example -- 4 Single-Cell Multi-omics Data Clustering -- 4.1 CITE-seq Data Structure -- 4.2 BREM-SC -- 4.3 Real Data Example -- 5 Concluding Remarks -- References -- Deep Learning Methods for Single-Cell Omics Data -- 1 Introduction -- 2 Factor-Model-Based Deep Learning Approaches -- 2.1 Regularization and Priors on the Latent Factors -- 2.1.1 Gaussian Prior and Variational Inference -- 2.1.2 Adjust for Batch Effects and Confounding Covariates: Identifiability -- 2.1.3 Adjust for Batch Effects and Confounding Covariates: Implementation -- 2.1.4 Model Cell Population Structure in the Latent Space -- 2.2 Distributional Assumptions on Observed Data -- 2.2.1 Model Observed Data from scRNA-seq -- 2.2.2 Model Observed Data from scATAC-seq -- 2.2.3 Model Observed Data from Single-Cell Multiomics Technologies -- 2.3 Post-training Statistical Analyses -- 2.3.1 Denoising -- 2.3.2 Visualization, Clustering, and Trajectory Analysis -- 2.3.3 Prediction -- 3 Deep Learning Methods for Dimension Reduction -- 3.1 Construct the Loss Function -- 3.2 Extra Penalties and Regularization -- 4 Discussion -- References -- Part II Network Analysis.
Probabilistic Graphical Models for Gene Regulatory Networks -- 1 Introduction -- 2 Probabilistic Graphical Models -- 2.1 Graphical Model Basics -- 2.2 Markov Networks -- 2.3 Bayesian Networks -- 3 Classic Graphical Models for Reconstructing GRNs -- 3.1 Frequentist Approach -- 3.2 Bayesian Approach -- 3.3 Graphical Models Incorporating Prior Knowledge -- 4 Testing in Graphical Models -- 4.1 Parametric Test -- 4.2 Non-parametric Test for Global Graph Structure -- 5 Conclusion -- References -- Additive Conditional Independence for Large and Complex Biological Structures -- 1 Additive Conditional Independence

(ACI) -- 1.1 Additive Reproducing Kernel Hilbert Spaces and Relevant Linear Operators -- 2 Variable Selection via ACI -- 2.1 Nonparametric Variable Selection -- 2.2 Penalized Least-Square Estimation with RKHS Operators -- 2.3 Matrix Representation of Operators and Algorithm -- 2.4 Data Example -- 3 Graphical Modeling Through ACI -- 3.1 Nonparametric Graphical Models -- 3.2 The Additive Conditional Covariance and Partial Correlation Operators -- 3.3 Operator-Level Estimation and the Algorithm -- 3.4 Data Examples -- References -- Integration of Boolean and Bayesian Networks -- 1 Introduction -- 2 Methods -- 2.1 s-p-scores Associated with Networks, SPAN -- 2.2 Network Learning -- 3 Results -- 3.1 An Example -- 3.2 Real Example -- 3.3 Complex Example -- 4 Discussion -- References -- Computational Methods for Identifying MicroRNA-Gene Regulatory Modules -- 1 Introduction -- 2 Identifying MiRNA-Gene Modules by Integrating Heterogeneous Data Sources -- 2.1 Bipartite Graph-Based Methods -- 2.2 Nonnegative Matrix Factorization Methods -- 2.3 Statistical Modeling Approaches -- 3 Evaluating the Performance of MiRNA-Gene Module Identification Methods -- 4 Discussion -- 5 Conclusions -- References -- Causal Inference in Biostatistics -- 1 Introduction.
1.1 Causation and Association -- 1.2 Two Conceptual Frameworks: Causal Effect and Causal Discovery -- 2 Causal Effect -- 2.1 Approaches to Causal Inference -- 2.2 Randomized Clinical Trials -- 2.2.1 Perfect Randomized Trials -- 2.2.2 Randomized Trials with Missing Data -- 2.2.3 Randomized Trials with Post-treatment Variables -- 2.3 Observational Studies -- 2.3.1 Unconfounded Treatment Assignment Conditional on Measured Covariates -- 2.3.2 Unmeasured Cofounding -- 3 Some Current Research Topics -- 3.1 Heterogenous Treatment Effect and Precision Medicine -- 3.2 Integrating Data from Randomized Controlled Trials and Observational Studies -- 3.3 Multiple Treatments -- 4 Software Appendix -- References -- Bayesian Balance Mediation Analysis in Microbiome Studies -- 1 Introduction -- 2 Bayesian Balance Mediation Model -- 2.1 Bayesian Balance Mediation Model with a Binary Treatment -- 2.2 Direct and Mediation Effect and Estimation Based on Predictive Posterior Distribution -- 3 MCMC Sampling -- 3.1 MCMC Sampling -- 3.2 Conditional Distributions -- 4 Applications to Real Data -- 4.1 Mediation Analysis at the Phylum Level -- 4.2 Analysis at the Order Level -- 5 Simulation Studies -- 5.1 Data Generation -- 5.2 Simulation Result -- 6 Discussion -- References -- Part III Systems Biology -- Identifying Genetic Loci Associated with Complex Trait Variability -- 1 Introduction -- 2 The Concept of vQTL -- 3 Statistical Methods for vQTL Mapping -- 3.1 Classical Nonparametric Tests -- 3.2 Regression-Based Methods -- 3.3 Two-Stage Methods -- 3.4 Quantile Integral Linear Model (QUAIL) -- 3.5 Dispersion Effects -- 4 Applications of vQTL -- 4.1 Examples of vQTL -- 4.2 Screening vQTL for Candidate Loci Involved in GxE Interaction -- 4.3 Variance Polygenic Score -- 4.4 Other Applications and Future Directions -- References.
Cell Type-Specific Analysis for High-throughput Data -- 1 Introduction -- 2 Cell Type Composition Estimation -- 3 Cell Type-Specific Differential Analysis -- 4 Step-by-step Tutorial -- References -- Recent Development of Computational Methods in the Field of Epitranscriptomics -- 1 Introduction -- 2 MeRIP-seq and Other Technologies for RNA Modification Profiling -- 3 Methods to Analyze MeRIP-seq Data -- 3.1 Count-Based Methods for Simple Study Designs -- 3.2 Methods Compatible with Confounding Factors -- 3.3 A Guide for RNA Differential Methylation Analysis Using RADAR -- 4 Web Resources on m6A Epitranscriptome -- 4.1 Web Servers with m6A Site